



NORDSTAT 2026
30th Nordic Conference
in
Mathematical Statistics
Helsinki, June 1-4, 2026

**Programme
and
Book of Abstracts**

June 4, 2026

Contents

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Preface

The 30th Nordic Conference in Mathematical Statistics, NORDSTAT 2026 brings together more than 200 participants in Helsinki. They will give talks and exchange ideas about the newest developments on the broad field of statistics and probability theory. The NORDSTAT2026 program consists of 7 keynote talks, 11 invited sessions, 8 topic-contributed sessions, 24 contributed sessions and a poster session.

NORDSTAT 2026 is sponsored by the Federation of Finnish Learned Societies, the University of Helsinki and the City of Helsinki. We thank the board of the Scandinavian Journal of Statistics (SJS) for sponsoring the SJS lecture.

The excellent scientific programme is a results of the enduring work of the scientific committee and responses from the scientific community. Thank you all!

We thank the organisers of Nordstat 2023 especially Umberto Picchini (Dept. Mathematical Sciences, Chalmers and the University of Gothenburg) and Mattias Villani (Stockholm University) for sharing their experiences and providing useful information for the organisation of the conference. We thank a team of students from the Department of Mathematics and Statistics, University of Helsinki for their help at various levels before, during and after the conference. We thank colleagues from the department, particularly Jyrki Möttönen and Petteri Piironen for their support. We also acknowledge IT services and administration of the University of Helsinki for their support.

Welcome to Helsinki and enjoy the conference!

The members of the Scientific committee are:

<i>Dario Gasbarra (Chair, Vaasa)</i>	<i>Mindaugas Bloznelis (Vilnius)</i>	<i>Birgir Hrafnkelsson (University of Iceland)</i>
<i>Aliaksandr Hubin (Oslo, Ås)</i>	<i>Kristi Kuljus (Tartu)</i>	<i>Klas Markström (Umeå)</i>
<i>Ida Scheel (Oslo)</i>	<i>Mikko Sillanpää (Oulu)</i>	<i>Aila Särkkä (Chalmers)</i>
<i>Helle Sørensen (Copenhagen)</i>	<i>Jun Yang (Copenhagen)</i>	<i>Leena Kalliovirta (Helsinki)</i>

Local organizing committee: Leena Kalliovirta (Chair) and Sangita Kulathinal.

Support team of students: Martin Härkönen and Lotta Niemi.

Conference website: <https://www.helsinki.fi/en/conferences/nordstat-2026>

Outline

	Monday		Tuesday		Wednesday		Thursday
09:00	Registration					09:00	Parallel session VII IS-11, F4050 TCS-08, F3020 CS-22, F3005 CS-23, F3017 CS-24, F3006
09:45	Opening Small Hall (F4050)	09:30	Keynote lecture III Small Hall (F4050)	09:30	Keynote lecture V Small Hall (F4050)		
10:00	Keynote lecture I Small Hall (F4050)	10:30	Coffee <i>Foyer Sirén</i>	10:30	Coffee <i>Foyer Sirén</i>	10:30	Coffee <i>Foyer Sirén</i>
11:00	Coffee <i>Foyer Sirén</i>	11:00	Parallel session III IS-05, F4050 IS-06, F3020 CS-06, F3005 CS-07, F3017 CS-08, U3041 CS-09, U3043	11:00	Parallel session V IS-09, F4050 TCS-05, F3020 CS-13, F3005 CS-14, F3017 CS-15, U3041 CS-16, U3043 CS-17, U4078	11:00	Keynote lecture VII Small Hall (F4050)
11:30	Parallel session I IS-01, F4050 IS-02, F3020 TCS-01, F3005 TCS-02, F3017 CS-01, U3041 CS-02, U3043	12:30	Lunch <i>Agora</i>	12:30	Lunch <i>Agora</i>	12:00	Poster prize and closing Small Hall (F4050)
13:00	Lunch <i>Agora</i>	13:30	Parallel session IV IS-07, F4050 IS-08, F3020 TCS-04, F3005 CS-10, F3017 CS-11, U3041 CS-12, U3043	13:30	Parallel session VI IS-10, F4050 TCS-06, F3020 TCS-07, F3005 CS-18, F3017 CS-19, U3041 CS-20, U3043 CS-21, U4078	12:15	
14:00	Parallel session II IS-03, F4050 IS-04, F3020 TCS-03, F3005 CS-03, F3017 CS-04, U3041 CS-05, U3043	15:00	Coffee <i>Foyer Sirén</i>	15:15	Keynote lecture VI Small Hall (F4050)		
15:30	Coffee <i>Foyer Sirén</i>	15:30	Keynote lecture IV Small Hall (F4050)	16:15			
16:00	Keynote lecture II Small Hall (F4050)	16:45	Panel Discussion II Small Hall (F4050)	16:30	Poster session and coffee <i>Agora 3)</i>		
17:00							
17:10	Panel Discussion I Small Hall (F4050)						
18:00		18:00		18:30			
	1)		2)				

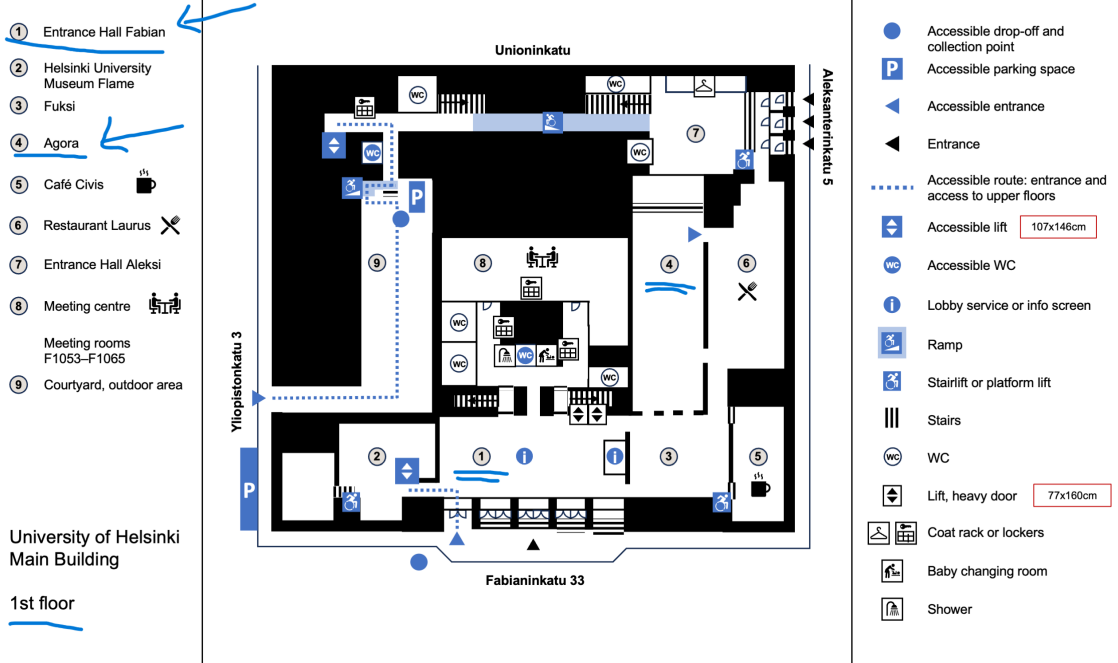
See next page on the details of the Main Building, Fabianinkatu 33.

Foyer Sirén is the 4th floor foyer of Small Hall (F4050). *Agora* is in the 1st floor.

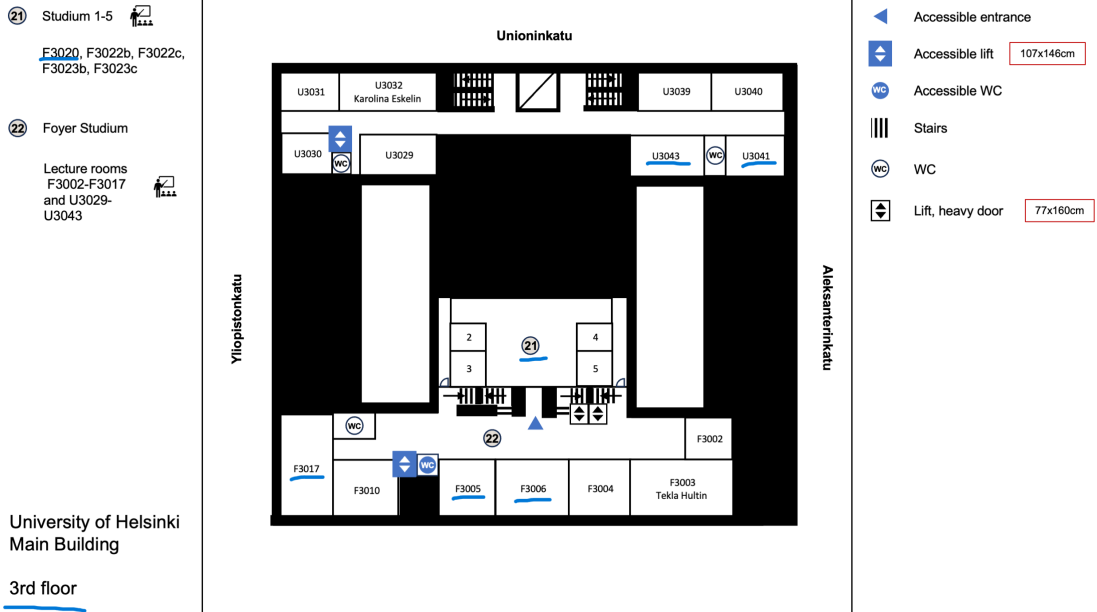
- 1) *For those who registered*, City of Helsinki Reception at Old Court House, Aleksanterinkatu 20.
- 2) Conference dinner starts at 19:00 in Restaurant Töölö, Runeberginkatu 14-16, Helsinki.
- 3) *SJS meeting* in lecture room F3005.

Information on the Main Building, Fabianinkatu 33

Link to the 1st floor map below



Link to the 3rd floor map below

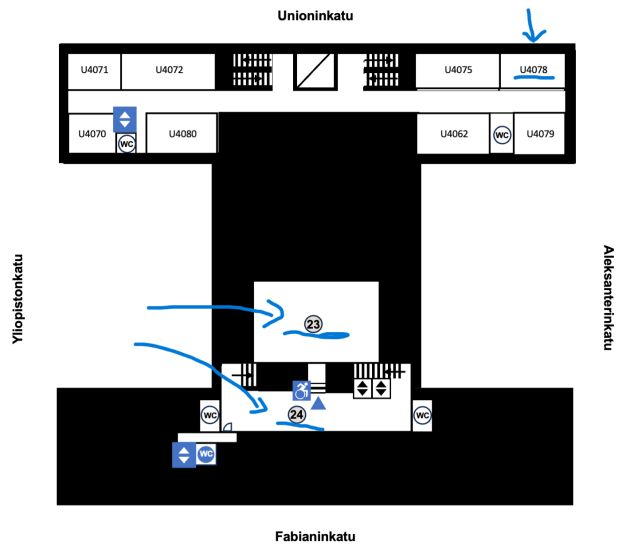


Link to the 4th floor map below

- ②③ Small Hall
- ②④ Fooyer F4001a
- Lecture rooms U4060-U4079

University of Helsinki
Main Building

4th floor



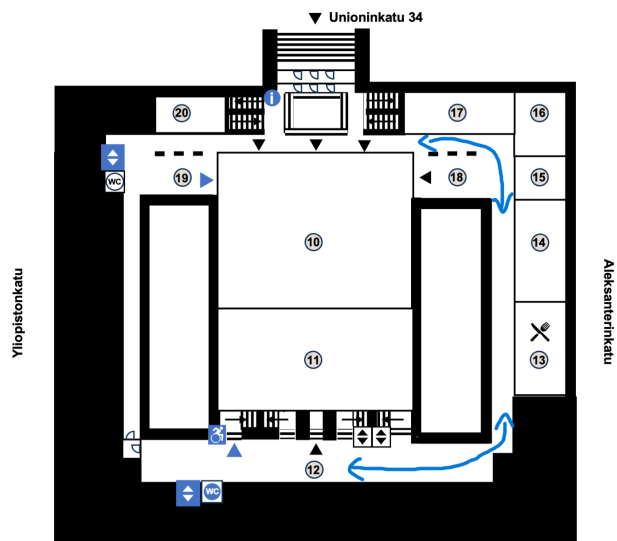
- Accessible entrance
- Accessible lift 107x146cm
- Accessible WC
- Lobby service or info screen
- Stairs
- WC
- Stairlift or platform lift
- Lift, heavy door 77x160cm

To access Fabianinkatu (F) and Unioninkatu (U) lecture halls, you need to use the 2nd floor corridor on the South side (Aleksanterinkatu).

- ⑩ Great Hall
- ⑪ Auditorium
- ⑫ Foyer Rectoria
- ⑬ Staff cafeteria
- ⑭ Runeberg
- ⑮ Pacius
- ⑯ Christina
- ⑰ Wexionius
- ⑱ Foyer U2087
- ⑲ Foyer U2065
- ⑳ Meeting room U2071

University of Helsinki
Main Building

2nd floor



- Accessible entrance
- Entrance
- Accessible lift 107x146cm
- Accessible WC
- Lobby service or info screen
- Stairlift or platform lift
- Stairs
- WC
- Lift, heavy door 77x160cm

Program

Monday, June 1

09:45-10:00

Small Hall (F4050)

Welcome words

Sangita Kulathinal and Leena Kalliovirta

10:00-11:00

Small Hall (F4050)

Chair: Kristi Kuljus

Keynote lecture I

Peter Grünwald

E is the new P

11:30-13:00

Parallel Sessions I

IS-01 Causality

Invited session, Small Hall (F4050)

Organizer: Søren Wengel Mogensen

Chair: Søren Wengel Mogensen

Susanne Dandl

Nonparanormal Adjusted Marginal Inference

Lucas Kook

Exact Graph learning via integer programming

Kjetil Røysland

On causal inference with marked point processes

IS-02 Computational Statistics

Invited session, F3020

Organizer: Jun Yang

Chair: Jun Yang

Sifan Liu

WALNUTS: A No-U-Turn Sampler with Locally Adaptive Step Size

Ruben Seyer

Non-reversible Birth-Death-Piecewise Deterministic Markov Process
samplers for Gibbs Spatial Point Processes

Claudia Strauch

Statistical guarantees for denoising reflected diffusion models

TCS-01 Recent Advances in Functional Data Analysis and Functional Time Series

Topic-contributed session, F3005

Organizer: Sebastian Kühnert

Chair: Sebastian Kühnert

Lujia Bai	A portmanteau test for multivariate non-stationary functional time series with an increasing number of lags
Alessia Caponera*	Low-Dose Tomography of Random Fields and the Problem of Continuous Heterogeneity
Sebastian Kühnert	An Operator-Level ARCH Model

*Alessia Caponera will give her talk via Zoom starting at 12:00.

TCS-02 Random matrices

Topic-contributed session, F3017

Organizer: Johannes Heiny

Chair: Johannes Heiny

Johannes Alt	Spectra of critical ErdHos-Rényi graphs
Teodor Bucht	Quantitative Tracy-Widom laws for sparse random matrices
Nina Dörnemann	Tracy-Widom, Gaussian, and Bootstrap: Approximations for Leading Eigenvalues in High-Dimensional PCA

CS-01 Bayesian Computation and Methods

Contributed session, U3041

Chair: Rolf Larsson

Joona Karjalainen	Mixing time of the conditional backward sampling particle filter
Emanuele Aliverti	Approximate Bayesian inference for semiparametric ordinal regression
Rolf Larsson	Implied priors for the exponential family

CS-02 Spatial data modelling and analysis

Contributed session, U3043

Chair: Klaus Nordhausen

Mehdi Moradi	Recent developments for marked spatial point processes
Perttu Saarela	Stationary subspace analysis for spatial data
Klaus Nordhausen	Consistent Distribution-Free and Affine-Invariant Tests for the Validity of Independent Component Models

14:00-15:30 Parallel Sessions II

IS-03 Bayesian Neural Networks

Invited session, Small Hall (F4050)

Organizer: Geir Storvik

Chair: Geir Storvik

August Arnstad	Dirichlet scale mixture priors for Bayesian Neural Networks
Eirik Høyheim	Explainable Bayesian Neural Networks through Active Paths: Global Structures and Local Insights
Luigi Acerbi	We Cannot Amortize Everything: Test-Time Approaches for Amortized Inference

IS-04 High-dimensional time series

Invited session, F3020

Organizers: Nina Dörnemann and Tim Kutta

Chair: Nina Dörnemann

Haeran Cho	Covariance scanning for adaptively optimal change point detection in high-dimensional linear models
Lujia Bai	Inference of time-varying precision matrices in high dimensional non-stationary time series
Tim Kutta	Multiscale Change Point Detection for Functional Time Series

TCS-03 (Statistical) guarantees for Bayesian inference in inverse problems

Topic-contributed session, F3005

Organizer: Maximilian Siebel

Chair: Maximilian Siebel

Dana Wrischnig	Wasserstein Stability of Bayesian Posteriors in the Concentrated Posterior Regime
Maximilian Siebel	Posterior contraction under misspecification and heteroscedasticity in non-linear inverse problems
Aurélien Castre	Computational guarantees for Bayesian inference in interacting particle system models

CS-03 Spatio-temporal modelling

Contributed session, F3017

Chair: Linnea Hallin

Gen Nowak	A vector time series approach for modelling spatio-temporal data
Diego Rondon	Seasonal Space Use and Habitat Associations of Golden Eagles in Finland: Insights from a Point Process Modelling
Linnea Hallin	Reconstructing the single-cell spatiotemporal dynamics of glioblastoma invasion

CS-04 Dynamic modelling and forecasting

Contributed session, U3041

Chair: Behnaz Pirzamanbin

Nourhan Shafik	Model-based clustering of abundance time series data
Moritz Otto	Subgraph counts in a dynamic random connection model
Behnaz Pirzamanbin	Bayesian inference for spatial compositional data with exact zeros using gradient-informed MCMC

CS-05 Environmental sciences

Contributed session, U3043

Chair: Albertas Dvirnas

Yang Han	Extreme Precipitation in Iceland: An Exploratory Analysis of IDF Curves Across Stations and Durations
Elling Svee	Bayesian estimation of subsurface properties in CO ₂ storage sites
Albertas Dvirnas	Bridging Matrix Profiles and Empirical Dynamic Modelling in Predictions for Environmental Data

16:00-17:00 Keynote lecture II

Small hall (F4050)

Chair: Jun Yang

Susanne Ditlevsen	Estimating early warning signals and tipping points in climate
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17:10-18:00 Panel Discussion I

Small hall (F4050)

Teaching statistics

Organizer and Chair: Kathrine Frey Frøslie, NMBU

Panel: Jo Røislien (Norway) and Bo Markussen (Denmark).

Tuesday, June 02

09:30-10:30 Keynote lecture III

Small hall (F4050)

Chair: Mindaugas Bloznelis

Gintare Karolina Dziugaite The Dynamics of Memorization and Generalization in Deep Learning
gaite

11:00-12:30 Parallel sessions III

IS-05 Statistics for stochastic processes and networks

Small hall (F4050)

Organizer: Almut E. D. Veraart

Chair: Almut E. D. Veraart

Luitgard A. M. Veraart Modelling contagious bank runs
aart

Leonardo Bardi Probabilistic forecast for spatio temporal Ornstein-Uhlenbeck processes

Almut E. D. Veraart Statistical inference for Lévy-driven graph supOU processes: From short-
to long-memory in high-dimensional time series

IS-06 Statistics in Peace Research

Invited session, F3020

Organizers: Celine Cunen and Nils Lid Hjort

Chair: Nils Lid Hjort

Dennis Christensen Why the decline-of-war question is so hard to answer

Jonathan P Williams Conformal prediction of fatalities from armed conflict

Kristian Skrede Escalation dynamics and the severity of wars

Gleditsch*

*Kristian Skrede Gleditsch will give his talk via Zoom starting at 12:00.

CS-06 Bayesian inference and applications 1

Contributed session, F3005

Chair: Jouni Helske

Lotta Eriksson BayesCNA: Detecting copy number alterations in noisy data

Javier E. Aguilar R2 priors for grouped variance decomposition in high-dimensional re-
gression

Jouni Helske Uncertainty-Aware Policy Evaluation with Bayesian Synthetic Control
Models

CS-07 Multivariate Analysis 1

Contributed session, F3017

Chair: Lauri Heinonen

Gero Szepannek	Clustering of Mixed-type Data
Joni Virta	Measure of shape for object data
Lauri Heinonen	Model-based mixed-type PCA

CS-08 Likelihood-based inference

Contributed session, U3041

Chair: Kristi Kuljus

Philip Stange	Maximum Likelihood Estimation of a Likelihood Ratio Ordered Family of Log-Concave Densities
Kristi Kuljus	Pseudo-likelihood approach for univariate normal mixture models
Carsten Wiuf	The <code>windowEM</code> algorithm

CS-09 Graphical Models

Contributed session, U3043

Chair: Joao Cordeiro

Marcus Gehrman	Sparsifying Transform Priors in Gaussian Graphical Models
Joao Cordeiro	Intrinsic Gaussian fields on metric graphs

13:30-15:00 Parallel sessions IV

IS-07 Random graph models

Invited session, Small hall (F4050)

Organizer: Victor Falgas-Ravry

Chair: Victor Falgas-Ravry

Matas Šileikis	Maximum local statistics in the random binomial graph
Timo Vilkas	Stochastic averaging processes on graphs
Cecilia Holmgren	Fringe trees in Split Trees

IS-08 Bayesian Nonparametric Statistics

Invited session, F3020

Organizer: Déborah Sulem

Chair: Jun Yang

Beatrice Franzolini	Complexity bounds for Dirichlet process slice samplers
Francesco Denti	Bayesian Multiresolution Functional Regression and Clustering via Self-Truncating Cumulative Shrinkage Processes
Sahoko Ishida*	Hierarchical additive interaction modelling with Gaussian process prior and its efficient implementation for multidimensional grid data

*Sahoko Ishida will give her talk via Zoom starting at 14:30.

TCS-04 Non-parametric testing for multivariate, functional and spatial data

Topic-contributed session, F3005

Organizer: Mari Myllymäki

Chair: Mari Myllymäki

Mari Myllymäki	Formal graphical statistics: The power of visualization in statistical tests and beyond
Martin Voigt Vejling	Semi-supervised group testing for point patterns

CS-10 Other topics in estimation

Contributed session, F3017

Chair: Hanna Bu Kvaløy

Daniel Rolandsgard Kjellevold	Estimation of intensity with small scale repulsion and medium scale clustering for river flow
Han Bao	Maximum spacing estimation under model misspecification
Hanna Bu Kvaløy	From Hypothesis Testing to Formal Proof: Disproving a Claimed G-Wishart Sampler

CS-11 Learning and adaptation techniques

Contributed session, U3041

Chair: Sebastian Grau Nielsen

Taariq Nazar	Transformed gradient based boosting
Mohammad Ghasempour	Unsupervised domain adaptation beyond label shift
Sebastian Nielsen	Grau Automatic Online Changepoint Detection with Recurrent Neural Networks

CS-12 Time series analysis

Contributed session, U3043

Chair: Helle Sørensen

Rana Bamdadi

Helle Sørensen

Samuel Modée

Model-Based Functional Clustering with Correlated Measurement Errors

Local inference for functional time series

Markov Regime-Switching Models with Time-Varying Transition Probabilities: A Monte Carlo Study and Application to U.S. Treasury Yield Changes

15:30-16:30 Keynote lecture IV

Small hall (F4050)

Chair: Aila Särkkä, the editor of *The Scandinavian Journal of Statistics*

The Scandinavian Journal of Statistics -lecture

Jüri Lember

Pairwise Markov models

16:45-18:00 Panel Discussion II

Small hall (F4050)

History of Statistical activities and Collaboration in Nordic and Baltic countries

Organizers: Sangita Kulathinal and Leena Kalliovirta

Chair: Susanne Ditlevsen (Denmark)

Panel: Elja Arjas (Finland), Nils Lid Hjort (Norway), Birgir Hrafnkels-son (Iceland), Rolf Larsson (Sweden) and Jüri Lember (Estonia)

Wednesday, June 3

09:30-10:30 Keynote lecture V

Small hall (F4050)

Chair: Helle Sørensen

Victor Panaretos Kernel Embeddings and Separation of Measure

11:00-12:30 Parallel sessions V

IS-09 Recent advances in nonparametric spatial point process statistics

Small hall (F4050)

Organizer: Mari Myllymäki

Chair: Mari Myllymäki

Chiara Fend Topological Data Analysis for Goodness-of-Fit Testing in Spatial Statistics

Jiří Dvořák Nonparametric testing of covariate significance for spatial point patterns

Tuomas Rajala Exploring local diversity in large, heterogeneous point patterns

TCS-05 High-Dimensional Modeling and Statistical Analysis 1

Topic-contributed session, F3020

Organizer: Nestor Parolya and Taras Bodnar

Chair: Nestor Parolya

Markus Reiß Inference on the maximal rank of time-varying covariance matrices using high-frequency data

Moritz Jirak Concentration and moment inequalities for heavy-tailed random matrices

Nestor Parolya Nonlinear shrinkage estimator for large covariance matrices with strong mean effects

CS-13 Time-to-event analysis and regression

Contributed session, F3005

Chair: Salme Kärkkäinen

Aapeli Nevala Bayesian hidden Markov model with time-to-event emissions to risk-prediction modelling in cancer screening

Salme Kärkkäinen Estimating mean lifetime from partially observed events in nuclear physics

Reza Arabi Belaghi Boruta-Based Variable Selection and Post-Estimation in High-Dimensional Regression: Theoretical Foundations and Simulation Evidence

CS-14 Bayesian inference and applications 2

Contributed session, F3017

Chair: Birgir Hrafnkelsson

Henri Pesonen	Efficient Likelihood-free Sequential Monte Carlo Sampling Using Probabilistic Surrogate Loss
Birgir Hrafnkelsson	Max-and-Smooth: An approximate Bayesian inference scheme for latent Gaussian models with a multivariate link function
Kasper Bågmard	Fast Bayesian Filtering for High-Dimensional Nonlinear SDEs with Deep Density Models

CS-15 Econometrics and Finance

Contributed session, U3041

Chair: Samuel Rauhala

Zbigniew Palmowski	Pricing time-capped American options: simulations and exact results
Onni Hinkkanen	Quantitative discrete time hedging under initial insider information
Samuel Rauhala	Network varying coefficient ridge regression

CS-16 Multivariate Analysis 2

Contributed session, U3043

Chair: Laura D'Angelo

Elle A. Saber	Beyond compositional validity: comparing distances for seemingly compositional data
Luis E. Nieto-Barajas	Directional models based on projected Pólya trees
Laura D'Angelo	Partition-based discriminant analysis

CS-17 Stochastic processes

Contributed session, U4078

Chair: Matti Vihola

Matti Vihola	On the forgetting of particle filters
Radu S. Stoica	Lévy - Cox Branching Point Processes
Grégoire Szymanski	Estimation of the invariant measure of a multidimensional diffusion from noisy observations

13:30-15:00 Parallel sessions VI

IS-10 Network Statistics

Small hall (F4050)

Organizer: Lasse Leskelä

Chair: Lasse Leskelä

- | | |
|------------------|---|
| Christian Hirsch | Asymptotic Normality of Topological Statistics in Dynamic Random Geometric Networks |
| Sofia Olhede | Multiplex weighted networks as decorated graphs for predicting binary outcomes |
| Ian Välimaa | Consistent spectral clustering in sparse tensor block models |

TCS-06 High-Dimensional Modeling and Statistical Analysis 2

Topic-contributed session, F3020

Organizer: Nestor Parolya and Taras Bodnar

Chair: Taras Bodnar

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|----------------|--|
| Angelike Rohde | Asymptotic equivalence for nonparametric additive regression |
| Johannes Heiny | Phase transitions for linear spectral statistics of sample correlation matrices in high dimension |
| Taras Bodnar | Nonlinear higher-order shrinkage estimation of the large-dimensional covariance and precision matrices |

TCS-07 Probabilistic Combinatorics

Topic-contributed session, F3005

Organizer: Matas Šileikis and Victor Falgas-Ravry

Chair: Matas Šileikis

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|--------------------------|---|
| Joel Danielsson | Random triangulations of the d -sphere with minimum volume |
| Victor Falgas-Ravry | A threshold for relative hyperbolicity in random right-angled Coxeter groups |
| Eero Rätty | Logical convergence laws for small permutation classes |
| Tomas Juškevičius | 'Asymptotically sharp anticoncentration in high dimensions' had to cancel participation. |

CS-18 Gaussian processes and related topics

Contributed session, F3017

Chair: Jaime C. Revenga

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|-----------------------|--|
| Kushagri Tandon | Investigating bivariate structure of non-Gaussian spatial fields |
| Erik Karlsson Strandh | Gaussian Processes on Directed Metric Graphs |
| Jaime C. Revenga | Self-supervised distributional regularization stabilizes estimators of decision boundaries in classification of functional data - an imaging spectroscopy case study |

CS-19 Causal inference

Contributed session, U3041

Chair: Juha Karvanen

Juha Karvanen	Simulating counterfactuals
Mikko Valtanen	Causal treatment effect decompositions with time-to-event outcomes under competing events

CS-20 Study design and simulation-based inference

Contributed session, U3043

Chair: Markku Kuismin

Jonas Bjermo	Algorithms for optimizing model-based incomplete block designs
Henrik Häggström	Semi-amortised simulation-based inference for stochastic nonlinear mixed-effects models
Markku Kuismin	Pushing the AR test beyond the limit: A novel goodness-of-fit test for high-dimensional applications

CS-21 Extreme value theory

Contributed session, U4078

Chair: Hamidreza Maleki Almani

Frank Röttger	Estimating Hüsler–Reiss Variogram Matrices via Noncanonical Half-spaces
Hamidreza Maleki Almani	Order Statistics for The Quantile Contribution

15:15-16:15 Keynote lecture VI

Small hall (F4050)

Chair: Mikko Sillanpää

Mattias Villani	Bayesian inference in non-Gaussian time series models with global-local shrinkage processes
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16:30-18:30 Poster session

Agora (1st floor)

Remember to give your vote for the best poster! Write the code 'P1-P21' in the blue ballot paper attached to your badge and drop it to the ballot box. Voting ended at 18:30 on Wednesday. Total 84 votes were given.

The two 500 euro poster prizes were given to William Nordansjö and Emmett Kendall.

P1	Kusti Aholainen Henrik Bengtsson	Comparing estimators in contaminated ARMA models Efficient sampling of excursion trajectories for stationary Gaussian processes via Slepian models
P2	Svitlana Drin	Estimation of minimum VaR and minimum CVaR optimal portfolios for small samples and singular covariance matrices
P3	Lulu Jiang	Modeling Spatially Obfuscated Street-Crime Data on Metric Graphs using a Log-Gaussian Cox Process
P4	Yuwei Jiang Leena Kalliovirta	Hypothesis Testing for Shape Constraints in Generalized Functional Linear Models Forecasting maritime in-situ observations using satellite data in the Gulf of Finland
P5	Oskar Keding	State space modelling of auditory attention using electroencephalography
P6	Emmett Kendall	Conflict Forecasting via Conformal Prediction for Markov Processes
P7	Mikko Kuronen	Uncertainty quantification for forest attribute maps with conformal prediction and k -Nearest Neighbor method
P8	Sebastian Kühnert	Pivotal inference for linear predictions in stationary processes
P9	Magnús Ingvi Magnússon	Fast likelihood ratio testing for case control GWAS on GPU with direct modeling of imputed genotypes
P10	Leonardo Miranda	Statistical Modeling of Saturated BJT Circuits with Component Tolerances
P11	Oliver Mortensen	On the learnability and sample complexity of RL with recursive OCE preferences
P12	William Nordansjö	Adaptive-Bias Random Walk in Static and Dynamic Percolation
P13	Hedvika Ranošová	Time Reversibility Testing for Stochastic Processes
P14	Rebecca Schmitz	Belyaev-Waiting model: From Waiting Times to Birth Control
P15	Øyvind H. Singsaas	Neural Simulation-Based Inference for Earthquake Modeling in the North Atlantic
P16	Tim Steinert	Triply Scalable Equivariant GP modeling
P17	David Sundström	Gaussian Process Sound Field Reconstruction Under Finite-Window Observations
P18	Ilmari Talo	Bayesian phenomenological modeling of the flight curve of a multi-voltine butterfly
P19	Maria Tirronen	Variational Bayesian inference for a nonlinear ODE inverse problem
P20	Denise Uwamariya	Disaggregation of residential building electricity consumption: Insights for energy efficiency and resilience
P21	Xiang Ye	A Bayesian regression framework for circular models with INLA
P22	Riha Anna	To select or not to select - predictively consistent priors instead of model selection

Thursday, June 4

09:00-10:30 Parallel sessions VII

IS-11 Algebraic Statistics

Small hall (F4050)

Organizer: Tobias Boege and Nataliia Kushnerchuk

Chair: Nataliia Kushnerchuk

Cecilie Olesen Recke Identifiability and Estimation in Continuous Lyapunov Models

Piotr Zwiernik Probabilistic PCA on tensors

Aida Maraj When is an algebraic statistical model toric?

TCS-08 Optimal Experimental Design

Topic-contributed session, F3020

Organizer: Maryna Prus

Chair: Maryna Prus

Luc Pronzato Random and Quasi-Random Designs for Quantisation in High Dimension

Frank Röttger Optimal designs for discrete choice models via graph Laplacians

Maryna Prus Optimal allocation of trials to sub-regions in crop variety testing with multiple years and correlated genotype effects

CS-22 Neural networks, machine learning and related topics 1

Contributed session, F3005

Chair: Sigrún Helga Lund

Peter Rudzisz Spectral gap in parallel tempering: a variational analysis

Geir Storvik Parameter estimation in Conditional Sequential Monte Carlo algorithms through Particle Learning

Sigrún Helga Lund Large Language Models as Tools for Statistics Education: Problem Generation and Mathematical Reasoning

CS-23 Stochastic processes

Contributed session, F3017

Chair: Stanislav Anatolyev

Stanislav Anatolyev Asymptotics of large-dimensional projection matrices

Soham Mukherjee Hilbert space methods for approximating multi-output latent variable Gaussian processes

Predrag Pilipović Strang Splitting Parameter Estimator for Nonlinear Multivariate Pearson-Type Diffusions

CS-24 Population modelling

Contributed session, F3006

Chair: Joel Kostensalo

Mikhail Shubin	Integrated Joint Distribution Modeling to Estimate the Biomass of Commercial Fish in the Baltic Sea from Acoustic and Trawl Data
Celia García-Pareja	Diffusion limit for Markovian models of evolution in structured populations with migration
Joel Kostensalo	Base rate problems in mapping rare ecological phenomena using remote sensing

11:00-12:00 Keynote lecture VII

Small hall (F4050)

Chair: Klas Markström

David Bolin	Gaussian random fields on metric graphs
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12:30-13:00 Poster prize and closing

Small hall (F4050)

Chair: Dario Gasbarra

Abstracts of Keynote lectures

E is the new P

Peter Grünwald

CWI and Leiden University (the Netherlands)

Monday 1
10:00-11:00
Small Hall (F4050)

E-values (<https://en.wikipedia.org/wiki/E-values>) are an alternative to p-values that effortlessly deal with optional continuation: with e-value based tests and the corresponding anytime valid (AV) confidence intervals, one can always gather additional data, while keeping statistically valid conclusions. Until 2019, publications on e-values were few and far between: the concept did not even have a name. Then, in the course of a few months, four papers by different research groups appeared on arXiv that firmly established them as an important statistical concept. The first of these was Safe Testing (see below) ; another one was Shafer's testing by betting, highlighting the interpretation of e-values in terms of betting strategies (nonnegative supermartingales). By now, there are 100s of papers and there have been four international workshops on e-values. Allowing for optional continuation is just one way in which e-values provide more flexibility than p-values – they also allow to set a type of significance/confidence level α after seeing the data, which is a mortal sin in classical testing, and this in turn has led to breakthroughs in multiple testing. In this talk I will introduce e-values, e-processes and AV confidence intervals, and discuss in detail the relation to Bayesian approaches, which are in some ways related and in others completely different.

Main literature:

Grünwald, De Heide, Koolen. "Safe Testing", *Journal of the Royal Statistical Society Series B*, 2024 (first version appeared on arXiv 2019).

Grünwald, "Beyond Neyman-Pearson: e-values enable hypothesis testing with a data-driven α ", *Proceedings National Academy of Sciences of the USA (PNAS)*, 2024.

Keynote speaker Peter Grünwald is founder and former head of the machine learning group at CWI in Amsterdam, the Netherlands, as well as full professor of statistics at the mathematical institute of Leiden University. He is interested in making statistical inference at the same time more robust and flexible using e-processes and related tools. In 2024 he received an ERC Advanced Grant for doing just this, in a project ranging from the very fundamental (a bridge between Bayesian and frequentist statistics) to the very applied (e-processes for generalized linear models). Earlier (and still related) work include a monograph on the Minimum Description Length (MDL) principle as well as various papers on adjusting Bayesian and MDL methods under misspecification.

Estimating early warning signals and tipping points in climate

Monday 1
16:00-17:00
Small Hall (F4050)

Susanne Ditlevsen

University of Copenhagen (Denmark)

Early warning signals for tipping are typically second order statistics, namely increasing variance (loss of resilience) and increasing autocorrelation (critical slowing down). However, it is statistically challenging to estimate these from non-stationary data, which is exactly the case for systems approaching tipping points. Moreover, the systems are typically highly non-linear and noisy, and this even more so, the closer to the tipping point. I will discuss such statistical challenges for estimating essential quantities and doing statistical inference related to tipping systems.

Keynote speaker Susanne Ditlevsen is President of the Royal Danish Academy of Sciences and Letters. Professor, Department of Mathematical Sciences, University of Copenhagen. Part of the Section Statistics and Probability Theory. Part of Data Science Laboratory.

The Dynamics of Memorization and Generalization in Deep Learning

Tuesday 2
09:30-10:30
Small Hall (F4050)

Gintare Karolina Dziugaite

Google DeepMind (USA)

Deep learning models exhibit a complex interplay between memorization and generalization. This talk will begin by exploring the ubiquitous nature of memorization, drawing on prior work on "data diets", example difficulty, pruning, and other empirical evidence. But is memorization essential for generalization? Our recent theoretical work suggests that eliminating it entirely may not be feasible. Instead, I will discuss strategies to mitigate unwanted memorization by focusing on better data curation and efficient unlearning mechanisms. Additionally, I will examine the potential of pruning techniques to selectively remove memorized examples and explore their impact on factual recall versus in-context learning.

Keynote speaker Gintare Karolina Dziugaite is a senior research scientist at Google DeepMind in Toronto, and an adjunct professor at the McGill University School of Computer Science. Prior to joining Google, she led the Trustworthy AI program at Element AI (ServiceNow). Her research combines theoretical and empirical approaches to understanding deep learning.

Pairwise Markov models Scandinavian Journal of Statistics -lecture

Jüri Lember
Tartu University (Estonia)

Tuesday 2
15:30-16:30
Small Hall (F4050)

A *multiple Markov model* consists of several stochastic processes – chains – that jointly satisfy the Markov property. Thus, the states of a multiple Markov model are vectors. However, a multiple Markov model is not defined by the dimensionality of the model, rather than the roles that the different chains play in the model. The most popular multiple Markov model is the *hidden Markov model (HMM)* – a two-dimensional chain consisting of observations and underlying states (Markov chain). It is a special case of *pairwise Markov model (PMM)*, which is just any two-dimensional Markov chain. A *triplet Markov model (TMM)* is a three-dimensional Markov chain. In the talk we mainly focus on PMM's, which is a surprisingly rich class of models. Several examples, subclasses and properties (e.g. lumpability) of PMMs are introduced and discussed. In multiple Markov models, often only one marginal process is observed, others are hidden. *Segmentation* (classification, decoding, pattern recognition) is the task of estimating or predicting the hidden realization, any such estimate is called a *path*. The best estimator in terms of average number of classification errors is the *pointwise maximum a posteriori (PMAP)* path (many alternative names). PMAP decoding allows paths of low or even zero probability and might fail in detecting an infrequent state. Therefore, the most popular estimator in practice is the *maximum a posteriori or Viterbi path* inheriting its name from the Viterbi algorithm. Unfortunately, it can be quite inaccurate. We consider the segmentation problem in a general framework of statistical learning. This framework defines a new and rich family of so-called *hybrid paths* (with corresponding dynamic programming algorithm). The hybrid decoding and some properties of hybrid paths will be discussed. In the end of the talks, some issues related to the asymptotics of segmentation will be discussed.

Keynote speaker Jüri Lember is Professor in Probability Theory at the Institute of Mathematics and Statistics, University of Tartu.

Kernel Embeddings and Separation of Measure

Victor Panaretos
EPFL (Switzerland)

Wednesday 3
09:30-10:30
Small Hall (F4050)

Nonparametric two-sample testing becomes notoriously difficult in high dimensions, where alternatives are vast and poorly structured. We show that kernel embeddings transform distinct probability distributions on a general space into mutually singular Gaussian measures on a Hilbert space, yielding information-theoretically perfect separation. This separation of measure phenomenon appears to be a blessing of infinite dimensionality underpinning the remarkable empirical success of the "kernel trick". We also show, however, that existing kernel-based criteria will typically fail to exploit this phenomenon. We demonstrate that the appropriate test criterion is the likelihood ratio of the Gaussian embeddings, which vanishes under the null and diverges under the alternative, and show how operationalize it for statistical inference. Joint work with Leonardo Santoro (EPFL) and Kartik Waghmare (ETH Zurich).

Keynote speaker Victor Panaretos research is Mathematical statistics motivated by/applied to the natural sciences.

Bayesian inference in non-Gaussian time series models with global-local shrinkage processes

Wednesday 3
15:16-16:15
Small Hall (F4050)

Mattias Villani
Stockholm University (Sweden)

Global-local shrinkage process priors for time-varying parameter models allow parameters to be essentially constant for longer spells, followed by periods of rapid change or jumps. Some recent work on computational algorithms for Bayesian inference with global-local shrinkage process prior will be presented, with emphasis on non-linear and non-Gaussian models.

Keynote speaker Mattias Villani is a professor of Statistics at Stockholm University, where he leads a research group developing flexible probabilistic models and scalable Bayesian methods for prediction and decision making. His applied work spans several areas, for example economics, neuroimaging, robotics, and transportation.

Gaussian random fields on metric graph

Thursday 4
11:00-12:00
Small Hall (F4050)

David Bolin
King Abdullah University of Science and Technology, KAUST (Saudi Arabia)

There is a growing interest in modeling data on networks and graphs. In statistics, typical applications are modeling traffic accidents or street crimes on road networks and modeling temperature or pollutants in river networks. In these cases, the statistical model is defined on both the edges and vertices of the graph, where the edges represent the roads or river segments. Importantly, distance between locations should then be measured on the network, and not by using the Euclidean distance. A graph coupled with a metric like this is referred to as a metric graph.

Gaussian random fields are essential for modeling spatially dependent data; however, the study of Gaussian random fields on metric graphs is challenging because it is difficult to construct valid covariance functions which are isotropic in the metric on the graph. In this talk, I will give an overview of our work on developing a comprehensive mathematical and statistical theory for Gaussian random fields on metric graphs, complemented by easy-to-use statistical software.

I will specifically introduce the Whittle-Matérn fields as a new flexible class of Gaussian random fields on metric graphs, and discuss their properties. I will also discuss various extensions and applications, including flexible non-stationary models and log-Gaussian Cox processes for point pattern data. Finally, I will demonstrate the proposed approaches in a few applications using the MetricGraph R package, which contains an extensive set of tools for statistical modeling on metric graphs.

Keynote speaker David Bolin leads the Stochastic Processes and Mathematical Statistics research group at KAUST, which develops methodology for statistical models involving stochastic processes and random fields. A main focus is the development of statistical methods based on stochastic partial differential equations (SPDEs), and some current areas of research are random fields on metric graphs and networks, stochastic processes formulated through fractional-order SPDEs, and non-Gaussian random fields.

Abstracts of Parallel sessions

Nonparanormal Adjusted Marginal Inference

Susanne Dandl

University of Zurich (Switzerland)

Monday 1
11:30-13:00
Lecture room F4050

Abstract Treatment effects quantify the causal effect of an intervention on an outcome, and randomized controlled trials (RCTs) are considered the gold standard for estimating these effects. For important noncollapsible treatment effects, such as odds ratios in a binary logistic regression model or hazard ratios in a Cox proportional hazards model, conditioning on different sets of covariates changes the interpretation of the treatment effect. This renders effect estimates obtained from different covariate sets incomparable.

To obtain a marginal effect estimate whose interpretation is not influenced by, but still benefits from, covariates, my coauthor Torsten Hothorn and I propose NAMI – a novel nonparanormal model for adjusted marginal inference. NAMI combines a marginal model of the outcome given the treatment variable with a nonparanormal model that estimates the joint distribution of the outcome and the covariates.

In addition to the treatment effect, our framework provides an overall coefficient of determination as well as covariate-specific measures of prognostic strength. The marginal models are based on transformation models, enabling broad applicability across diverse outcome types (e.g., continuous, binary, ordinal, or survival). A reference implementation is available in the R add-on package `tram`.

For the special case of Cohen’s standardized mean difference d we theoretically show that adjusting for an informative prognostic variable improves the precision of this marginal, noncollapsible effect. Empirical results confirm this not only for Cohen’s d but also for log-odds ratios and log-hazard ratios in simulations and across four applications.

Exact Graph learning via integer programming

Lucas Kook

Vienna University of Economics and Business

Monday 1
11:30-13:00
Lecture room F4050

Learning the dependence structure among variables in complex systems is a central problem across medical, natural, and social sciences. These structures can be naturally represented by graphs, and the task of inferring such graphs from data is known as graph learning or as causal discovery if the graphs are given a causal interpretation. Existing approaches typically rely on restrictive assumptions about the data-generating process, employ greedy oracle algorithms, or solve approximate formulations of the graph learning problem. As a result, they are either sensitive to violations of central assumptions or fail to guarantee globally optimal solutions. We address these limitations by introducing a nonparametric graph learning framework based on nonparametric conditional independence testing and integer programming. We reformulate the graph learning problem as a mixed-integer program and prove that solving this integer-programming problem provides a globally optimal solution to the original graph learning problem. Our method leverages efficient encodings of graphical separation criteria, enabling the exact recovery of larger graphs than was previously feasible. We provide an implementation in the openly available R package ‘`glip`’ which supports learning (acyclic) directed (mixed) graphs and chain graphs. From the resulting

output one can compute representations of the corresponding Markov equivalence classes or weak equivalence classes. Empirically, we demonstrate that our approach is faster than other existing exact graph learning procedures for a large fraction of instances and graphs of various sizes. GLIP also achieves state-of-the-art performance on simulated data and benchmark datasets across all aforementioned classes of graphs.

Monday 1
11:30-13:00
Lecture room F4050

On causal inference with marked point processes

Kjetil Røysland
University of Oslo

We will present a general, yet rigorous, class of causal models for event history data that forms a direct generalization of the so-called RCISTG-models for finite families of random variables and potential outcomes to marked point processes in continuous time. This enables a rigorous treatment of potential outcomes at random event times that we have not been able to find elsewhere in the literature. We will discuss a very particular notion of intervention that enables us to carry out this construction.

Identifying the efficient influence function (EIF) is crucial for machine learning methods in causal inference, e.g., TMLE and double/debiased ML. There are however some phenomena that occur in continuous time models that do not have analogies in discrete time, leading to subtleties related to identification of EIFs. Aad van der Vaart (2004) pointed at analogous problems with the "Robins-formula" for EIFs in coarsening models that are CAR and only CAR, and then followed up with a rather formal construction in order to give precise meaning, and an actual proof, to the claim by Robins.

We will present a formula for the EIFs for causal estimands. Analogously to van der Vaart, we offer a formal construction that coincides with the Robins formula in discrete time. Our method, however, takes a slightly different route, and is largely based on operators on Hilbert spaces and martingale representations. We will use this construction to address the validity of various formulas for EIFs found elsewhere in the literature on continuous time causal inference.

This is joint work with Pål Ryalen and Mats Stensrud.

Monday 1
11:30-13:00
Lecture room F3020

WALNUTS: A No-U-Turn Sampler with Locally Adaptive Step Size

Sifan Liu
Duke University

Adapting parameters locally in Markov chain Monte Carlo while preserving reversibility remains a fundamental challenge. The No-U-Turn Sampler (NUTS) addresses this issue by dynamically adjusting the integration time through a geometric U-turn criterion, enabling robust performance across a wide range of posterior geometries. However, when the target distribution exhibits multi-scale structure, such as funnel-shaped posteriors, the local curvature can vary dramatically along a trajectory. In such settings, adapting only the integration length is often insufficient; the step size must also vary locally to maintain numerical stability and efficiency.

We introduce WALNUTS (Within-orbit Adaptive Leapfrog No-U-Turn Sampler), a generalization of NUTS that dynamically adjusts the leapfrog step size at each integration step within an orbit. Like NUTS, WALNUTS is rejection-free and uses biased progressive sampling to favor proposals farther from the starting point. By adapting both the duration and the resolution of the integration, WALNUTS achieves improved robustness and sampling efficiency in challenging geometries. Empirical results on difficult posterior distributions demonstrate substantial gains in effective sample size and exploration efficiency.

Non-reversible Birth-Death-Piecewise Deterministic Markov Process samplers for Gibbs Spatial Point Processes

Ruben Seyer

Chalmers University of Technology and University of Gothenburg

Monday 1
11:30-13:00
Lecture room F3020

Markov chain Monte Carlo methods are often viewed as impractical by spatial statisticians because they can converge slowly and become computationally expensive in challenging models. We develop a class of non-reversible continuous-time samplers that exploit a distinctive feature of point patterns: their natural ordering by cardinality. This allows us to introduce directed birth–death dynamics that improve exploration over the number of points while preserving the target distribution, and to combine these dynamics with continuous movement based on piecewise deterministic Markov processes to maintain efficient spatial mixing. We provide a general algorithm for these samplers and establish their ergodicity under standard conditions on the target point process. Across Poisson, hardcore, and Geyer saturation models, the proposed methods show shorter burn-in, improved local and global mixing, and better exploration of difficult regions of the state space than standard reversible samplers. The gains are especially pronounced in challenging regimes, indicating that non-reversibility provides a practical route to simulation for models that are otherwise difficult to sample from.

Statistical guarantees for denoising reflected diffusion models

Claudia Strauch

Heidelberg University and Aarhus University

Monday 1
11:30-13:00
Lecture room F3020

Denoising diffusion models are a powerful class of generative models, yet their theoretical properties in bounded domains are often addressed via truncation heuristics. We study models driven by reflected diffusions, which naturally confine the dynamics and provide a rigorous alternative to such heuristics. Under Sobolev smoothness assumptions, we establish minimax-optimal convergence rates in total variation distance, up to polylogarithmic factors. Our analysis combines spectral methods for score approximation with neural network estimation to provide formal statistical guarantees. Furthermore, we discuss how the performance of the model is impacted by the underlying simulation schemes and discretisation errors.

A portmanteau test for multivariate non-stationary functional time series with an increasing number of lags

Lujia Bai

Ruhr University Bochum; Bochum (Germany)

Monday 1
11:30-13:00
Lecture room F3005

Multivariate locally stationary functional time series provide a flexible framework for modeling complex data structures exhibiting both temporal and spatial dependencies while allowing for time-varying data generating mechanism. In this paper, we introduce a portmanteau-type test for assessing white noise assumptions tailored for multivariate locally stationary functional time series without dimension reduction. A simple bootstrap procedure is proposed to implement the test because the limiting distribution can be non-standard or even does not exist. Our approach is based on a Gaussian approximation result for a degenerate U -statistic of second-order functional time series involving an increasing number of lags, which is of independent interest. Through theoretical analysis and simulation studies, we demonstrate the efficacy and adaptability of the proposed method in detecting departures from white noise assumptions in multivariate locally stationary functional time series.

Low-Dose Tomography of Random Fields and the Problem of Continuous Heterogeneity

Monday 1

11:30-13:00

Lecture room F3005

Alessia Caponera

LUISS Guido Carli University; Rome (Italy)

We consider the problem of nonparametric estimation of the conformational variability in a population of related structures, based on low-dose tomography of a random sample of representative individuals. In this context, each individual represents a random perturbation of a common template and is imaged noisily and discretely at but a few projection angles. Such problems arise in the cryo Electron Microscopy of structurally heterogeneous biological macromolecules. We model the population as a random field, whose mean captures the typical structure, and whose covariance reflects the heterogeneity. We show that consistent estimation is achievable with as few as two projections per individual, and derive uniform convergence rates reflecting how the various parameters of the problem affect statistical efficiency, and their trade-offs. Our analysis formulates the domain of the forward operator to be a reproducing kernel Hilbert space, where we establish representer and Mercer theorems tailored to question at hand. This allows us to exploit pooling estimation strategies central to functional data analysis, illustrating their versatility in a novel context. We provide an efficient computational implementation using tensorized Krylov methods and demonstrate the performance of our methodology by way of simulation.

An Operator-Level ARCH Model

Monday 1

11:30-13:00

Lecture room F3005

Sebastian Kühnert

Ruhr University Bochum; Bochum (Germany)

We consider the problem of nonparametric estimation of the conformational variability in a population of related structures, based on low-dose tomography of a random sample of representative individuals. In this context, each individual represents a random perturbation of a common template and is imaged noisily and discretely at but a few projection angles. Such problems arise in the cryo Electron Microscopy of structurally heterogeneous biological macromolecules. We model the population as a random field, whose mean captures the typical structure, and whose covariance reflects the heterogeneity. We show that consistent estimation is achievable with as few as two projections per individual, and derive uniform convergence rates reflecting how the various parameters of the problem affect statistical efficiency, and their trade-offs. Our analysis formulates the domain of the forward operator to be a reproducing kernel Hilbert space, where we establish representer and Mercer theorems tailored to question at hand. This allows us to exploit pooling estimation strategies central to functional data analysis, illustrating their versatility in a novel context. We provide an efficient computational implementation using tensorized Krylov methods and demonstrate the performance of our methodology by way of simulation.

Spectra of critical ErdHos-Rényi graphs

Monday 1

11:30-13:00

Lecture room F3017

Johannes Alt

University of Bonn

The ErdHos-Rényi graph is a common random graph model with intricate behaviours, e.g., a connectivity transition when the expected degree scales like the logarithm of the number of vertices. In this regime, we established a transition in the eigenvector structure of the adjacency matrix of the ErdHos-Rényi graph. For large enough expected degree, all eigenvectors are delocalized, i.e. their mass spreads out approximately uniformly over all vertices. Below a certain threshold, localized eigenvectors emerge. More precisely, the mass of each eigenvector with large eigenvalue is concentrated in a ball around a unique vertex and decays exponentially in the graph distance from this vertex.

We refine this spectral information to study the Schrödinger time evolution of a free quantum particle hopping on the ErdHos-Rényi graph. These results have been obtained in joint works with Antti Knowles and Raphael Ducatez.

Quantitative Tracy-Widom laws for sparse random matrices

Teodor Bucht

KTH Royal Institute of Technology

Monday 1
11:30-13:00
Lecture room F3017

In this talk I will consider the fluctuations of the largest eigenvalue of sparse random matrices, the class of random matrices that includes the normalized adjacency matrices of the Erdős-Rényi graph $G(N, p)$. I will discuss edge universality for this model and present joint work with Kevin Schnelli and Yuanyuan Xu. Our main result is that the fluctuations of the largest eigenvalue converge to the Tracy-Widom law at a rate almost $O(N^{-1/3} + p^{-2}N^{-4/3})$ in the regime $p \gg N^{-2/3}$. Our proof builds upon the Green function comparison method initiated by Erdős, Yau, and Yin (2012). To show a Green function comparison theorem for fine spectral scales, we implement algorithms for symbolic computations involving averaged products of Green function entries.

Tracy-Widom, Gaussian, and Bootstrap: Approximations for Leading Eigenvalues in High-Dimensional PCA

Nina Dörnemann

Aarhus University

Monday 1
11:30-13:00
Lecture room F3017

Under certain conditions, the largest eigenvalue of a sample covariance matrix undergoes a well-known phase transition when the sample size n and data dimension p diverge proportionally. In the subcritical regime, this eigenvalue has fluctuations of order $n^{-2/3}$ that can be approximated by a Tracy-Widom distribution, while in the supercritical regime, it has fluctuations of order $n^{-1/2}$ that can be approximated with a Gaussian distribution. However, the statistical problem of determining which regime underlies a given dataset is far from resolved. We develop a new testing framework and procedure to address this problem. In particular, we demonstrate that the procedure has an asymptotically controlled level, and that it is power consistent for certain alternatives. Also, this testing procedure enables the design of a new bootstrap method for approximating the distributions of functionals of the leading sample eigenvalues within the subcritical regime—which is the first such method that is supported by theoretical guarantees.

Mixing time of the conditional backward sampling particle filter

Joona Karjalainen

University of Jyväskylä (Finland)

Monday 1
11:30-13:00
Lecture room U3041

The conditional backward sampling particle filter (CBPF) is a powerful Markov chain Monte Carlo sampler for general state space hidden Markov model (HMM) smoothing. We show that the CBPF has $O(T \log T)$ time complexity under strong mixing: its mixing time is upper bounded by $O(\log T)$, for any sufficiently large number of particles N independent of T . This $O(\log T)$ mixing time is optimal. To prove our main result, we introduce a novel coupling of two CBPFs, which employs a maximal coupling of two particle systems at each time instant. The coupling is implementable and we use it to construct unbiased, finite variance, estimates of functionals which have arbitrary dependence on the latent state's path, with a total expected cost of $O(T \log T)$. We use this to construct unbiased estimates of the HMM's score function, and also investigate other couplings which can exhibit improved behaviour.

Monday 1
11:30-13:00
Lecture room U3041

Approximate Bayesian inference for semiparametric ordinal regression

Emanuele Aliverti
University of Padova (Italy)

Ordinal categorical variables—such as Likert-scale responses—are widely used across many scientific fields. In several applications, it is of interest to characterize how their distribution depends on one or more covariates through flexible smooth effects. Under a Bayesian framework, this can be addressed using additive cumulative probit models with penalized regression splines, where smoothness is induced via derivative-based penalties on the basis coefficients. When the sample size is large, however, posterior inference based on Markov chain Monte Carlo becomes computationally demanding, motivating the use of scalable deterministic approximations. In this talk, we consider two approaches relying on Variational Inference: a partially factorized Mean-Field approximation and an Expectation Propagation routine. We discuss their construction, computational properties, and empirical performance, showing that they provide blazing fast and accurate alternatives to simulation-based methods for semiparametric ordinal regression models.

Monday 1
11:30-13:00
Lecture room U3041

Implied priors for the exponential family

Rolf Larsson
Uppsala University (Sweden)

Given a random sample from a distribution with unknown parameter(s), the implied prior is defined as the ratio of the confidence density and the likelihood function. The confidence density of a parameter is a frequentist counterpart of a Bayesian posterior density. The calculation of a confidence density does not require any prior distribution.

The present paper gives conditions for when the implied prior, in the context of a one-parameter continuous exponential family distribution, equals Jeffreys' prior. In a sense, this is a generalization of a previously well-known result about exponential families that holds when conditioning on an ancillary statistic. Some simple examples illustrate the matter.

Discrete one-parameter exponential family distributions are also briefly discussed.

Monday 1
11:30-13:00
Lecture room U3043

Recent developments for marked spatial point processes

Mehdi Moradi
Umeå University (Sweden)

Many environmental and biological systems are naturally represented as marked spatial point processes, where events occur at spatial locations, and carry associated attributes, often called marks. Understanding how these marks vary across space and how they are associated between nearby events is a central statistical problem. Classical mark correlation functions provide global summaries of such associations as a function of interpoint distance, but they can perform poorly when the underlying point pattern is spatially inhomogeneous or when distinct local mark behaviours coexist within the same dataset. In this work, I present recent methodological developments for analysing mark associations in spatial point patterns that address these challenges. First, we introduce inhomogeneous mark correlation functions, which explicitly account for spatial inhomogeneity while quantifying how marks vary or associate as a function of pairwise spatial distance. Nonparametric estimators are developed and evaluated through simulation studies, demonstrating their ability to reliably detect both positive and negative mark associations and to identify the spatial scales at which these associations occur. Second, to capture spatially varying mark behaviour, we introduce local indicators of mark association (LIMA). Unlike global summaries, LIMA functions identify mark associations at the level of individual points and determine the interpoint distances at which these associations are significant. This local perspective allows the detection of distinct mark behaviours that may otherwise be masked by dominant global patterns. Finally, these methodological developments are implemented in the R package `markstat`, which provides

tools for computing both global and local mark correlation functions for spatial point patterns in Euclidean spaces and on linear networks, accommodating both real-valued and function-valued marks. The proposed methods are illustrated through simulation studies and forestry applications involving tree attributes such as diameter and height, demonstrating how they provide deeper insight into spatial variation and interaction in marked point patterns.

Stationary subspace analysis for spatial data

Perttu Saarela

University of Helsinki (Finland)

Monday 1
11:30-13:00
Lecture room U3043

Stationary subspace analysis (SSA) is a blind source separation framework that decomposes linearly mixed multivariate data into stationary and nonstationary components. We extend SSA to spatially indexed data by introducing spatial stationary subspace analysis (spSSA), which explicitly accounts for spatial dependence. We propose three estimation procedures for the unmixing matrix based on first- and second-order spatial statistics. Each procedure targets a different type of nonstationarity and can be formulated as the solution to a generalized eigenvalue problem. To address situations where multiple forms of nonstationarity are present simultaneously, we combine the three procedures using approximate joint diagonalization. Simulation studies demonstrate that this combined approach yields superior separation performance. When the dimension of the nonstationary subspace is known, the proposed methods reliably recover the latent stationary and nonstationary components. However, determining this dimension remains a fundamental challenge in SSA, for which no generally accepted solution currently exists. Building on our estimation procedures, we propose a novel data augmentation approach to estimate the dimension of the nonstationary subspace and demonstrate its effectiveness through simulation studies. The proposed methodology is easily transferable to time series settings, making it of broader methodological interest.

Consistent Distribution-Free and Affine-Invariant Tests for the Validity of Independent Component Models

Klaus Nordhausen

University of Helsinki (Finland)

Monday 1
11:30-13:00
Lecture room U3043

We propose a family of tests of the validity of the assumptions underlying independent component analysis methods. The tests are based on empirical characteristic functions computed from estimated independent components; rank-based versions are also proposed. The test statistics involve weights; proper choices of these weights and the estimation method for the mixing matrix yield universally consistent and affine-invariant tests. The asymptotic null distribution of the test statistics, however, is extremely complex and numerically untractable. Implementation, therefore, is based on permutational and resampling strategies which, remarkably, lead to distribution-free procedures despite the fact that they are performed on estimated independent components or their componentwise ranks. A Monte Carlo study is conducted, involving various estimation methods for the mixing matrix, different weights, and a competing test based on distance covariance, under both the null hypothesis and alternative scenarios. A real-data application demonstrates the practical utility and effectiveness of the method.

Monday 1
14:00-15:30
Lecture room F4050

Dirichlet scale mixture priors for Bayesian Neural Networks

August Arnstad
University of Oslo

Neural networks are the cornerstone of modern machine learning, yet can be difficult to interpret, give overconfident predictions and are vulnerable to adversarial attacks. Bayesian neural networks (BNNs) provide some alleviation of these limitations, but have problems of their own. The key step of specifying prior distributions in BNNs is no trivial task, yet is often skipped out of convenience. In this work, we propose a new class of prior distributions for BNNs, the Dirichlet scale mixture (DSM) prior, that addresses current limitations in Bayesian neural networks through structured, sparsity-inducing shrinkage. Theoretically, we derive general dependence structures and shrinkage results for DSM priors and show how they manifest under the geometry induced by neural networks. In experiments on simulated and real world data we find that the DSM priors encourages sparse networks through implicit feature selection, show robustness under adversarial attacks and deliver competitive predictive performance with substantially fewer effective parameters. In particular, their advantages appear most pronounced in correlated, moderately small data regimes, and are more amenable to weight pruning. Moreover, by adopting heavy-tailed shrinkage mechanisms, our approach aligns with recent findings that such priors can mitigate the cold posterior effect, offering a principled alternative to the commonly used Gaussian priors.

Monday 1
14:00-15:30
Lecture room F4050

Explainable Bayesian Neural Networks through Active Paths: Global Structures and Local Insights

Eirik Høyheim
Norwegian Defence Research Establishment

Artificial neural networks (ANNs) can offer highly accurate predictions by approximating complex input-output relationships, but their over-parametrisation often hinders interpretability and limits their ability to provide uncertainty measures. Bayesian neural networks (BNNs) address some of these challenges by representing weights as probability distributions, while latent binary Bayesian neural networks (LBBNNs) further account for structural uncertainty by learning inclusion probabilities for individual weights and inducing sparsity via the median probability model. However, although LBBNNs often drastically reduce the network density, the resulting architectures typically remain too dense to interpret, offering limited insight into how covariates contribute to predictions. In this talk, we present an extension of the LBBNN framework that incorporates input-skip connections. These skip connections allow each covariate to contribute to any subsequent layer directly or be excluded entirely from the network, enabling the model to adapt its complexity to the problem at hand and recover simpler structures (e.g. linear or even constant models) when appropriate. Input-skip LBBNNs (ISLaBs) substantially reduces network density compared to standard LBBNNs, achieving density reductions of over 99% for small networks and over 99.9% for larger ones, while maintaining high predictive performance and providing uncertainty measures. A central component of ISLaB is the concept of active paths, which make it feasible to obtain global structures, as well as local explanations with theoretical guarantees. This removes the need for post-hoc interpretability tools and helps to clarify how covariates contribute to predictions. ISLaB thus offer a deep learning framework that unifies sparsification, uncertainty quantification, and built-in explainability.

We Cannot Amortize Everything: Test-Time Approaches for Amortized Inference

Luigi Acerbi
University of Helsinki

Monday 1
14:00-15:30
Lecture room F4050

In recent years, amortized Bayesian methods have emerged to address two key challenges of traditional probabilistic inference: computational expense and limited generalization. By pre-training neural networks on priors, simulators, or historical data, amortized inference approaches provide rapid probabilistic solutions to new problem instances across scientific and engineering applications. However, amortization alone is not enough – some problems demand computation that cannot be anticipated at training time. For example, new information might become available at test time, such as task-relevant priors or related datasets. How can we extend amortized methods to meaningfully allocate compute and improve predictive performance at test time? In this talk, I will present recent work from our group on amortized inference for predictive modelling and simulator-based inference, showing how adaptive test-time computation can complement and extend amortized solutions when the problem demands it.

Covariance scanning for adaptively optimal change point detection in high-dimensional linear models

Haeran Cho
University of Bristol

Monday 1
14:00-15:30
Lecture room F3020

This paper investigates the detection and estimation of a single change in high-dimensional linear models. We derive minimax lower bounds for the detection boundary and the estimation rate, which uncover a phase transition governed by the sparsity of the covariance-weighted differential parameter. This form of "inherent sparsity" captures a delicate interplay between the covariance structure of the regressors and the change in regression coefficients on the detectability of a change point. Complementing the lower bounds, we introduce two covariance scanning-based methods, McScan and QcSan, which achieve minimax optimal performance (up to possible logarithmic factors) in the sparse and the dense regimes, respectively. In particular, QcScan is the first method shown to achieve consistency in the dense regime and further, we devise a combined procedure which is adaptively minimax optimal across sparse and dense regimes without the knowledge of the sparsity. Computationally, covariance scanning-based methods avoid costly computation of Lasso-type estimators and attain worst-case computation complexity that is linear in the dimension and sample size. Additionally, we consider the post-detection estimation of the differential parameter and the refinement of the change point estimator. Simulation studies support the theoretical findings and demonstrate the computational and statistical efficiency of the proposed covariance scanning methods.

This is joint work with Housen Li (Goettingen).

Inference of time-varying precision matrices in high dimensional non-stationary time series

Monday 1
14:00-15:30
Lecture room F3020

Lujia Bai

Ruhr University Bochum

Inference of the precision matrix is fundamental to understanding conditional dependence structures in multivariate time series. Classical methods typically rely on stationarity, an assumption frequently violated in practice when dependence patterns evolve over time. In this paper, we investigate the estimation and inference of time-varying precision matrices for high-dimensional, non-stationary time series. We propose a flexible framework in which the precision matrix is modeled as a smooth function of time, allowing conditional dependencies to evolve dynamically. Under a mild cross-sectional weak dependence condition, which induces sparsity in the precision matrices, we develop an estimation procedure that combines sieve approximations with group lasso regularization to ensure stability in high dimensions. We establish theoretical guarantees for uniform consistency of the time-varying precision matrices based on the lasso-type estimator under mild assumptions on temporal smoothness and dependence. Furthermore, we introduce a refined estimator that enables simultaneous inference of the associated partial correlation functions, along with a bootstrap procedure for implementing the inference. Simulation studies demonstrate that the proposed method accurately recovers evolving network structures. An application to brain imaging data illustrates its practical effectiveness in uncovering time-dependent conditional dependencies in complex systems.

Multiscale Change Point Detection for Functional Time Series

Monday 1
14:00-15:30
Lecture room F3020

Tim Kutta

Aarhus University

We study the problem of detecting and localizing multiple changes in the mean parameter of a Banach space-valued time series. The goal is to construct a collection of narrow confidence intervals, each containing at least one (or exactly one) change, with globally controlled error probability. Our approach relies on a new class of weighted scan statistics, called Hölder-type statistics, which allow a smooth trade-off between efficiency (enabling the detection of closely spaced, small changes) and robustness (against heavier tails and stronger dependence). For Gaussian noise, maximum weighting can be applied, leading to a generalization of optimality results known for scalar, independent data. Even for scalar time series, our approach is advantageous, as it accommodates broad classes of dependency structures and non-stationarity. Its primary advantage, however, lies in its applicability to functional time series, where few methods exist and established procedures impose strong restrictions on the spacing and magnitude of changes.

Wasserstein Stability of Bayesian Posteriors in the Concentrated Posterior Regime

Monday 1
14:00-15:30
Lecture room F3005

Dana Wrischnig

Freie Universität Berlin

Understanding the stability of Bayesian posterior distributions under perturbations of the data is a classical problem in inverse problems and uncertainty quantification. This talk develops a Wasserstein-based perspective in regimes where the posterior concentrates, such as the small noise or large data setting.

While established bounds ensure local stability of the posterior under variations of the likelihood, the associated constants deteriorate in the concentration regime. In contrast, we show that, under standard assumptions, the Wasserstein distance between posterior distributions associated with different datasets admits a decomposition into the Euclidean distance between the

corresponding maximum a posteriori estimators and a remainder of the order of the posterior contraction rate.

The framework applies both to the small noise setting and to large data regimes in which the likelihood evolves with increasing observations, and allows for multimodal posterior distributions. These results offer a perspective on posterior stability in the concentration regime that is relevant across a wide range of inverse problems.

Posterior contraction under misspecification and heteroscedasticity in non-linear inverse problems

Maximilian Siebel
Heidelberg University

Monday 1
14:00-15:30
Lecture room F3005

In many practical and numerical inverse problems, the exact data log-likelihood is not fully accessible, motivating the use of surrogate models. We study heteroscedastic nonparametric non-linear regression problems with Gaussian errors and establish contraction results for posterior distributions arising from a surrogate log-likelihood constructed from proxy error variances, an approximate forward map, and an appropriate Gaussian process prior.

Under general assumptions on the approximation quality, we show that the resulting surrogate posterior is statistically reliable and contracts about the true parameter at rates comparable to those of the exact posterior.

The analysis leverages consistency properties of the maximum a posteriori (MAP) estimator to effectively handle heteroscedastic noise and to control the impact of likelihood approximation errors. We apply the framework to PDE-constrained inverse problems for a reaction–diffusion equation and the two-dimensional Navier–Stokes equation. In the latter case, we consider misspecified viscosity and forcing terms as well as Oseen-type linearization models, highlighting the relevance of our results for numerical analysis applications.

Computational guarantees for Bayesian inference in interacting particle system models

Aurélien Castre
University of Cambridge

Monday 1
14:00-15:30
Lecture room F3005

We consider the inverse problem of inferring the interaction potential W in a weakly interacting particle system from noisy measurements of its mean-field density. We adopt a Bayesian approach, placing a Gaussian prior on W and studying the resulting posterior distribution.

We rigorously compute the Fréchet derivative of the parameter-to-solution map using a Banach space version of the implicit function theorem to verify the gradient stability condition of Nickl & Wang (JEMS, 2024). This implies that the posterior is locally log-concave in a neighbourhood of the true potential.

Combined with posterior contraction results of Nickl, Pavliotis & Ray (AoS, 2025), which ensure the posterior concentrates in this neighbourhood, this yields polynomial-time mixing of a warm-start Unadjusted Langevin Algorithm (ULA): for any prescribed accuracy level ϵ , a suitable step size ensures the ULA iterates are ϵ -close to the posterior in Wasserstein-2 distance, in a number of steps polynomial in the data size N , the discretisation dimension D , and the inverse accuracy. We thus obtain an end-to-end computational guarantee: the posterior mean can be approximated by ULA in polynomially many iterations, and the output is close to the true interaction potential with high probability.

Monday 1
14:00-15:30
Lecture room F3017

A vector time series approach for modelling spatio-temporal data

Gen Nowak
Australian National University

We propose a hierarchical model for spatio-temporal data that is based on a vector time series approach and incorporates geographic spatial information and deterministic temporal components. The model can be used to produce temporal predictions for future time points, spatial predictions at unobserved locations, and spatio-temporal predictions for future time points at unobserved locations. We use the model to analyse monthly rainfall data from the Murray-Darling Basin and to generate predictions. The Murray-Darling Basin is an important agricultural area in southeastern Australia that produces more than a third of Australia's food supply and therefore understanding rainfall patterns in this area is crucial. We compare the performance of our model to a previous model developed on this data that was based on a singular value decomposition of the data. Our model addresses some limitations imposed by the singular value decomposition of the previous model, has very comparable predictive performance, and is more applicable to a wider variety of spatio-temporal data types.

Monday 1
14:00-15:30
Lecture room F3017

Seasonal Space Use and Habitat Associations of Golden Eagles in Finland: Insights from a Point Process Modelling

Diego Rondon
University of Helsinki

We quantified the seasonal and nationwide distribution of golden eagles (*Aquila chrysaetos*) in Finland from 2018 to 2021 by integrating citizen science observations with nest-survey records in a spatio-temporal point process framework. We fitted a log-Gaussian Cox process that shares a spatially continuous Gaussian random field (GRF) across different datasets, where spatial autocorrelation was modelled using Matérn covariance function and temporal dependence with an autoregressive term, linking occurrence to continuous environmental variables. We present continuous maps for the distribution of breeding (April-July) and non-breeding (November-February) seasons, based on joint data set and single dataset estimation, respectively. Results show high densities in the northern part of Finland and low densities in the south and southwest. Larger dispersal is observed during the non-breeding season, while breeding season distribution is more concentrated. We quantified the effects of environmental variables and translated the outputs into conservation guidance. This integrated workflow takes advantage of the integrated nested Laplace approximation (INLA) framework and delivers high-resolution spatio-temporal maps that improve understanding of golden eagle distribution across Finland while supporting conservation and decision-making.

Monday 1
14:00-15:30
Lecture room F3017

Reconstructing the single-cell spatiotemporal dynamics of glioblastoma invasion

Linnea Hallin
University of Gothenburg

Glioblastoma invasion into healthy brain tissue remains a major barrier to effective treatment, yet its spatiotemporal dynamics are difficult to quantify at single-cell resolution in a scalable and patient-specific manner. Here we introduce GlioTrace, an ex vivo imaging and computational framework for real-time tracking of glioblastoma invasion. By combining whole-specimen confocal microscopy with machine learning-based morphology classification and probabilistic modeling of state transitions, GlioTrace reconstructs how tumor cells switch between distinct invasion phenotypes over time and how these dynamics are shaped by local tissue context and therapeutic perturbation. The transitions between different morphologies are modeled by a Hidden Markov Model (HMM), with the true morphological states as hidden states, and the class probabilities

from a CNN classifier as the observed states. To allow transitions to depend on track-derived covariates, we modeled the probability of moving from one hidden state to another using multinomial regression. The resulting HMM transition matrix then consisted of one multinomial logistic linear regression model per "from"-state. Applied to six patient-derived models, GlioTrace reveals that invasion plasticity, the ability of tumor cells to transition between morphologically and behaviorally distinct states, is patient-specific, spatially organized, and modulated by microenvironmental features including vascular proximity and microglial interaction. Targeted therapies selectively alter phenotype composition and transition probabilities, whereas standard-of-care treatment enriches a branching state consistent with a treatment-tolerant invasive phenotype. GlioTrace therefore provides a scalable framework for quantifying glioblastoma invasion dynamics and comparing anti-invasive responses across patient-derived models.

Model-based clustering of abundance time series data

Nourhan Shafik
University of Helsinki

Monday 1
14:00-15:30
Lecture room U3041

In Ecology, community stability is commonly quantified as the temporal variability of abundance (or biomass) within a community. To better characterize ecological communities, we propose a Bayesian model-based clustering framework for grouping ecological communities and species based on shared fluctuation dynamics. This approach aims to cluster ecological time-series data with particular attention to missing data, sampling errors, and uncertainty estimation. Our proposed method differs from existing approaches in that it automatically handles missing data without need for imputation methods, provides uncertainty estimates, and incorporates additional covariates, such as functional traits and environmental variables, to explain (and predict) the clusters. Latent dynamic characteristics are embedded within a finite mixture model, where cluster membership is treated as an unobserved random variable and inferred probabilistically. A fully Bayesian formulation enables joint estimation of model parameters and cluster assignments, while naturally accounting for uncertainty through posterior inference. We consider both finite mixtures and non-parametric extensions (e.g., Dirichlet process mixtures) to allow flexible inference on the number of clusters. Posterior summaries are used to identify groups exhibiting distinct stability regimes and differential responses to perturbations. We further examine associations between inferred clusters and species' functional traits within a hierarchical framework, providing insight into the mechanisms driving community stability and identifying potential stabilizing taxa. Overall, this work demonstrates how Bayesian model-based clustering of ecological time series data can uncover latent structure in ecosystem dynamics, offering a principled and uncertainty-aware foundation for conservation prioritization in changing environments.

Subgraph counts in a dynamic random connection model

Moritz Otto
Leiden University

Monday 1
14:00-15:30
Lecture room U3041

We consider a dynamic version of the Poisson point process, in which the points independently appear and disappear over time with exponentially distributed on- and off-times. At each time instance, the active points form the vertex set of a time-dependent random connection model (RCM), where edges are formed probabilistically based on pairwise distances via a prescribed connection function. We study the evolution of subgraph counts in this dynamic RCM. Specifically, we fix a finite collection of connected graphs and track the time-dependent vector of subgraph counts. Our main result is a multivariate functional central limit theorem for this vector. After suitable centering and normalization, we show that, as the intensity of the Poisson process grows, the subgraph count process converges in distribution to a multidimensional Gaussian process. This talk is based on joint work with Rajat Subhra Hazra, Nikolai Kriukov and Michel Mandjes.

Bayesian inference for spatial compositional data with exact zeros using gradient-informed MCMC

Monday 1
14:00-15:30
Lecture room U3041

Behnaz Pirzamanbin
Lund University (Sweden)

Spatial compositional data with exact zeros arise in many applications but remain challenging for models that often assume strictly positive components. We develop a Bayesian spatial model that combines the Dirichlet Composition Distribution, which accommodates exact zeros through component-specific zero probabilities, with a Gaussian Markov random field representation of the latent compositional field. The resulting framework supports joint inference on zero occurrence, compositional structure, and spatial dependence. For efficient posterior computation, we derive gradient-based expressions in additive log-ratio coordinates and investigate how MCMC performance depends on the update strategy for both the high-dimensional latent field and the parameters.

We compare four latent-field samplers, MALA, pCN, gradient-informed pCN (gpCN), and the auxiliary-gradient sampler, combined with joint and decoupled updates for the Dirichlet precision parameter α , and random-walk Metropolis updates for the spatial range parameter κ .

In a simulation study on a 35×35 grid with three compositional components and structural zeros, only the Q-preconditioned samplers, gpCN and auxiliary-gradient, reliably recover the spatial structure. In addition, decoupling α via slice sampling is essential: joint updates lead to slow mixing in α and downward bias in κ , while decoupled updates recover the true parameters more accurately. We apply the best-performing strategy to the LANDCLIMII pollen-based REVEALS dataset for Europe, comprising 303 sites and 13 plant functional types with zero rates ranging from 0.3% to 78.2%. Ten-fold cross-validation confirms out-of-sample predictive performance, and stable parameter estimates across folds. These results show that accurate spatial inference for compositional data with exact zeros requires both a likelihood that respects zero structure and MCMC updates adapted to the geometry of the latent field.

Extreme Precipitation in Iceland: An Exploratory Analysis of IDF Curves Across Stations and Durations

Monday 1
14:00-15:30
Lecture room U3043

Yang Han and Birgir Hrafnkelsson
University of Iceland

Extreme precipitation poses growing risks to infrastructure and private property in Iceland. In July 2024, Grundarfjörur in West Iceland recorded 227 mm of rainfall in 24 hours, the highest daily rainfall in July nationwide, leading to five landslides in the area. This study presents an exploratory analysis of precipitation data from the Icelandic Meteorological Office (IMO), forming the foundation for a PhD project on Bayesian hierarchical modelling of spatial precipitation extremes in Iceland. Raw tipping-bucket measurements at 10-minute intervals from 74 automatic weather stations (1990-2024) were post-processed by IMO using a neutral aggregating filter (NAF). Annual maxima series (AMS) were extracted for each station across accumulation durations ranging from 10 minutes to 72 hours, considering both full-year and summer (May-October) periods. Each AMS is assumed to follow a generalized extreme value (GEV) distribution. Intensity-Duration-Frequency (IDF) curves were constructed subsequently using the `extRemes` and `IDF` package in R for each station and for return periods of 2-100 years.

Fitting GEV models independently per duration using the `extRemes` package yields non-monotonically decreasing IDF curves at some stations, which is physically unrealistic. In contrast, the `IDF` package enforces a duration-dependent structure and produces monotonic IDF curves across all stations. Both approaches show high sensitivity to extreme observations. Summer-based IDF curves appear less spread out than full-year results, as anomalous values (e.g., 41.0 mm over a 10 minute-window in March) are excluded from the AMS. These findings highlight two key considerations: the importance of selecting an appropriate modelling framework for spatiotemporal precipitation data, and the need for rigorous quality check of the NAF-processed observations

prior to statistical modelling. Distinguishing genuine extremes from snow slump/gauge malfunction/maintenance is essential and particularly important, which can possibly be facilitated in collaboration with domain experts.

Bayesian estimation of subsurface properties in CO₂ storage sites

Elling Svee

Norwegian University of Science and Technology

Monday 1
14:00-15:30
Lecture room U3043

Uncertainty in subsurface properties is central to determining the long-term behavior of CO₂ plumes in geological storage sites. However, the computational cost of inference with full physics-based models motivates the need for more efficient alternatives. We present a likelihood-free Bayesian framework to model subsurface uncertainty and predict plume migration.

Approximate Bayesian Computation with Sequential Monte Carlo is used to estimate posterior distributions (4). The approach iteratively refines the parameter space by comparing simulated and observed plume extents. Simulations are run using the open-source Julia package `CO2BatchFill.jl` (3). It combines a buoyancy-driven theory for vertical migration with spill-point analysis (1; 2), and is fast enough to perform the thousands of simulations required in the sampling approach.

The framework is assessed on both synthetic data with known parameters and field data from the Sleipner CO₂ storage site. Synthetic experiments show that the method recovers migration paths and geometries in the multi-layer storage system. For Sleipner, we estimate parameters from seismic observations collected between 1996 and 2010, and use the calibrated model to forecast future CO₂ migration. Together, the results demonstrate the framework as a practical tool for uncertainty quantification in complex storage settings

References:

[1] Odd A. Andersen. Topography-based surface water modeling in Julia, with support for infiltration and temporal developments. *Journal of Open Source Software*, 10(109):7785, May 2025.

[2] Daniel J. Carruthers. AAPG/Datapages Discovery Series No. 7, Multidimensional Basin Modeling, Chapter 3: Modeling of Secondary Petroleum Migration Using Invasion Percolation Techniques. pages 21–37, 2003.

[3] Elling Svee. `CO2BatchFill.jl`: Fast simulation of CO₂ migration in layered reservoirs, 2026.

[4] Tina Toni, David Welch, Natalja Strelkowa, Andreas Ipsen, and Michael P. H. Stumpf. Approximate Bayesian computation scheme for parameter inference and model selection in dynamical systems. *Journal of The Royal Society Interface*, 6(31):187–202, February 2009. arXiv:0901.1925 [stat].

Bridging Matrix Profiles and Empirical Dynamic Modelling in Predictions for Environmental Data

Albertas Dvirnas

Umeå University

Monday 1
14:00-15:30
Lecture room U3043

Empirical dynamical modelling (EDM) and matrix profiles offer complementary approaches to discovering structure in complex time series. EDM reconstructs low-dimensional attractors from high-dimensional observations, enabling local analogue forecasting and causal inference, while matrix profiles provide a scalable, domain-agnostic mechanism for fast motif discovery, anomaly detection, and nearest-neighbour search. This talk presents a unified framework that bridges these two perspectives for the analysis of high-dimensional environmental data, with a focus on multi-species environmental DNA (eDNA) time series.

The central idea is to interpret matrix profile subsequences as embedded states in EDM's reconstructed phase space. This connection yields a principled method for identifying recurrent dynamical patterns and constructing local, interpretable forecasts. The framework extends naturally to streaming settings, where incremental updates to the matrix profile enable real-time pattern tracking and prediction as new observations arrive.

We demonstrate the approach on examples from seasonal environmental monitoring, showing how the joint use of matrix profiles and EDM can reveal candidate mechanisms, regime shifts, and nonlinear dependencies that are obscured by purely statistical or purely mechanistic models. We argue that this synergy constitutes a practical and scalable toolkit for exploratory analysis and prediction in modern, high-dimensional environmental datasets.

Keywords: empirical dynamical modelling, matrix profiles, environmental DNA, nonlinear time series, motif discovery, anomaly detection, streaming data.

Tuesday 2
11:00-12:30
Lecture room F4050

Modelling contagious bank runs

Luitgard A. M. Veraart

London School of Economics and Political Science

We develop a modelling framework for contagion in financial networks arising from bank runs. We show how interacting channels of contagion, namely funding withdrawals in the interbank network and price-mediated contagion arising from fire sales can turn a bank run on one institution into a systemic crisis. We provide an empirical case study and show how the new framework can be used in financial stress testing even if only partial information about the underlying financial network is available. We use a Bayesian approach to conduct the stress test under partial information. We find that the extent of systemic risk is highly sensitive to the choices of withdrawal strategies used by the market participants. We also discuss policy implications.

Tuesday 2
11:00-12:30
Lecture room F4050

Probabilistic forecast for spatio temporal Ornstein-Uhlenbeck processes

Leonardo Bardi

TU Chemnitz

We present a novel methodology, called mixed moving average field (MMAF, in short) guided learning, that can be employed to forecast spatio-temporal random fields as a spatio-temporal Ornstein-Uhlenbeck process or its mixed versions, the so-called STOU or MSTOU processes. We assume to observe 3D raster data generated from the latter processes, i.e., a set of spatio-temporal observations on a regular grid in space and time. STOU and MSTOU processes impose a dependence structure and a causal model on such data, based on the concept of cone-shaped ambit sets. However, in general, they have an unknown predictive distribution, and observed data cannot be directly employed to infer it. We then employ an ensemble of feedforward neural networks with Gaussian-distributed weights to produce probabilistic forecasts for such fields at specific spatial positions, incorporating the data generation process in the learning routine as follows. The networks are trained using a generalized Bayesian methodology on a specific embedding of the 3D raster data. Such embedding can be designed when the parameters shaping the autocovariance function and the causal model of the data-generating process are known. We then define a novel (weighted) least-squares estimator for θ -lex weakly dependent random fields to infer them, holding for exponential or power-shape covariogram functions, and prove its asymptotic properties. Finally, the trained networks in inference mode are used to generate ensemble forecasts, which we can show are calibrated across multiple time horizons. This is joint work with Imma V. Curato and Lorenzo Proietti.

Statistical inference for Lévy-driven graph supOU processes: From short- to long-memory in high-dimensional time series

Almut E. D. Veraart
Imperial College London

Tuesday 2
11:00-12:30
Lecture room F4050

We introduce Lévy-driven graph supOU processes, a parsimonious parametrisation for high-dimensional time series in which dependence between components is governed by a graph structure. Specifically, our model bridges short- and long-range dependence within a single parametric family while accommodating a wide range of marginal distributions. We further develop a generalised method of moments estimator, establish its consistency and asymptotic normality, and assess its finite-sample performance through a simulation study. Finally, we illustrate the practical relevance of our model and estimation method in an empirical study of wind capacity factors in a European electricity network context. This is joint work with Shreya Mehta.

Why the decline-of-war question is so hard to answer

Dennis Christensen
Norwegian Defence Research Establishment (FFI)

Tuesday 2
11:00-12:30
Lecture room F3020

The question of whether wars have become less violent over the last 200 years remains controversial. Advocates for this claim suggest that a ‘long peace’ has endured since the end of the Second World War, or shortly thereafter. Others find no evidence of such a decline and thus argue that the mechanisms governing lethality of war are unlikely to have changed. This talk will cover some of the major attempts to assess whether war is in decline, beginning with Lewis Fry Richardson’s pioneering work in 1960. In doing so, we will highlight the conceptual, methodological, and data challenges that make this question particularly difficult to answer and help explain why the debate remains unresolved. We will also examine the new interstate wars of the last four years and consider how they affect on the decline-of-war thesis.

Conformal prediction of fatalities from armed conflict

Jonathan P Williams
North Carolina State University

Tuesday 2
11:00-12:30
Lecture room F3020

Forecasting of armed conflicts is a critical area of research with the potential to save lives and mitigate suffering. While existing forecasting models offer valuable point predictions, they often lack individual-level uncertainty estimates, limiting their usefulness for decision-making. Several approaches exist to estimate uncertainty, such as parametric and Bayesian prediction intervals, bootstrapping, quantile regression, but these methods often rely on restrictive assumptions, struggle to provide well-calibrated intervals across the full range of outcomes, or are computationally intensive. Conformal prediction offers a model-agnostic alternative that guarantees a user-specified level of coverage but typically provides only marginal coverage, potentially resulting in non-uniform coverage across different regions of the outcome space. In this talk, I will discuss constructions of conformal prediction algorithms for prediction of fatalities in the context of both bin-conditional exchangeability and partial exchangeability. The latter arises in the formulation of hidden Markov models.

Tuesday 2
11:00-12:30
Lecture room F3020

Escalation dynamics and the severity of wars

Kristian Skrede Gleditsch
University of Essex (United Kingdom)

Although very large wars remain an enduring threat in global politics, we lack a clear understanding of how some wars become large and costly, while most do not. There are three possibilities: large conflicts begin with intense fighting, accumulate severity over a long duration, or escalate in intensity over time. Using detailed within-conflict data on civil and interstate wars (1946–2008), we show that escalation dynamics—variations in fighting intensity within an armed conflict—are the primary mechanism for producing large conflicts. Civil wars, however, tend to deescalate once they become very large, limiting their overall severity, while interstate wars exhibit a persistent risk of continual escalation. Simple models of within-conflict severity dynamics show that this distinction compactly explains the historical size distributions of civil and interstate wars, and unconditioned escalation is a plausible mechanism for Richardson’s Law—the power-law pattern in the frequency and severity of interstate conflicts. The dynamics of escalation within conflicts have broad implications for conflict theory and risk assessment.

Tuesday 2
11:00-12:30
Lecture room F3005

BayesCNA: Detecting copy number alterations in noisy data

Lotta Eriksson
Chalmers University of Technology (Sweden)

Liquid biopsies, coupled with analysis of copy number alterations (CNAs), have emerged as a promising tool for non-invasive monitoring of cancer progression and tumor composition. CNAs, which involve large genomic gains or losses, are prevalent in cancer and can be detected using low-pass liquid biopsy sequencing. This approach offers a cost-effective and minimally invasive alternative to traditional tissue biopsies. However, methods utilizing CNA data from liquid biopsies are limited by the low signal in the samples, caused by a low percentage of cancer DNA in the blood, and the inherent noise introduced during sequencing, which limits the strength of the detectable signal. To address this challenge, we developed BayesCNA, a method designed to improve signal extraction from low-quality liquid biopsy sequencing data, by utilizing a Bayesian changepoint detection algorithm [1, 2]. We identify positions in the genome with high posterior changepoint probability to identify the locations of CNAs. We show the effectiveness of the method on synthetically generated datasets, and compare the method to state-of-the-art bioinformatics tools under noisy conditions. Our results show that this novel approach increases sensitivity in detecting CNAs, particularly in low-quality cases.

References:

- [1] D. Barry, J.A. Hartigan, "Product Partition Models for Change Point Problems", *The Annals of Statistics*, 20(1):260-279, 1992.
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R2 priors for grouped variance decomposition in high-dimensional regression

Javier E. Aguilar
TU Dortmund (Germany)

Tuesday 2
11:00-12:30
Lecture room F3005

We introduce the Group-R2 decomposition prior, a hierarchical shrinkage prior that extends R2-based priors to structured regression settings with known groups of predictors. By decomposing the prior distribution of the coefficient of determination R^2 in two stages, first across groups, then within groups, the prior enables interpretable control over model complexity and sparsity. We derive theoretical properties of the prior, including marginal distributions of coefficients, tail behavior, and connections to effective model complexity. Through simulation studies, we evaluate the conditions under which grouping improves predictive performance and parameter recovery compared to priors that do not account for groups. Our results provide practical guidance for prior specification and highlight both the strengths and limitations of incorporating grouping into R2-based shrinkage priors.

Uncertainty-Aware Policy Evaluation with Bayesian Synthetic Control Models

Jouni Helske
University of Turku (Finland)

Tuesday 2
11:00-12:30
Lecture room F3005

In the last two decades, the synthetic control method (SCM) has emerged as a popular tool for observational causal inference in the evaluation of policy reforms and other interventions. One appealing feature of SCM is the simplicity of its core idea: counterfactual outcomes for the treated unit are constructed as a convex combination of non-treated units. However, standard SCM provides only point estimates of treatment effects and offers limited tools for principled uncertainty quantification, particularly in typical small-sample settings.

We recast SCM within a fully Bayesian framework as a Bayesian synthetic control model (BSCM), enabling interpretable, uncertainty-aware inference for treatment effects, donor weight composition, and other quantities of interest. The model naturally accommodates time-varying covariates, multiple treated units with staggered adoption, and robustness checks based on variants of leave-one-out cross-validation. We implement the approach in the `bscm` R package, which provides tools for model estimation, diagnostics, and model comparison. Computationally efficient posterior inference is obtained via Markov chain Monte Carlo using Stan.

Through simulation studies, we compare BSCM with existing SCM variants and demonstrate improved predictive performance in terms of root mean squared error and frequentist coverage of treatment effect estimates. Finally, we illustrate the method using a real-world policy evaluation example.

Clustering of Mixed-type Data

Gero Szepannek
Stralsund University of Applied Sciences

Tuesday 2
11:00-12:30
Lecture room F3017

Traditionally, most literature in clustering is dedicated to numeric data while in practical problems variables are often of both types numeric and categorical. In the recent years several approaches have been developed for clustering mixed-type data.

A brief overview on the most popular approaches will be given. The k-prototypes algorithm [1] as implemented in the R package `clustMixType` [2] will be presented in more detail together with several extensions of the original algorithm with regard to ordinal variables, missing values, its initialization or cluster validation.

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Tuesday 2
11:00-12:30
Lecture room F3017

Measure of shape for object data

Joni Virta
University of Turku

Object data analysis is concerned with statistical methodology for datasets whose elements reside in an arbitrary, unspecified metric space. In this talk we discuss the *object shape*, a novel measure of shape/symmetry for object data. The object shape is easy to compute and interpret, owing to its intuitive characterization as interpolation between two extreme forms of symmetry. We apply object shape in various metric spaces and show that it manages to unify several pre-existing, classical forms of symmetry. We also present a new visualization tool called the *peeling plot*, which allows using the object shape for outlier detection and principal component analysis of object data.

Tuesday 2
11:00-12:30
Lecture room F3017

Model-based mixed-type PCA

Lauri Heinonen
University of Turku

Principal component analysis (PCA) is a well-known method for extracting the latent structure behind observed variables. Its restriction is that PCA is mainly suitable for continuous variables. By mixed-type data, we mean that some variables are continuous with values ranging on the real line, some are restricted to positive values, some are counts (natural numbers) and some are binary.

We propose a model-based PCA-type method for mixed-type data. It is based on assuming a parametric distribution for the observations, where the parameter is dependent on a latent variable. The method gives a way to interpret the latent variable scores and loadings between observed and latent variables. Sparsity can also be added to the proposed method using techniques similar to sparse PCA.

The presentation consists of introducing the method, showing simulations comparing popular methods and a real data example of an analysis using the proposed method.

Tuesday 2
11:00-12:30
Lecture room U3041

Maximum Likelihood Estimation of a Likelihood Ratio Ordered Family of Log-Concave Densities

Philip Stange
University of Bern

Imposing a nonparametric shape constraint such as log-concavity has proven to be a useful regularization technique and a powerful alternative to classical smoothness constraints. Building on this idea, we study the problem of estimating a likelihood ratio ordered family $(f_x)_{x \in \mathcal{X}}$, where $\mathcal{X} \subset \mathbb{R}$ is fixed, of log-concave probability densities based on samples $(X_1, Y_1), \dots, (X_n, Y_n)$. Conditional on the X_i , the Y_i are assumed independent with density f_{X_i} . Our approach follows the maximum likelihood (Kullback-Leibler minimization) paradigm, under which we establish the existence and uniqueness of the maximum likelihood estimator. In particular, the log-concavity constraint is essential to guarantee boundedness of the likelihood function. The estimator can be computed via a variant of the pool-adjacent-violators algorithm. We evaluate its predictive performance, in terms of the continuous ranked probability score (CRPS), and compare it with other isotonic distributional regression approaches. To enable this comparison, we also discuss interpolation procedures that preserve both the likelihood ratio order and log-concavity.

Pseudo-likelihood approach for univariate normal mixture models

Kristi Kuljus
University of Tartu

Tuesday 2
11:00-12:30
Lecture room U3041

We consider a new approach for parameter estimation in univariate normal mixture distributions. The proposed method combines distance-based parameter estimation with maximum likelihood estimation, and is therefore referred to as a pseudo-likelihood approach. In the pseudo-likelihood approach, the weights of the mixture components can be considered as functions of mixture component means and standard deviations. The proposed method has two main advantages in comparison to the traditional likelihood approach: 1) the pseudo-likelihood is always bounded from above, thus the global maximum exists; 2) since the mixture weights are functions of component means and standard deviations, the number of estimated parameters is reduced, which may play an important role in models with many mixture components.

The pseudo-likelihood estimator is strongly consistent. We present simulation examples to demonstrate the behaviour of the proposed method in different situations in comparison to other parameter estimation methods. It is interesting to observe that in some models, where it is more difficult to separate the components and the number of components is large, the pseudo-likelihood method beats the maximum likelihood method even for large sample sizes.

This is a joint work with Jüri Lember and Raul Kangro.

The windowEM algorithm

Carsten Wiuf
University of Copenhagen

Tuesday 2
11:00-12:30
Lecture room U3041

A stochastic version of the EM algorithm (called **windowEM**) is proposed based on averaging parameter estimates within a rolling window. The motivation is to do inference on very large-scale genetics data with latent variables. In this setting, where the dataset potentially comprises billions of data points, the standard EM algorithm becomes impractical since it makes use of all data in each iteration. A particular issue is to keep data out of RAM as this drastically speeds up convergence.

Similar to other stochastic EM algorithms, **windowEM** splits data randomly into blocks. However, in the **windowEM** algorithm, these blocks are placed on a circle. Inspired by Polyak-Ruppert averaging, estimates are then averaged over a rolling window of blocks on this circle. The effect of this windowing is to produce a sequence of *dampened estimates*, counteracting the aforementioned noise, while still allowing frequent updates and fast convergence. For block k , a preliminary estimate is obtained by performing one iteration of the standard EM algorithm with data from block k , using the estimate of the previous block k as input value. A final estimate is obtained by averaging all estimates in the window.

Furthermore, we investigate the convergence properties of the **windowEM** algorithm. We distinguish two cases, depending on the number of blocks B : B is finite, and B is infinite.

In the first case, the whole data is repeatedly used to update parameter estimates in a circular manner. In effect, this yields a population of B block estimates. We show that a fixed point exists for one block if and only if a fixed point exists for all blocks. A single estimate might be obtained by averaging over all B estimates.

In the second case, the number of blocks is considered so large that we never see the same block twice. We give conditions under which convergence of estimates occur to a fixed point (for large block indices), based on random function iteration theory for dependent data. A single combined estimate might be obtained by taking the average of block estimates, and we give conditions that guarantee convergence of this average in the limit as $B \rightarrow \infty$.

Having a population of estimates rather than a single ‘best’ estimate might give a better idea about the true parameter. The window size determines how much variation in the estimates is allowed. In concrete applications in genomics, we have shown that when estimating the site frequency spectrum (SFS) of the rarer allele in large samples, averaging across a window smooths out the estimate of the SFS, contrary to maximum likelihood estimation that leaves ‘bump’ in

the SFS spectrum because of rare events that artificially raises an estimated frequency. `windowEM` might therefore also be a tool to prevent over-fitting.

Tuesday 2
11:00-12:30
Lecture room U3043

Sparsifying Transform Priors in Gaussian Graphical Models

Marcus Gehrmann

Norwegian University of Science and Technology (Norway)

In Gaussian Graphical Models (GGMs) we assume data to follow a Gaussian distribution, where the precision matrix has a zero structure in accordance with a conditional independence graph. In Bayesian structure learning, a joint prior is assigned to the graph and the precision matrix, yielding a corresponding posterior distribution when conditioning on data. The parameters are inferred by generating samples from the posterior distribution with Markov chain Monte Carlo (MCMC). Historically, the most common choice for the prior is to assign a suitable prior to the conditional independence graph and let the precision matrix conditioned on the graph follow a so called G-Wishart distribution. The G-Wishart distribution is conjugate to the Gaussian likelihood, but lacks a closed form expression for the normalizing constant. This gives rise to the problem of *double intractability* in the updating step of the MCMC algorithm.

We propose a new family of priors for the precision matrix, termed Sparsifying Transform priors, where a realization from this prior is obtained by applying a sparsifying transform on a sample from a distribution with support in the set of full positive definite matrices. When performing inference, we make use of auxiliary variables by having a parameter set that consists of a full matrix in addition to the graph. The precision matrix, that is needed for evaluation of the likelihood, is then given by said transformation of the full matrix. The prior distribution for the full matrix is specified in such a manner that the prior for the precision matrix coincides with the prior from the proposed family that we have specified. In addition, the full matrix and the conditional independence graph are specified to be a priori independent. In this way, the problem of double intractability is avoided. We carry out numerical experiments that are compared to results obtained with G-Wishart based algorithms from the literature, where our algorithm shows satisfactory results in terms of convergence and mixing.

Tuesday 2
11:00-12:30
Lecture room U3043

Intrinsic Gaussian fields on metric graphs

Joao Cordeiro^{*1}, David Bolin¹, Alexandre Simas¹ and Jonas Wallin²

¹King Abdullah University of Science and Technology (Saudi Arabia) and ²Lund University (Sweden).

^{*}Speaker, corresponding author

Intrinsic random fields play a central role in spatial statistics, providing flexible models for structured dependence, for example, as latent priors in hierarchical models. The increasing interest in network-structured data motivates the extension of such objects to compact metric graph domains. However, this endeavour poses significant challenges, as the topologies along networks may substantially diverge from those on classical surfaces. To address these challenges, we define intrinsic Gaussian fields on metric graphs as the solutions u of the stochastic partial differential equation

$$(-\Delta_\Gamma)^{\alpha/2} u = \mathcal{W}$$

on a compact metric graph Γ , where $\alpha > 1/2$ is a smoothness parameter, Δ_Γ is the Kirchhoff-Laplacian, and \mathcal{W} denotes Gaussian white noise.

Existence, uniqueness, and regularity results are exhibited. Considering the particular case $\alpha = 1$, by establishing Markov properties, we show that the finite-dimensional distributions coincide with those of polynomial intrinsic Gaussian Markov random fields of order 1 (IGMRF).

As an application, we propose a structured regression method on networks with intrinsic priors. The Markov structure of the IGMRF enables us to construct a sparse precision matrix, yielding computational efficiency and scalability. Numerical experiments to assess and demonstrate the efficacy of the method are presented as well.

Maximum local statistics in the random binomial graph

Matas Šileikis
Vilnius University

Tuesday 2
13:30-15:00
Lecture room F4050

Maximum degree of the random binomial graph $G(n, p)$ was thoroughly studied by Ivchenko (1973) and Bollobás (1980). We consider the following generalization of the maximum degree. For a fixed rooted tree T , let X_v be the number of copies (injective homomorphisms) of T into $G(n, p)$ such that the root of T is mapped to a vertex v . This is also a special case of so-called extension counts, introduced by Spencer (1990).

We investigate where the maximum of X_v over all vertices is concentrated. For $p = p(n)$ tending to zero not too fast, we show that the maximum is asymptotically attained by the vertex of maximum degree. That is, if the maximum degree is concentrated at value $D = D(n, p)$, then $\max_v X_v$ is concentrated at $D^d (pn)^{e(T)-d}$, where d is the degree of the root in T . However, for smaller p , the maximum is concentrated at a value of higher order and the answer crucially depends on the structure of T . We illustrate this by treating fully the case when T is a path rooted at one end.

This is joint work with Pedro Araújo, Simon Griffiths and Lutz Warnke.

Stochastic averaging processes on graphs

Timo Vilkas
Lund Universitet (Sweden)

Tuesday 2
13:30-15:00
Lecture room F4050

There is a growing range of stochastic processes on graphs which feature local updates in the form of pairwise averaging. I will shortly introduce three prominent examples (compass model, edge-averaging process and Deffuant-Weisbuch model) and with their help highlight the different regimes in long-term behavior one can expect: Disagreement on the one hand, local and global consensus on the other. While the picture is fairly clear for the former two, there are still wide open questions when it comes to the limiting behavior of bounded-confidence models (e.g. Deffuant-Weisbuch).

This talk is based on joint work with Nina Gantert and Markus Heydenreich.

Fringe trees in Split Trees

Cecilia Holmgren
Uppsala Universitet (Sweden)

Tuesday 2
13:30-15:00
Lecture room F4050

Split trees were introduced by Devroye (1998) as a novel approach for unifying many important random trees of logarithmic height. They are interesting not least because of their usefulness as models of sorting algorithms in computer science; for instance, the well-known Quicksort algorithm (introduced by Hoare [1960]) can be depicted as a binary search tree (which is one example of a split tree).

In this talk we study so-called fringe trees in split trees and in so-called fractional split trees (a novel model which we introduce where the components in the split vector does not need to sum up to 1). A fringe tree is a node together with all its descendants. We will study sums of functions of fringe trees, which are called additive functionals. These additive functionals are quite general and can describe e.g. the number of nodes (which is often a random number in split trees), number of leaves, the number of fringe trees of a certain size and the number of fringe trees isomorphic to a given tree T . In the talk I will discuss some of our results on these additive functionals in split trees and fractional split trees. In particular I will discuss our results on the expected value and weak law of large numbers for these additive functionals. Our methods are mainly based on renewal theory and analysis of Fourier series, which I will briefly discuss.

Joint work with Jasper Ischebeck and Svante Janson

Tuesday 2
13:30-15:00
Lecture room F3020

Complexity bounds for Dirichlet process slice samplers

Beatrice Franzolini

University of Milano-Bicocca and Bocconi University (Italy)

Slice sampling is a standard Monte Carlo technique for Dirichlet process (DP)–based models, widely used in posterior simulation. However, formal assessments of the scalability of posterior slice samplers have remained largely unexplored, primarily because the computational cost of a slice-sampling iteration is random and potentially unbounded. In this work, we obtain high-probability bounds on the computational complexity of DP slice samplers. Our main results show that, uniformly across posterior cluster-growth regimes, the overhead induced by slice variables, relatively to the number of clusters supported by the posterior, is $O_P(\log n)$. As a consequence, even in worst-case configurations, superlinear blow-ups in per-iteration computational cost occur with vanishing probability. Our analysis applies broadly to DP–based models without any likelihood-specific assumptions, still providing complexity guarantees for posterior sampling on arbitrary datasets. These results establish a theoretical foundation for assessing the practical scalability of slice sampling in DP-based models.

Tuesday 2
13:30-15:00
Lecture room F3020

Bayesian Multiresolution Functional Regression and Clustering via Self-Truncating Cumulative Shrinkage Processes

Francesco Denti

University of Padua (Italy)

We introduce a Bayesian multiresolution framework for functional data analysis designed to capture locally varying complexity. Similar to standard approaches, our model expresses each function as a sum of layers with increasing flexibility, where each layer is constructed using a basis expansion (such as B-splines) and gains higher resolution at deeper levels. By employing spike-and-slab Lasso priors, the model adaptively activates basis coefficients, allowing each layer to focus on specific regions and facilitating a clear distinction between smooth and highly variable parts of the function. To achieve ordered shrinkage across layers, we propose the Self-Truncating Cumulative Shrinkage Process (ST-CUSP): a prior that controls the number of active layers in the model. ST-CUSP generalizes the original Cumulative Shrinkage Process by introducing a probabilistic self-truncation mechanism, which discourages redundant layers through spike-and-slab distributions on the stick-breaking variables. This approach encourages parsimony and interpretability, while preserving the adaptive shrinkage behavior of the original CUSP. Additionally, we extend the prior to a partially exchangeable framework, allowing for nested clustering of functions based on their complexity, as measured by the number of active layers. Despite its flexibility, the model remains tractable, enabling straightforward derivation of full conditionals, efficient Gibbs sampling, and structured variational inference. Simulations across various complexities and noise levels show that ST-CUSP provides competitive estimation accuracy while activating significantly fewer layers than the original CUSP. We further demonstrate the method’s practical utility and interpretability by applying it to several real-world datasets from diverse domains.

Hierarchical additive interaction modelling with Gaussian process prior and its efficient implementation for multidimensional grid data

Sahoko Ishida
University of Oxford

Tuesday 2
13:30-15:00
Lecture room F3020

Additive Gaussian process (GP) models offer flexible tools for modelling complex non-linear relationships and interaction effects among covariates. While most studies have focused on predictive performance, relatively little attention has been given to identifying the underlying interaction structure, which may be of scientific interest in many applications. In practice, the use of additive GP models in this context has been limited by the cubic computational cost and quadratic storage requirements of GP inference. This paper presents a fast hierarchical additive interaction GP model for multi-dimensional grid data. A hierarchical ANOVA decomposition kernel forms the foundation of our model, which incorporate main and interaction effects under the principle of marginality. Kernel centring ensures identifiability and provides a unique, interpretable decomposition of lower- and higher-order effects. For datasets forming a multi-dimensional grid, efficient implementation is achieved by exploiting the Kronecker product structure of the covariance matrix. Our contribution is to extend Kronecker-based computation to handle any interaction structure within the proposed class of hierarchical additive GP models, whereas previous methods were limited to separable or fully saturated cases. The benefits of the proposed approach are demonstrated through simulation studies and an application to high-frequency nitrogen dioxide concentration data in London.

Formal graphical statistics: The power of visualization in statistical tests and beyond

Mari Myllymäki

Natural Resources Institute Finland (Luke); Dept. of Mathematics and Statistics, University of Helsinki

Tuesday 2
13:30-15:00
Lecture room F3005

Global envelopes are useful for formal testing of various hypotheses using functional or multivariate statistics when interpretation of the test results is of key interest, for determining central regions of functional or multivariate data, and also for determining confidence or prediction bands. In this talk, I describe the global envelopes, illustrate the methodology on different applications including the functional general linear model and distributional tests and show examples of the usage of the R package GET (Myllymäki and Mrkvička, 2024) that implements global envelopes. Further, I discuss the multiple testing correction in the global envelope tests for functional test statistics, which are discretized to m highly correlated hypotheses. While we first developed the global envelopes to control the family-wise error rate (Myllymäki et al., 2017), also control of false discovery rate can be introduced (Mrkvička and Myllymäki, 2023).

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Semi-supervised group testing for point patterns

Martin Voigt Vejling

Dept. of Mathematical Sciences & Dept. of Electronic Systems, and Aalborg University, Denmark

Biscio et al. (2025) introduced the concept of conformal novelty detection, see Marandon et al. (2024), to the context of replicate point patterns. A semi-supervised setting was considered, in which a calibration sample consisting of point patterns labelled as inliers was observed, and the objective was to detect novelties in a test sample of point patterns. Their methodology relied on parametric data augmentation using conformal scores defined through global envelopes, see Myllymäki et al. (2017). In this presentation, we improve the methodology along two directions: (i) using adaptive conformal scores yielding more powerful tests, and (ii) presenting a flexible framework for non-parametric data augmentation based on Brochard et al. (2022). Additionally, we explore a group testing scenario, often occurring in medical datasets, with a calibration sample of point patterns consisting of both labelled inliers and outliers, motivating the use of techniques similar to Huo et al. (2025). Under weak conditions, this framework yields conformal p-values, hence, adaptive Benjamini-Hochberg procedures provide false discovery rate control. The methodology is compared to that of Biscio et al. (2025) and applied to two medical datasets.

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Estimation of intensity with small scale repulsion and medium scale clustering for river flow

Daniel Rolandsgard Kjellevoid

Norwegian University of Science and Technology - NTNU

In water flow, many interesting properties are found near the surface. One such property is the heat-mass transfer between the river and the atmosphere. However, this quantity is not easy to measure in the field. As a proxy, we utilize easily observable surface features - called dimples and scars - to do inference on properties of the flow near the surface.

We regard spatial patterns of dimples and scars, sampled with sufficiently large time intervals, as independent realizations of the same spatial point process. The dimples and scars show clustering behavior at medium scale, but physical restrictions mean they show hard-core repulsion at small scales. We model the patterns of dimples and scars using a *Matérn Thinned Variance Gamma Cluster Process*. Here the dependent Matérn thinning mechanism is used to model small scale repulsion which is not available for the original variance gamma process. While the model is easy to specify, closed form theoretical expressions for first and second order summary statistics are intractable.

The main contribution of our work is inference on the model parameters where we propose to estimate parameters using a simulation based minimum contrast estimation procedure, which has not previously been applied to Matérn thinned Cox processes. In this regard we introduce a novel form of importance sampling to enhance computational efficiency.

We finally link parameter estimates to physical properties of the flow. We present results based on both numerically simulated and experimental datasets.

Maximum spacing estimation under model misspecification

Han Bao

Tartu University (Estonia)

Tuesday 2
13:30-15:00
Lecture room F3017

Maximum spacing (MSP) method is a parameter estimation method for continuous distributions based on spacings. It offers two main advantages over maximum likelihood estimation: 1) it is applicable in situations where the maximum likelihood approach can fail (for example, when the likelihood function is unbounded like in normal mixture distributions); 2) it can be applied with different information-type divergence measures (for example, the Kullback-Leibler information measure, the Hellinger distance, Jeffreys' divergence, Rényi's divergence) yielding estimators with different properties. This flexibility of obtaining MSP estimators with varying properties is particularly useful for detecting model misspecification.

We consider MSP estimation for multivariate observations under model misspecification. A broad class of MSP estimators is studied, including the MSP estimator corresponding to the Kullback-Leibler information measure obtained with the logarithmic function, which enables direct comparison with maximum likelihood estimators. Under model misspecification, the MSP estimator converges to a well-defined limit that depends on the chosen divergence measure; this establishes consistency.

We explore the behaviour of MSP estimator under different divergence measures using simulation studies and demonstrate how their asymptotic properties can be exploited to detect model misspecification in sufficiently large samples. The results indicate that estimators based on the Kullback-Leibler information are sensitive to perturbations and outliers, whereas those based on Rényi's divergence and the Hellinger distance are quite robust. Finally, we illustrate the application of the MSP method to model validation using a real data example.

This is a joint work with Kristi Kuljus and Bo Ranneyby.

From Hypothesis Testing to Formal Proof: Disproving a Claimed G-Wishart Sampler

Hanna Bu Kvaløy

Norges Bank / Norwegian University of Science and Technology

Tuesday 2
13:30-15:00
Lecture room F3017

When faced with a proposed simulation algorithm claiming to produce exact samples from a specified target distribution, but whose correctness is uncertain, how should one proceed? Ideally, one would either prove correctness or find a counterexample. However, trying to prove correctness of a potentially incorrect proposed algorithm is unappealing, as is trying to prove incorrectness by constructing a counterexample when the proposed algorithm may be correct. A natural first step is empirical validation. Only if this provides strong evidence of incorrectness does constructing a formal counterexample become worthwhile. This work demonstrates this approach through a concrete application.

We formulate a hypothesis test where the null hypothesis is that the proposed algorithm generates correct samples from the specified target distribution $p(\cdot)$. We generate multiple samples from the proposed algorithm and use each to initialize a Metropolis-Hastings chain fulfilling detailed balance with respect to the target distribution $p(\cdot)$. The test exploits a fundamental property: if we run each chain for a fixed number of updates, the initial and final states are exchangeable if and only if the sampler is correct. Combining this property with a permutation test on these pairs of initial and final states yields a valid p-value.

Our main motivation for considering the above discussed situation is a simulation algorithm that is proposed in the literature, and that is claimed to generate exact samples from the G-Wishart distribution. The G-Wishart distribution, defined for a given graph structure, is the conjugate prior for precision matrices in Gaussian graphical models. The proposed algorithm claims to efficiently generate exact samples, a significant advancement if correct. It has since been incorporated into several Bayesian structure learning methods, widening its potential impact. However, it is presented with limited theoretical justification. Applying our hypothesis test across multiple graph

structures yields extremely low p -values (often below 10^{-6}), providing strong empirical evidence that the algorithm does not generate samples from the G-Wishart distribution.

The hypothesis test provides overwhelming empirical evidence of incorrectness, making it worthwhile to pursue a formal proof. To this end, we construct a counterexample by deriving the exact probability density induced by the proposed algorithm for a simple three-node graph and strategically chosen parameters. By computing density ratios evaluated at carefully selected arguments, we demonstrate explicit disagreement with the true G-Wishart distribution, providing definitive proof that the proposed algorithm does not generate exact samples from the specified target G-Wishart distribution.

Transformed gradient based boosting

Taariq Nazar
Stockholm University

This work introduces a boosting method based on transformed gradients (TGB), a framework encompassing standard gradient boosting machines (GBMs), NGBoost, and XGBoost as special cases. For the TGB method, we derive explicit sufficient conditions to guarantee in-sample loss improvement and convergence for general base learners. When applied to regression trees, this framework provides alternative proofs of in-sample loss improvement and convergence for both GBMs and XGBoost. Furthermore, our theoretical results demonstrate that NGBoost is not guaranteed to converge unless weighted regression trees are utilized. By introducing weighted regression trees into the NGBoost procedure, we reveal that this adjusted method functions as a variant of XGBoost where the Hessians are replaced by their corresponding expected Fisher information matrices. Finally, we analyze the maximum likelihood estimation of exponential dispersion family (EDF) models, detailing the effects of combining these models with natural gradients and NGBoost.

Tuesday 2
13:30-15:00
Lecture room U3041

Unsupervised domain adaptation beyond label shift

¹Mohammad Ghasempour, ¹Xavier de Luna and ²Yanyuan Ma

¹Department of Statistics, School of Business, Economics and Statistics, Umeå University and

²Department of Statistics, Pennsylvania State University

Consider the motivating example where we have K cohorts (source labelled datasets) born in consecutive years $k = 1, \dots, K$, and a target unlabelled cohort τ born in year $K + 1$. Labels Y are the number of days of hospitalization of an individual in any of the cohorts the year that s/he turns 80 years of age. Because cohort τ is 79 years of age we do not have their labels. We, however, want to estimate $E_\tau(Y)$ for this cohort, engaging labels in all other cohorts and covariates \mathbf{X} available for all datasets. This type of situation falls into the realm of unsupervised domain adaptation. We introduce and study a framework beyond label-shift to perform inference on $E_\tau(Y)$ as well as more general target estimands. We leave the density functions $f_{k,Y|\mathbf{X}}(y, \mathbf{x})$ unspecified in all cohorts, while allowing for a conditional shift from one cohort to another, whereby $f_{k+1,\mathbf{X}|Y}(\mathbf{x}, y)$ is modelled as an exponential tilt of $f_{k,\mathbf{X}|Y}(\mathbf{x}, y)$. We give conditions for identification of the target estimand, deduce the efficient influence function and thereby propose semiparametric estimators, which are \sqrt{n} -consistent, asymptotically normal and locally efficient. Several nuisance functions need to be estimated and we propose feasible and robust estimators allowing for the simultaneous misspecification of three of these nuisance functions. The implementation of the estimators is supplied to complement the proven asymptotic theory and to illustrate the finite sample performance of the estimators and their inference.

Key words: Domain adaptation, efficient influence function; label shift; robustness.

Automatic Online Changepoint Detection with Recurrent Neural Networks

Sebastian Grau Nielsen
University of Oslo

Tuesday 2
13:30-15:00
Lecture room U3041

Online changepoint detection is the task of detecting distributional changes in time series data observed in real time. This problem imposes strict demands on the computational complexity of algorithms, since the current observation needs to be processed before the next one arrives. Recently, feedforward neural networks have attracted interest for changepoint detection in the offline (non-sequential) setting. In the online setting, however, these approaches may fail because they are non-sequential and may thus be highly computationally expensive. In this work, we propose a class of recurrent neural networks (RNNs) for online changepoint detection that are inherently sequential, and we show that multiple well-known grid- and window-based statistical tests can be represented as simple RNNs. Leveraging these representations, we present theoretical results that give high-probability bounds on the error rate and detection delay of our trained RNN classifiers. These bounds imply that, with sufficient data, a trained RNN will have a performance that is comparable with these statistical methods when their underlying assumptions are fulfilled. In numerical experiments, we show that our RNNs perform on par with state-of-the-art online statistical algorithms under independent Gaussian noise. Under autocorrelated and heavy-tailed noise, our RNNs appear to significantly outperform these methods. Finally, we present an analysis of the runtimes and show that the runtime of RNN changepoint detection is competitive with existing methods.

This is joint work with Idris Eckley (University of Lancaster), Ingrid Glad (University of Oslo), Martin Tveten (Norwegian Computing Center), Michael Kampffmeyer (UiT The Arctic University of Norway), and Per August Jarval Moen (University of Oslo).

Model-Based Functional Clustering with Correlated Measurement Errors

Rana Bamdadi, Sara Sjöstedt de Luna, Per Arnvqvist and Natalya Pya Arnvqvist
Umeå University (Sweden)

Tuesday 2
13:30-15:00
Lecture room U3043

Functional data analysis focuses on data where each observation is represented as a continuous function. Clustering such data aims to identify homogeneous groups of curves while accounting for their infinite-dimensional structure. Model-based functional clustering assumes that observations are generated according to a mixture distribution with G components (clusters). Arnvqvist and Sjöstedt de Luna (2019) propose a flexible model-based framework that allows for cluster-specific mean and covariance structures, as well as the inclusion of covariates, with parameter estimation carried out via the EM algorithm. In this work, we extend this framework by incorporating correlated measurement errors within each curve. In particular, the error is modelled using a Gaussian process with an exponential covariance structure. We also investigate simplified representations of the covariance structures (based on a diagonalisation approach), aimed to improve computational efficiency without loss of information. To improve computational efficiency, we investigate a simplified representation of the covariance structure based on a diagonalisation approach. To investigate the impact of modelling error dependence, we conduct simulation studies under varying levels of correlation, signal-to-noise ratios, and sample sizes. The results show that accounting for dependence in the error structure can improve clustering stability and classification accuracy, particularly in settings with stronger correlation and higher noise levels. The study is motivated by functional data arising from varved lake sediment records from Lake Kassjön in northern Sweden. The obtained results highlight the importance of incorporating dependence structures when applying model-based clustering methods to functional data.

Local inference for functional time series

Helle Sørensen

University of Copenhagen (Denmark)

Local inference is a technique in functional data analysis where hypotheses are tested along the domain of the functional data—in principle involving infinitely many tests. The multiple testing problem is addressed by performing tests over intervals and exploiting the continuity of the data. In this talk we consider local inference for the situation where data is a time series with each data unit being a curve. We approach two questions: (1) In which parts of the functional domain is there dependence in the time series, and (2) how can local inference for hypotheses concerning fixed effects be carried out in the presence of dependence? Our tests are based on permutations and are thus non-parametric of nature. As an application we consider data consisting of daily ice cover in the Baffin Bay in the period from 1979 to 2023.

Markov Regime-Switching Models with Time-Varying Transition Probabilities: A Monte Carlo Study and Application to U.S. Treasury Yield Changes

Samuel Modée

University of Bergen (Norway)

Markov regime-switching models with time-varying transition probabilities (TVTP) allow the likelihood of regime changes to respond to economic conditions, which can improve turning-point detection and forecasting over constant-probability specifications. While Bazzi et al. (2017) developed a score-driven framework for updating transition probabilities and validated it via Monte Carlo simulation, their study was restricted to $K = 2$ regimes with a common variance. This setting is considerably simpler than the many regime structures commonly encountered in empirical macroeconomics and finance.

We extend the analysis to $K \geq 3$ regimes with regime-specific variances and conduct a comprehensive Monte Carlo study building on the TVTP frameworks of Diebold et al. (1994), Filardo (1994), and Creal et al. (2013). We compare three TVTP specifications:

- (I) Transition probabilities driven by the lagged dependent variable,
- (II) Transition probabilities driven by exogenous covariates,
- (III) Score-driven dynamics based on the predictive likelihood.

All three specifications are evaluated in terms of parameter recovery, coverage rates, forecast precision, and filtered probability accuracy across nine data-generating processes, under both correct specification and systematic cross-model misspecification.

Our results show that distribution parameters are generally well recovered in the three-regime setting, with performance varying across specifications, while the TVTP driving coefficients require larger samples ($T = 1000$) for acceptable precision. Coverage rates for transition probabilities under TVTP models fall systematically below nominal levels for $K = 3$, suggesting that alternative standard error procedures may be warranted. Point forecast accuracy is robust to the choice of TVTP specification across all three models, extending this conclusion from the two-regime setting of Bazzi et al. (2017) to $K = 3$.

We apply the three-regime models to U.S. Treasury zero-coupon yield changes (Liu and Wu, 2021) across four maturities spanning the yield curve, using monthly data from 1961 to 2024. All methods are implemented in a modular, open-source R package supporting general K -regime TVTP estimation.

Topological Data Analysis for Goodness-of-Fit Testing in Spatial Statistics

Chiara Fend

Department of Mathematics, RPTU University Kaiserslautern-Landau (Germany)

Wednesday 3
11:00-12:30
Lecture room F4050

Spatial statistics focuses on analyzing spatial data coming from random phenomena with complex dependencies such as the positions of trees in a forest or the microstructure of a material. The model validation of stochastic models for these phenomena has seen many advances in recent years in particular in terms of goodness-of-fit (GoF) testing using functional summary statistics. Classical summary statistics often fail to distinguish complex higher-order dependencies and subtle topological properties that are present in the data.

Topological Data Analysis (TDA) addresses this by quantifying shape-based properties (e.g., connectivity, holes) in data. Using persistent homology, TDA allows us to extract multiscale topological descriptors that are robust to noise and invariant to deformations. This makes TDA ideal for characterizing complex spatial interactions.

In this talk, we present how TDA can be incorporated into a general framework for GoF testing in spatial statistics, covering both point processes and random tessellations. For both types of structures we explain how we can build a filtration of topological spaces that captures the multiscale properties. In particular our proposed filtration for the tessellation takes the geometry of the structure into account. From these filtrations we then extract functional topological summary statistics that can be used individually or in combination with classical summary statistics in GoF tests.

Through an extensive simulation study for planar point processes, we demonstrate which types of test statistics are suitable when working with topological characteristics in Monte Carlo tests. Additionally our study shows that the combination of topological and classical characteristics yields more powerful tests in comparison to the classical GoF tests.

Nonparametric testing of covariate significance for spatial point patterns

Jiří Dvořák

Faculty of Mathematics and Physics, Charles University, Prague (Czech Republic)

Wednesday 3
11:00-12:30
Lecture room F4050

In this talk, we discuss the problem of deciding which covariates influence the distribution of a point process. Before formulating a parametric model including all available covariates, it is useful to try reducing the number of covariates by discarding the unnecessary ones. Deciding which covariates should be included in the analysis is a complicated task, especially in the case of correlated covariates. We describe a nonparametric way of determining the significance of individual covariates, under the presence of nuisance covariates. The method is based on random shifts, which constitute a popular approach to testing independence of two spatial objects (random fields, point processes, random measures) in a nonparametric way. It is based on randomly shifting one of the objects while keeping the other one fixed. This breaks the possible spatial dependence between the objects without affecting the marginal distributions, allowing to study the distribution of the chosen test statistic under the null hypothesis of independence.

Wednesday 3
11:00-12:30
Lecture room F4050

Exploring local diversity in large, heterogeneous point patterns

Tuomas Rajala

Natural Resources Institute Finland, Luke (Finland)

Large, heterogeneous point pattern datasets, with millions or billions of points, are becoming commonplace. For example, all trees can be located nationally using remote sensing, and all cells can be located in a tissue sample using medical multi-imaging. The need to summarize and analyze such diverse datasets is therefore also increasing. For the practitioners dealing with large, heterogeneous point pattern data, not many useful statistical methods are available, especially of the kind that are easy, fast and reliable to compute. In this talk, we address this topic by studying diversity indices for heterogeneous marked point patterns. With example data from forestry and spatial biology, we discuss what local versions of diversity indices can be, how they can be estimated, and how they can be used in data exploration and discovering areas of exceptional diversity.

Wednesday 3
11:00-12:30
Lecture room F3020

Inference on the maximal rank of time-varying covariance matrices using high-frequency data

Markus Reiß

Humboldt-Universität zu Berlin

We study the rank of the instantaneous or spot covariance matrix of a multidimensional continuous semi-martingale. Given high-frequency observations, we test the null hypothesis that the rank of the spot covariance matrix is at most r , uniformly on the observation interval, against local alternatives where the average $(r + 1)$ st eigenvalue is larger than a signal detection rate. A major problem is that the inherent averaging in local covariance statistics produces a bias that distorts the rank statistics. We show that the bias depends on the regularity and a spectral gap in the covariance. Using matrix perturbation and lower bounds for the minimal eigenvalue of non-i.i.d. Wishart matrices, non-asymptotic uniform critical values and optimal signal detection rates are derived. The methods are illustrated by simulations and an application to high-frequency data of U.S. government bonds.

Wednesday 3
11:00-12:30
Lecture room F3020

Concentration and moment inequalities for heavy-tailed random matrices

Moritz Jirak

University of Vienna

Fuk-Nagaev and Rosenthal-type inequalities are proven for the sums of independent random matrices, focusing on the situation when the norms of the matrices possess finite moments of only low orders. The bounds depend on the intrinsic dimensional characteristics, such as the effective rank, as opposed to the dimension of the ambient space. The advantages of such results are illustrated in several applications, including new moment inequalities for sample covariance matrices and the corresponding eigenvectors of heavy-tailed random vectors.

Nonlinear shrinkage estimator for large covariance matrices with strong mean effects

Nestor Parolya

Delft University of Technology

Wednesday 3
11:00-12:30
Lecture room F3020

The aim of this paper is to develop a nonlinear shrinkage estimator for high-dimensional covariance matrices that explicitly incorporates the effects arising from the estimation of the population mean vector via its sample counterpart. The resulting nonlinear shrinkage formula differs fundamentally from the classical version. We analyze its asymptotic properties and derive a bona fide estimator. Surprisingly, the influence of the sample mean proves to be asymptotically non-negligible and must be taken into account when applying nonlinear shrinkage. We illustrate the practical relevance of our theoretical results in two settings - linear discriminant analysis and optimal portfolio selection - both of which typically involve estimation risk in the mean vector and the covariance matrix simultaneously.

Bayesian hidden Markov model with time-to-event emissions to risk-prediction modelling in cancer screening

Aapeli Nevala

University of Helsinki (Finland)

Wednesday 3
11:00-12:30
Lecture room F3005

Biphasic testing protocols with sub-100% sensitive primary test to detect asymptomatic disease state are widely applied in decision-making and testing scenarios. In this setting, we have a positive real primary test τ that is mapped into scale positive-negative with pre-specified cutoff as $\tilde{\tau} = \mathbb{I}\{\tau \geq \rho\}$. Positive primary test cannot confirm existence of a disease X , but it triggers a confirmation sequence that accelerates the eventual detection time of disease, T , with possible censoring δ . In our example scenario of cancer screening, these latent states become detected eventually, but later, in absence of primary testing. We propose a model using eventual detection times of cancer to predict the prevalence of the latent state of interest. We first describe a model for predicting initial screening round latent state prevalence, building a mixture model of X as $\sum_{X \in \{0,1\}} p(X | Z, \theta_1) p(\tau | Z, X, \theta_2) p(\tilde{\tau} | \tau) p(T, \delta | X, \tilde{\tau}, \theta_3)$. The model takes into account the accelerated detection due to screening. Then, we generalise the approach into a sequence of screening rounds using a discrete-time hidden Markov model, where the emission is multivariate with time-to-event component $Y_k = (\tau_k, \tilde{\tau}_k, T_k)$. The model parameters are estimated in Bayesian setting. We evaluate the estimation performance in a simulation study using two different estimation algorithm and estimate the model is estimated with real data, to show how Bayesian approach allows producing different relevant metrics for risk-prediction and real-world impact. This is a joint work with Tytti Sarkeala, Sirpa Heinävaara and Sangita Kulathinal. The work is under review currently, and we wish that the abstract would thus to be treated discreetly.

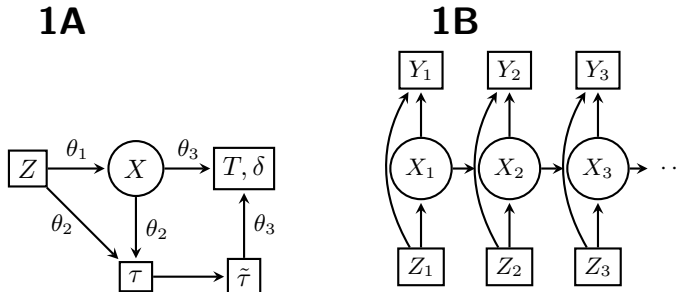


Figure 1: 1A: Dependence structure over over screening round. 1B: dependence structure accross multiple screening rounds.

Estimating mean lifetime from partially observed events in nuclear physics

Wednesday 3
11:00-12:30
Lecture room F3005

Salme Kärkkäinen

University of Jyväskylä (Finland)

In nuclear physics, particle detectors are used for estimating the lifetime of radioactive nuclei. There are several challenges in the observation of the lifetimes. First, the observation is based on the separate identification of the arrival and departure of single radioactive nuclei. Second, the arrival and departure are not matched. Third, on average the half of the departures is not observed. To solve these problems in practice, this means experiments with low arrival rates which is time-consuming. In our work, we tackle these issues by proposing an estimation method working for a wider range of arrival rates. We propose an initial estimator which is post-corrected by using a numerical bias correction technique. The method is evaluated by using simulation experiments.

This presentation is based on the joint work Karvanen, Niilo-Rämä, Saren & Kärkkäinen (2022).

Reference:

Karvanen, Niilo-Rämä, Saren & Kärkkäinen (2022). Estimating mean lifetime from partially observed events in nuclear physics. *Journal of the Royal Statistical Society, Series C*. 71:3–26. DOI: 10.1111/rssc.12519

Boruta-Based Variable Selection and Post-Estimation in High-Dimensional Regression: Theoretical Foundations and Simulation Evidence

Wednesday 3
11:00-12:30
Lecture room F3005

Reza Arabi Belaghi (Joint work with Hulya Yurekli)

Swedish University of Agricultural Sciences (Sweden)

Boruta is an increasingly popular all-relevant feature selection algorithm for high-dimensional data, particularly in settings with complex dependence structures and heterogeneous signals. Despite its strong empirical performance, its theoretical justification in regression settings remains limited.

This talk presents a novel high-dimensional justification for Boruta within a two-stage screen-then-shrink framework for beta regression. In the first stage, Boruta is used to screen predictors; in the second stage, the retained variables are combined with ridge-type shrinkage estimation to address multicollinearity and weak effects. Under mild regularity conditions—including sub-Gaussian fluctuations of random forest importance scores, a signal-gap condition, sparsity of the true active set, and bounded predictor correlations—we show that the Boruta screening stage satisfies a sure-screening property and controls false positives. Consequently, the post-screening model dimension is of order $O_p(n/\log n)$, and the second-stage estimator operates in an effectively low-dimensional regime and achieves oracle efficiency (Arabi Belaghi et al., 2026, *accepted*).

To place these theoretical results in a broader applied context, the talk also synthesizes evidence from two simulation studies of Boruta in logistic regression for variable selection. Across both low- and high-dimensional correlated settings, Boruta demonstrates high sensitivity to true signals, particularly under strong correlation. However, this sensitivity may be accompanied by over-selection relative to sparsity-oriented competitors such as LASSO, Elastic Net, and SCAD (Arabi Belaghi et al., under review; Arabi Belaghi and Yurekli, under review).

Applications to real datasets, including ovarian cancer miRNA data and prostate gene-expression data, further illustrate Boruta's practical utility for biomarker discovery and high-dimensional statistical learning. Overall, this presentation bridges new asymptotic theory with empirical evidence and clarifies when Boruta can be expected to serve as a principled and effective screening tool in modern high-dimensional regression.

Efficient Likelihood-free Sequential Monte Carlo Sampling Using Probabilistic Surrogate Loss

Henri Pesonen
Tampere University

Wednesday 3
11:00-12:30
Lecture room F3017

Likelihood-free inference (LFI) refers to techniques for inferring model parameters using simulations from complex models without relying on the analytic form of the simulator. In recent years, LFI has been significantly accelerated through the use of surrogate models that efficiently capture the relationship between parameters and observations, and leverage this information to select informative parameter values for querying the simulator. These surrogate-based LFI methods are often Bayesian, drawing posterior samples from an approximated posterior distribution. A flexible alternative to traditional Bayesian inference is the Generalized Bayesian Inference (GBI) framework, which relies on a highly general mechanism for updating parameter beliefs in light of observed data. The formulation of GBI makes it a natural complement to surrogate model-based LFI. We introduce a novel iterative algorithm that uses sequential Monte Carlo to simultaneously generate samples from the approximate generalized posterior and determine which parameter values should be queried to further improve the surrogate. This active learning strategy is guided by the uncertainty in Monte Carlo importance weights induced by the probabilistic surrogate models.

Max-and-Smooth: An approximate Bayesian inference scheme for latent Gaussian models with a multivariate link function

Birgir Hrafnkelsson
University of Iceland

Wednesday 3
11:00-12:30
Lecture room F3017

With modern high-dimensional data, complex statistical models are necessary, requiring computationally feasible inference schemes. We introduce Max-and-Smooth, an approximate Bayesian inference scheme for a flexible class of latent Gaussian models (LGMs) in which one or more likelihood parameters are modeled by latent additive Gaussian processes. Our proposed inference scheme is a two-step approach. In the first step (Max), the likelihood function is approximated by a Gaussian density with mean and covariance equal to the maximum likelihood estimate and the inverse observed information, respectively. In the second step (Smooth), the latent parameters and hyperparameters are inferred and smoothed with the approximated likelihood function. The proposed method ensures that the uncertainty from the first step is correctly propagated to the second step. The prior densities for the latent parameters and the approximated likelihood function are Gaussian. Thus, the approximate conditional posterior density of the latent parameters is also Gaussian, which facilitates efficient posterior inference in high dimensions, especially when the Gaussian prior density is specified with a sparse precision matrix. The approximate marginal posterior distribution of the hyperparameters is tractable; thus, the hyperparameters can be sampled independently of the latent parameters. The proposed inference scheme is demonstrated on three spatially referenced real datasets, namely, (i) average summer surface air temperature in Europe, (ii) flood frequency data from the UK, and (iii) extreme precipitation from the UK Climate Projections. A discussion on how dependence at the response level can be tackled will be given.

Fast Bayesian Filtering for High-Dimensional Nonlinear SDEs with Deep Density Models

Kasper Bågmark

University of Technology and University of Gothenburg (Sweden)

We propose deep density models for fast nonlinear Bayesian filtering in discretely observed, continuous-time stochastic differential equations (SDE). The filter is characterized by a prediction–update recursion: between observation times the (unnormalized) filtering density evolves according to a Fokker–Planck equation, while each new observation triggers a Bayesian reweighting. In high dimensions, likelihood-based density learning becomes numerically fragile because the filtering density can take extremely small values, leading to underflow and unstable training. To address this, we work with a log-density formulation (obtained via a reverse Cole–Hopf transform), which yields stable learning signals and a principled way to represent high-dimensional posteriors.

Methodologically, we exploit a nonlinear Feynman–Kac representation that expresses the prediction step through a forward backward stochastic differential equation (FBSDE). We approximate the resulting forward–backward systems with the deep BSDE method, producing an amortized filtering surrogate: after offline training, posterior quantities can be computed rapidly for new observation sequences. We provide theoretical guarantees in the form of a hybrid error bound in the number of discretization steps under a parabolic Hörmander condition on the underlying SDE.

We evaluate the approach against a deep splitting filter, extended/ensemble Kalman filtering, and particle filtering on linear and nonlinear benchmarks, including partially observed Lorenz–96 up to dimension 100. In this regime particle filters degrade, whereas the deep density approach remains stable. Empirically, we observe two to five orders of magnitude faster inference than particle filtering in high-dimensional settings, enabling scalable sequential Bayesian inference.

This is joint work with Adam Andersson, Stig Larsson, and Filip Rydin.

Pricing time-capped American options: simulations and exact results

Zbigniew Palmowski

Wrocław University of Science and Technology

This talk investigates the valuation of perpetual American put options under exercise constraints driven by a price-dependent random time. In particular, we examine the case where the optimal exercise time is limited by the first time when the asset experiences a drawdown exceeding a predetermined level.

Within the Black–Scholes framework, we derive an explicit pricing formula and show that the optimal exercise strategy is characterized by the first passage of the asset price below a critical threshold. We then extend the analysis to a more general setting in which the logarithm of the asset price follows a spectrally negative Lévy process. In this case, analytical results are obtained using martingale methods and the fluctuation theory of Lévy processes.

Finally, we implement a Least Squares Monte Carlo approach to compute option values numerically and illustrate our theoretical findings through a series of numerical experiments.

Quantitative discrete time hedging under initial insider information

Onni Hinkkanen

University of Jyväskylä (Finland)

Wednesday 3
11:00-12:30
Lecture room U3041

The problem of quantitative discrete time hedging within the Black-Scholes model has been intensively studied for many years. In this presentation we study this problem under initial insider information. To include non-smooth terminal conditions, which induce a blow-up of trading strategies, we use adapted, i.e. not equidistant, deterministic time-nets. It is well known that the best possible rate of the L_2 -hedging error in the setting without insider information is $n^{-1/2}$, when the number n of trading dates tends to infinity.

We investigate the question to what extent this convergence improves in the presence of insider information. Moreover, we compute the limit of the re-scaled L_2 -hedging error. Because of the insider information, the underlying stochastic analysis in order to treat this models changes, for example Skorohod integration has to be used. Examples using parametrized Black-Scholes PDEs are given.

This is joint work with Hannah Geiss and Stefan Geiss.

Network varying coefficient ridge regression

Samuel Rauhala, Joni Virta

Department of Mathematics and Statistics, 20014 University of Turku (Finland)

Wednesday 3
11:00-12:30
Lecture room U3041

Time Varying Parameter (TVP) regression models are common in time series econometrics. This paper generalizes the TVP framework for environments where parameters do not change only in time but in an arbitrary number of dimensions. The framework is flexible and represents each dimension as a separate network allowing for easy interpretation of the results. We derive a closed-form solution to the associated least squares problem, study conditions under which it exists, and show how the model can easily be modified to accommodate missing values. We build a bridge between state space models and graphs to provide the tools necessary for construction of informative networks. These methods are applied to study a time, location and commodity specific New-Keynesian Phillips Curve in the EU.

Beyond compositional validity: comparing distances for seemingly compositional data

Elle A. Saber

Australian National University

Wednesday 3
11:00-12:30
Lecture room U3043

Microbiome and community ecology data are often described as compositional because they convey relative abundance information. This has led to strong advocacy for log-ratio transformations of microbiome data and use of log ratio transformations and Aitchison distance when analysing this data. However, the prevalence of zeros in such data complicates the assumptions underlying standard compositional data analysis. For this reason such data are referred to here as ‘seemingly compositional’.

Alternative criteria for comparing candidate distances are proposed and applied to Aitchison, Euclidean, Jensen-Shannon, and Hellinger distances. The comparison combines visualisation approaches, simulation, and selected analytical results to examine how these distances behave, particularly near zeros. The results show that distances that appear attractive on compositional grounds can behave poorly under realistic sparse data conditions. In contrast, distances not traditionally considered ‘compositionally valid’, such as Jensen-Shannon and Hellinger distances, demonstrate more reliable statistical behaviour. Notably, the Jensen-Shannon distance emerges as a compromise between the extremes of Aitchison and Euclidean distances, exhibiting an unexpected similarity to the Hellinger distance.

These results have broad implications for practitioners in microbiome analysis, multi-omics, and ecological studies. Compositional validity alone is an insufficient criterion for distance selection, and that the behaviour of a distance under realistic data conditions, including zeros, must be part of the evaluation.

Wednesday 3
11:00-12:30
Lecture room U3043

Directional models based on projected Pólya trees

Luis E. Nieto-Barajas
ITAM (Mexico)

Projected distributions have proved to be useful in the study of circular and directional data. Although any multivariate distribution can be used to produce a projected model, these distributions are typically parametric. In this article we consider a multivariate Pólya tree on \mathbb{R}^k and project it to the unit hypersphere \mathbb{S}^k to define a new Bayesian nonparametric model for directional data. We study the properties of the proposed model and in particular, concentrate on the implied conditional distributions of some directions given the others to define a directional-directional regression model. We also define a multivariate linear regression model with Pólya tree errors and project it to define a linear-directional regression model. We obtain the posterior characterisation of all models via their full conditional distributions. Metropolis-Hastings steps are required, where random walk proposal distributions are optimised with a novel adaptation scheme. We show the performance of our models with simulated and real datasets.

Wednesday 3
11:00-12:30
Lecture room U3043

Partition-based discriminant analysis

Laura D'Angelo (Joint work with Bernardo Nipoti and Tommaso Rigon)
University of Milano-Bicocca (Italy)

We propose a Bayesian nonparametric framework that enhances classical discriminant analysis in settings characterized by limited sample sizes and high estimation uncertainty. The proposed method provides a flexible approach that encompasses both linear and quadratic discriminant analysis as special cases. This is accomplished through a scale-only nonparametric mixture model defined on the space of positive definite matrices. Within this framework, observations are modeled as Gaussian with class-specific mean vectors and covariance matrices that may be unique or shared across classes. The key innovation lies in allowing information sharing across classes, which improves the estimation of covariance matrices and stabilizes classification boundaries in small-sample regimes. A conjugate nonparametric prior ensures remarkable ease of implementation and tractability. This allows closed-form characterization of several posterior quantities of interest, including the induced partition of classes and the number of covariance clusters. The resulting methodology is straightforward to implement and avoids the need for numerical approximations. The tractability of the proposed model further enables theoretical investigation of its asymptotic behavior, providing insight into its large-sample properties. Through experiments on both simulated and real datasets, we demonstrate the adaptability and effectiveness of the proposed methodology.

On the forgetting of particle filters

Matti Vihola

University of Jyväskylä (Finland)

Wednesday 3
11:00-12:30
Lecture room U4078

We study the forgetting properties of the particle filter when its state — the collection of particles — is regarded as a Markov chain. Under a strong mixing assumption on the particle filter’s underlying Feynman–Kac model, we find that the particle filter is exponentially mixing, and forgets its initial state in $O(\log N)$ ‘time’, where N is the number of particles and time refers to the number of particle filter algorithm steps, each comprising a selection (or resampling) and mutation (or prediction) operation. We present an example which shows that this rate is optimal. We also establish new propagation of chaos type results using our proof techniques. Our forgetting result extends relatively directly to the conditional particle filter (CPF), once we establish new time-uniform L^p error estimates for CPF, which can be of independent interest. The talk is based on the article [1].

Reference:

[1] Joona Karjalainen, Anthnoy Lee, Sumeetpal S. Singh and Matti Vihola. *On the forgetting of particle filters*, arXiv:2309.08517. <https://arxiv.org/abs/2309.08517>

Lévy - Cox Branching Point Processes

Radu S. Stoica

Université de Lorraine, CNRS, IECL, Inria, F-54000 Nancy (France)

Wednesday 3
11:00-12:30
Lecture room U4078

Spatial point patterns with hierarchical or cascading structures arise in a wide range of applications, including environmental sciences, biology, and astrophysics.

In this work, we introduce Lévy-driven branching Cox processes, a class of spatial point processes that extends classical Cox models by incorporating a spatial branching mechanism. In the proposed framework, an initial configuration of points is generated by a Lévy basis, while successive generations of points are produced according to a branching kernel, leading to hierarchical spatial structures.

Expressions for key summary characteristics are derived, including the intensity and pair correlation function. Because these quantities become analytically complex, an alternative characterization based on Choquet capacities is proposed. This provides a tractable description of the process as a random set.

The proposed framework broadens the class of Cox-type models available for spatial statistics and provides a basis for the development of statistical inference methods for spatial branching processes.

The presented results are joint work with ¹L. Beznea and ²O. Lupascu - Stamate, ¹Simion Stoilow Institute of Mathematics of the Romanian Academy and ²“Gheorghe Mihoc – Caius Iacob” Institute of Mathematical Statistics and Applied Mathematics.

Estimation of the invariant measure of a multidimensional diffusion from noisy observations

Grégoire Szymanski

University of Luxembourg (Luxembourg)

We introduce a new approach for estimating the invariant density of a multidimensional diffusion when dealing with high-frequency observations blurred by independent noises. We consider the intermediate regime, where observations occur at discrete time instances $k\Delta_n$ for $k = 0, \dots, n$, under the conditions $\Delta_n \rightarrow 0$ and $n\Delta_n \rightarrow \infty$. Our methodology involves the construction of a kernel density estimator that uses a pre-averaging technique to proficiently remove noise from the data while preserving the analytical characteristics of the underlying signal and its asymptotic properties. The rate of convergence of our estimator depends on both the anisotropic regularity of the density and the intensity of the noise. We establish conditions on the intensity of the noise that ensure the recovery of convergence rates similar to those achievable without any noise. Furthermore, we prove a Bernstein concentration inequality for our estimator, from which we derive an adaptive procedure for the kernel bandwidth selection.

Asymptotic Normality of Topological Statistics in Dynamic Random Geometric Networks

Christian Hirsch

Aarhus University (Denmark)

We study dynamic random geometric networks generated by a marked Poisson process in \mathbb{R}^d , where vertices arrive over time and edges are formed through spatial interactions. This produces an evolving random intersection graph whose connectivity and higher-order structure change dynamically. We analyze topological characteristics of this network, including connected components and higher-order cycles encoded by persistent Betti numbers of the associated nerve complex. Under subcritical percolation assumptions, we prove a functional central limit theorem for suitably recentered and rescaled persistent Betti numbers in expanding observation windows. The fluctuations converge to a centered Gaussian field in a two-parameter Skorokhod space.

These results provide a fluctuation theory for time-evolving geometric networks and establish asymptotic normality for a broad class of topological network statistics. If time permits, we illustrate the theory with simulations and with data from black silicon materials. This talk is based on ongoing joint work with Nikolaj N. Lundbye.

Multiplex weighted networks as decorated graphs for predicting binary outcomes

Sofia Olhede

EPFL (Switzerland)

Accurate early prediction of neurological outcomes in comatose patients after cardiac arrest is critical for guiding therapeutic decisions and improving individualized care. Current electroencephalographic (EEG) approaches typically rely on threshold-based or binarized measures of functional connectivity to this purpose, which may overlook key subtleties of brain dynamics and limit clinical interpretability. We have developed an explainable machine learning framework using weighted EEG connectivity over frequency bands and topological network features to improve early outcome prediction after cardiac arrest from multiple decorated graphs. This talk will discuss making useful summary statistics from weighted multiplex graph, and discuss their interpretation.

This is joint work with Arthur Verdeyme, Jake Grainger and Marzia de Lucia

Consistent spectral clustering in sparse tensor block models

Ian Välimaa
Aalto University (Finland)

Wednesday 3
13:30-15:00
Lecture room F4050

High-order clustering aims to classify objects in multiway datasets that are prevalent in various fields such as bioinformatics, recommendation systems, and social network analysis. Such data are often sparse and high-dimensional, posing significant statistical and computational challenges. This talk introduces a tensor block model specifically designed for sparse integer-valued data tensors. We propose a simple spectral clustering algorithm augmented with a trimming step to mitigate noise fluctuations, and identify a density threshold that ensures the algorithm's consistency. Our approach models sparsity using a sub-Poisson noise concentration framework, accommodating heavier than sub-Gaussian tails. Remarkably, this natural class of tensor block models is closed under aggregation across arbitrary modes. Consequently, we obtain a comprehensive framework for evaluating the tradeoff between signal loss and noise reduction incurred by aggregating data. The analysis is based on a novel concentration bound for sparse random Gram matrices. The theoretical findings are illustrated through numerical experiments.

Joint work with Lasse Leskelä. <https://arxiv.org/abs/2501.13820>.

Asymptotic equivalence for nonparametric additive regression

Angelike Rohde
Freiburg University

Wednesday 3
13:30-15:00
Lecture room F3020

We prove asymptotic equivalence of nonparametric additive regression and a Gaussian white noise model in which a multidimensional Wiener process is observed with a drift depending on the additive components of the regression function and the one- and two-dimensional marginal distributions of the covariates. The number of additive components is allowed to increase moderately with respect to the sample size. Moreover we study the special case of pairwise independent components of the covariates and approximation in some specific semiparametric setting.

Phase transitions for linear spectral statistics of sample correlation matrices in high dimension

Johannes Heiny
KTH Royal Institute of Technology

Wednesday 3
13:30-15:00
Lecture room F3020

We investigate linear spectral statistics (LSS) of a sample correlation matrix R , constructed from n observations of a p -dimensional random vector with iid components. If the entries have finite fourth moment and p and n grow proportionally, it is known that LSS satisfy a central limit theorem (CLT) and the centering and scaling sequences are universal in the sense that they do not depend on the entry distribution. Under a symmetry and a regular variation assumption with index α and any growth rate of the dimension, we prove that the universal CLT remains valid for $\alpha > 3$. Moreover, for $\alpha \leq 3$ we establish a non-universal CLT with norming sequences depending on the value of α . Our findings include specific conditions under which the CLT holds for LSS and the implications for hypothesis testing in multivariate settings.

Nonlinear higher-order shrinkage estimation of the large-dimensional covariance and precision matrices

Taras Bodnar

Linköping University

In this paper, we develop nonlinear higher-order shrinkage estimators for both the covariance and precision matrices. Our results cover scenarios where the sample size is either larger or smaller than the dimensionality of the data-generating process. The derivation relies on mild assumptions about the underlying model, such as the existence of the fourth moment and a bounded spectrum for the true population covariance matrix. The finite-sample performance of the proposed shrinkage methods is assessed through an extensive simulation study, comparing them against existing approaches.

Wednesday 3
13:30-15:00
Lecture room F3020

Random triangulations of the d -sphere with minimum volume

Joel Larsson Danielsson

Lund University (Sweden)

We study a higher-dimensional analogue of the Random Travelling Salesman Problem: let the complete d -dimensional simplicial complex K_n^d on n vertices be equipped with i.i.d. volumes on its facets, uniformly random in $[0, 1]$. What is the minimum volume $M_{n,d}$ of a sub-complex homeomorphic to the d -dimensional sphere \mathbb{S}^d , containing all vertices? We determine the growth rate of $M_{n,2}$, and prove that it is well-concentrated. For $d > 2$ we prove such results to the extent that current knowledge about the number of triangulations of \mathbb{S}^d allows.

Wednesday 3
13:30-15:00
Lecture room F3005

Asymptotically sharp anticoncentration in high dimensions

Tomas Juškevičius

Vilnius University

We shall address anticoncentration for sums of random vectors in \mathbb{R}^d . Given partial information on the distributions of individual summands we shall establish an asymptotically sharp version of the well-known Kolmogorov-Rogozin inequality for sums of real valued random variables. The main ingredient of the proof that is new to the context is the use of the Strong Perfect Graph Theorem from structural graph theory.

Wednesday 3
13:30-15:00
Lecture room F3005

A threshold for relative hyperbolicity in random right-angled Coxeter groups

Victor Falgas-Ravry

Umeå University

The right-angled Coxeter group (or RACG) $W = W(\Gamma)$ with presentation graph $\Gamma = (V, E)$ is the group with generators V and relations $aa = \text{id}$ and $ab = ba$ for all $a \in V$ and $ab \in E$. By taking Γ to be an instance of the Erdős-Rényi random graph model on n vertices with edge probability $p = p(n)$, one can generate a model for random RACG. Geometric group theorists have investigated this model in recent years, with a particular emphasis on the typical geometric properties of the random RACG.

In this talk I will explain how one can obtain a rough threshold for relative hyperbolicity in this model and discuss the related problem of square percolation in random graphs. While motivation for the problem comes from geometric group theory, the focus of this talk will be on certain combinatorial problems about random graphs that arise in its resolution.

Based on joint work with Jason Behrsock, R. Altar Çiçeksiz and Tim Susse.

Wednesday 3
13:30-15:00
Lecture room F3005

Logical convergence laws for small permutation classes

Eero Rätty

ECOPRO research group, Institute for Basic Science

Wednesday 3
13:30-15:00
Lecture room F3005

A permutation class \mathcal{F} is said to be small if it has growth-rate less than κ , where $\kappa \approx 2.20557$. Vatter established a structural classification result on small permutation classes and conjectured that every small permutation class has a rational generating function. The conjecture was later settled by Albert, Ruškuc and Vatter.

In this talk, I will discuss our recent result which states that every small permutation class satisfies a first-order convergence law. In fact, we prove the following slightly more general result. Given a small permutation class \mathcal{F} , we construct a regular language $L_{\mathcal{F}}$ and a length-preserving bijection $f_{\mathcal{F}} : L_{\mathcal{F}} \rightarrow \mathcal{F}$ that is a first-order homomorphism, i.e. for every first-order sentence Ψ in \mathcal{F} there exists a first-order sentence Φ in $L_{\mathcal{F}}$ so that

$$f_{\mathcal{F}}^{-1}(\{\sigma \models \Psi : \sigma \in \mathcal{F}\}) = \{w \models \Phi : w \in L_{\mathcal{F}}\}.$$

This is based on joint work with Klas Markström.

Investigating bivariate structure of non-Gaussian spatial fields

Kushagri Tandon

University of Oslo (Norway)

Wednesday 3
13:30-15:00
Lecture room F3017

Many environmental variables, such as precipitation, wind speed and soil moisture, exhibit skewed, heavy-tailed and nonlinear dependence structures, yet spatial modelling practice still heavily relies on Gaussian random fields and linear correlation. A common workaround is Gaussian anamorphosis: each marginal is transformed to standard normal, and Gaussian methods are then applied on this transformed scale. However, for genuinely non-Gaussian spatial fields it is unclear what correlation structure this procedure actually induces, and how well it agrees with standard Gaussian-copula constructions.

This talk considers two classes of explicitly non-Gaussian spatial models: Gamma convolution (random particle) fields built from independently scattered Gamma measures and spatial kernels, and non-Gaussian Matérn fields defined as solutions to SPDEs (stochastic partial differential equations) driven by type-G Lévy noise with finite element discretisation. For both classes, tractable bivariate Laplace transforms and low-order mixed moments are derived and used to approximate bivariate densities and the field-implied Gaussian anamorphosis correlations via two complementary approaches: a Fourier inversion of the bivariate Laplace transform, and an operator-theoretic (Lancaster) expansion based on orthonormal polynomials.

These field-implied correlations are then compared with those obtained by standard Gaussian copula matching based on Hermite–Mehler expansions, and the impact on observed-scale dependence summaries and kriging performance is assessed in simulation experiments. The results highlight when Gaussian copula practice is close to what explicit non-Gaussian models would imply, and when it can lead to systematic distortions in dependence and prediction.

Gaussian Processes on Directed Metric Graphs

Erik Karlsson Strandh
Lund university (Sweden)

We introduce directed Gaussian processes on metric graphs as solutions to a system of stochastic ordinary differential equations (SODE) defined on a metric graph. We relate this construction to earlier work on non-directed Gaussian processes on metric graphs and show that the distinction can be made precise through their reproducing kernel Hilbert spaces (RKHSs).

We also connect the proposed framework to earlier stream-network models, showing that these can be represented as solutions to the same SODE system under particular boundary conditions. In addition, we introduce new boundary conditions and argue that they yield more physically realistic processes than existing alternatives.

From a computational perspective, we show that the SODE representation enables efficient inference and prediction. In particular, we develop a novel domain-reduction technique that uses a minimal data-spanning subgraph while still providing exact inference for the full graph. This makes the method applicable to large data sets without requiring approximations. We illustrate and compare the methods through an application to temperature modelling on river networks, where we observe substantial computational speed-ups and improved performance when physically conservative confluence conditions are imposed at vertices.

Self-supervised distributional regularization stabilizes estimators of decision boundaries in classification of functional data - an imaging spectroscopy case study

Jaime C. Revenga^{1*}, Fabian D. Schneider^{2,3}, Zhaoyue Wu^{2,3}, Federico Grillini⁴, Ankit Kariryaa^{5,6}

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*: presenting author

Self-Supervised Learning (SSL) is a family of learning methods designed to learn object representations with few to no labeled instances (i.e. a functional data instance with its corresponding ground-truth category). Since costly, labor-intensive label acquisition is no longer a strict requirement, the applications of SSL hold the promise of e.g., enabling the upscaling of machine learning identification routines to ever larger datasets at significantly reduced costs.

However, until recently, SSL has seen mainly empirical progress, with theoretical work remaining limited. Existing theory in SSL has largely focused on post-hoc explanations, rather than on the development of principled theoretical foundations. In contrast to other areas of machine learning which have seen decades of theoretical work grounding empirical findings (e.g. supervised learning), in SSL, on the other hand, solid theoretical development has lagged behind, as empirical applications have consistently outpaced theoretical progress.

To close this gap and reduce the degree of heuristics involved in SSL, a current line of work attempts to ground the field in formal justification, contributing proofs for optimal embedding distributions based on a penalization that focuses on the joint probability distribution of learned embeddings, in a manner agnostic to the specific architecture employed, or functional data type (Ballestrero & LeCun, 2026). Such distributional regularization of the embedding space is obtained through a tailored loss function: Sketched Isotropic Gaussian Regularization (SIGReg).

Here, we evaluate the effect of this loss function (SIGReg) on the embedding space it enforces. As application, we employ a functional dataset of vegetation reflectances acquired by the imaging spectroscopy mission Surface Biology and Geology High-Frequency Time Series (SHIFT, NASA, 2022) over the protected area Dangermond Preserve (Santa Barbara Bay, California, US). Specifically, we assess the effect of the SIGReg loss function on estimator variance of decision boundaries for the classification task of vegetation community identification.

Our current observations show that the SIGReg loss function enforces distributional regularity, leading to an isotropic embedding space and lower estimator variance of class boundaries. This property provides particular benefits in learning tasks where labeled instances are scarce—suggesting potential implications for environmental imaging spectroscopy missions.

Simulating counterfactuals

Juha Karvanen
University of Jyväskylä

Wednesday 3
13:30-15:00
Lecture room U3041

Counterfactual inference considers a hypothetical intervention in a parallel world that shares some evidence with the factual world. If the evidence specifies a conditional distribution on a manifold, counterfactuals may be analytically intractable. We present an algorithm for simulating values from a counterfactual distribution where conditions can be set on both discrete and continuous variables. We show that the proposed algorithm can be presented as a particle filter leading to asymptotically valid inference. The algorithm is applied to fairness analysis in credit scoring.

Keywords: Causality, Fairness, Particle filter, Sequential Monte-Carlo, Structural causal model
Reference:

J. Karvanen, S. Tikka, M. Vihola (2024). Simulating counterfactuals, *Journal of Artificial Intelligence Research*, 80, 835-857.

Causal treatment effect decompositions with time-to-event outcomes under competing events

Mikko Valtanen
University of Turku

Wednesday 3
13:30-15:00
Lecture room U3041

Inference about treatment effects for time-to-event outcomes is often obscured by the presence of competing events. A particularly complex situation arises when the treatment also influences the occurrence of the competing event. A comprehensive assessment should then account for different mechanisms by which the treatment and the competing event together produce the apparent treatment effect. Here, we propose a decomposition of the treatment's effect on the event of interest (target), characterising how it arises due to four distinct mechanisms involving both the target and competing events. Based on a causal model, the decomposition relies on cross-world estimands reflecting counterfactual scenarios in which the treatment affects the two events as if they were set to conflicting levels. We specify exchangeability and consistency assumptions under which the decomposition can be estimated from empirical observations. We discuss how the new decomposition can reveal the role of the competing event and serve as a basis for defining causally interpretable estimands in the presence of competing events. Finally, we demonstrate the use of the four-way decomposition with datasets from two randomised trials.

Algorithms for optimizing model-based incomplete block designs

Jonas Bjermo^{1,2,3}, Frank Miller¹

¹Department of Computer and Information Science, Linköping University, Sweden, and ²Department of Statistics, Stockholm University, Sweden. ³Presenting author

Because of time limitations or participation burden, the total number of treatments in an experimental design can be too large for a single subject. This is traditionally addressed using combinatorial incomplete block designs, which ensure treatment block symmetry and balance. However, we propose a treatment allocation design based on a parametric model, enabling the selection of a design that optimizes model parameters. This model-based approach offers several distinct advantages over combinatorial methods: it straightforwardly incorporates subject-specific covariates to tailor treatment allocation to individual characteristics, allows for varying block sizes to adjust for different treatment burdens, and eliminates the requirement for equal treatment replication across the study.

Despite these benefits, the model-based approach is limited by model dependence and a lack of developed software. Furthermore, the search space in many applications becomes prohibitively large, making exact optimization methods computationally intractable, which requires heuristic approaches. To address this, we present algorithms based on local search techniques and compare them to existing methods adapted for this setting.

Specifically, we evaluate first and best improvement algorithms, simulated annealing (SA), threshold accepting (TA), and two novel algorithms utilizing directional derivatives to guide exchanges. These directional derivative algorithms serve as discrete versions of continuous gradient-based methods, and are combinations of the first improvement algorithm and a chained local search method using TA criteria. The idea of using directional derivatives is to take smaller, smoother steps in the objective values. It prioritizes the exchanges with the largest directional derivative difference, effectively avoiding flat regions.

Our approach is broadly applicable to most models, including linear, non-linear, generalized linear (GLM), and generalized non-linear models (GNLM). In this presentation, we use item calibration in achievement tests as a comparative example, and we evaluate final objective values and computational time across different settings. Our results demonstrate that while SA and TA often produce the lowest objective values, they are computationally intensive. Conversely, for larger problems, algorithms based on directional derivatives achieve near-optimal solutions significantly faster. Given the importance of computational efficiency in practical applications, our developed algorithms offer a highly appealing approach for optimizing model-based incomplete block designs.

Semi-amortised simulation-based inference for stochastic nonlinear mixed-effects models

Henrik Häggström

Department of Mathematical Sciences, Chalmers University of Technology and the University of Gothenburg (Sweden)

The analysis of data from multiple experiments, such as observations of several individuals, is commonly approached using mixed-effects models, which account for variation between individuals through hierarchical representations. This makes mixed-effects models widely applied in fields such as biology, pharmacokinetics, and sociology. In this work [1], we propose a novel methodology for scalable Bayesian inference in hierarchical mixed-effects models. Our framework first constructs amortized approximations of the likelihood and the posterior distribution, which are then rapidly refined for each individual dataset, to ultimately approximate the parameters posterior across many individuals. The framework is easily trainable, as it uses mixtures of experts but without neural networks, leading to parsimonious yet expressive surrogate models of the likelihood and the posterior. We demonstrate the effectiveness of our methodology using challenging stochastic models, such as mixed-effects stochastic differential equations emerging in systems biology-driven problems. However, the approach is broadly applicable and can accommodate both stochastic and deterministic models. We show that our approach can seamlessly handle inference for many

parameters. Additionally, we applied our method to a real-data case study of mRNA transfection. When compared to exact pseudomarginal Bayesian inference, our approach proved to be both fast and competitive in terms of statistical accuracy.

Reference:

[1] H. Häggström, S. Persson, M. Cvijovic and U. Picchini. Simulation-based inference for stochastic nonlinear mixed-effects models with applications in systems biology. *Statistics and Computing*, 36(99), <https://doi.org/10.1007/s11222-026-10850-8>, 2026.

Pushing the AR test beyond the limit: A novel goodness-of-fit test for high-dimensional applications

Markku Kuusmin

University of Oulu, Research Unit of Mathematical Sciences (Finland)

Wednesday 3
13:30-15:00
Lecture room U3043

High-dimensional methods have arguably become one of the most notable areas of statistical research in the 21st century. However, developing high-dimensional tests remains a challenging task. Many state-of-the-art methods are either inapplicable to high-dimensional data or exhibit low power in high-dimensional scenarios. Additionally, the evaluation of uncertainty is often neglected in modern multivariate tests. To address these challenges, an experimental high-dimensional goodness-of-fit test based on the Accept-Reject (AR) test is introduced. The proposed method is suitable for high-dimensional applications where existing methods are not applicable. Additionally, the AR test includes built-in methods for quantifying the uncertainty of its output. Extensive Monte Carlo simulation studies of heavy-tailed alternatives are used to demonstrate how far the AR test can be pushed in high-dimensional data analysis. These results indicate that the AR test not only extends applicability to data beyond the reach of state-of-the-art methods but also exhibits strong power performance in extremely high-dimensional settings.

Estimating Hüsler–Reiss Variogram Matrices via Noncanonical Halfspaces

Frank Röttger

University of Twente

Wednesday 3
13:30-15:00
Lecture room U4078

The variogram matrix is a natural and interpretable summary statistic for characterizing extremal dependence in multivariate data. As a parameter matrix, it completely determines the Hüsler–Reiss family of distributions, which can be considered as an extremal analogue of Gaussian models. In this talk, we introduce an empirical estimator of the variogram matrix based on threshold exceedances lying in noncanonical halfspaces, a construction that generalizes the estimator of Engelke and Volgushev (2022, 11) and enables a broader class of ensemble-type estimators. Using simulated data in the domain of attraction of a Hüsler–Reiss random vector, we investigate how different choices of halfspaces and ensembles induce a bias–variance tradeoff presented in Hentschel, Röttger and Engelke (2026). Finally, we present a geometric perspective on variogram matrices, highlighting their connection to Euclidean distance matrices and identifying a bounded subset that corresponds to the Gaussian elliptope presented in Devriendt, Echave-Sustaeta Rodríguez and Röttger (2026).

References:

- [1] Devriendt, K., I. Echave-Sustaeta Rodríguez, and F. Röttger (2026). Extremal conditional independence for Hüsler-Reiss distributions via modular functions.
 - [2] Engelke, S. and S. Volgushev (2022, 11). Structure learning for extremal tree models. *Journal of the Royal Statistical Society Series B: Statistical Methodology* 84 (5), 2055–2087.
 - [3] Hentschel, M., F. Röttger, and S. Engelke (2026). Hüsler-Reiss distributions on noncanonical halfspaces. In preparation.
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Wednesday 3
13:30-15:00
Lecture room U4078

Order Statistics for The Quantile Contribution

Hamidreza Maleki Almani
University of Vaasa (Finland)

Heavy-tailed phenomena appear across diverse domains—from wealth and firm sizes in economics to network traffic, biological systems, and physical processes—characterized by the disproportionate influence of extreme values. These distributions challenge classical statistical models, as their tails decay too slowly for conventional approximations to hold. Among their key descriptive measures are quantile contributions, which quantify the proportion of a total quantity (such as income, energy, or risk) attributed to observations above a given quantile threshold. This paper presents a theoretical study of the quantile contribution statistic bridging it to order statistics. We derive a closed-form expression for the joint cumulative distribution function (CDF) of order statistics and, based on it, obtain an explicit CDF for quantile contributions applicable to small samples. We then investigate the almost sure convergence of these contributions as the sample size increases.

Thursday 4
09:00-10:30
Lecture room F4050

Identifiability and Estimation in Continuous Lyapunov Models

Cecilie Olesen Recke
University of Copenhagen (Denmark)

We study a class of models which we denote continuous Lyapunov models, which models cross-sectional data of a dynamical model. They arise as the steady state distributions of a stationary stochastic differential equation with a linear drift matrix parametrized by a directed graph. We derive equations for the k^{th} -order cumulants of this distribution, a generalization of the well-known covariance Lyapunov equation. Under a non-Gaussianity assumption we are able to prove generic identifiability for any connected graph with all self-loops using the equations of the higher order cumulants. Based on the identifiability result we propose a new semi-parametric estimator of the drift matrix and show it is asymptotically normal and investigate it in simulations.

Thursday 4
09:00-10:30
Lecture room F4050

Probabilistic PCA on tensors

Piotr Zwiernik
Universitat Pompeu Fabra & Barcelona School of Economics

In probabilistic principal component analysis (PPCA), an observed vector is modeled as a linear transformation of a low-dimensional Gaussian factor plus isotropic noise. We generalize PPCA to tensors by constraining the loading operator to have Tucker structure, yielding a probabilistic multilinear PCA model that enables uncertainty quantification and naturally accommodates multiple, possibly heterogeneous, tensor observations. We develop the associated theory: we establish identifiability of the loadings and noise variance and show that—unlike in matrix PPCA—the maximum likelihood estimator (MLE) exists even from a single tensor sample. We then study two estimators. First, we consider the MLE and propose an expectation maximization (EM) algorithm to compute it. Second, exploiting that Tucker maps correspond to rank-one elements after a Kronecker lifting, we design a computationally efficient estimator for which we provide provable finite-sample guarantees. Together, these results provide a coherent probabilistic framework and practical algorithms for learning from tensor-valued data. (Joint work with Yaoming Zhen)

When is an algebraic statistical model toric?

Aida Maraj

Max Planck Institute of Molecular Cell Biology and Genetics

Thursday 4
09:00-10:30
Lecture room F4050

Determining whether a statistical model or a variety in general can be represented as a vanishing set of a toric ideal, possibly after a linear change of variables, is important for theory and applications. We introduce and discuss how the new approach using the Lie algebra of the variety helps.

Random and Quasi-Random Designs for Quantisation in High Dimension

Luc Pronzato

Université Côte d'Azur

Thursday 4
09:00-10:30
Lecture room F3020

The greedy-packing algorithm for selecting points from a finite (yet large) candidate set is an efficient approach for the incremental construction of space-filling designs. Its computational complexity scales linearly with the design size, and when the algorithm terminates at step k , the resulting design of size k achieves at least 50% efficiency in terms of both packing radius (PR) and covering radius (CR). Furthermore, as the design size grows, these constructions become asymptotically optimal among all incremental methods with respect to the mesh ratio (CR/PR) [2]. When the space \mathcal{X} is a d -dimensional hypercube, variants of the basic algorithm can avoid selecting vertices as design points and prevent excessive clustering near the boundary of \mathcal{X} . In high-dimensional settings ($n \approx 2^d$) or extremely high-dimensional ones ($n \ll 2^d$), evaluating space-filling properties via the covering radius loses relevance. Instead, the L_s -mean quantisation error provides a more meaningful metric. Unfortunately, while greedy minimisation of the L_s -mean quantisation error is computationally feasible in low dimensions [1], it becomes intractable for large d .

In this talk, we focus on random designs composed of i.i.d. points drawn from a suitable distribution in \mathcal{X} . We show that when \mathcal{X} is a high-dimensional ball, unless n is astronomically large (so that Zador's theorem [3] applies), the optimal distribution is uniform on a sphere of appropriate radius. For a d -dimensional hypercube, sampling points uniformly (or quasi-uniformly) from a smaller hypercube, or selecting suitable subsets of vertices from an even smaller hypercube, yields designs with low quantisation error. In this context, greedy packing among a fractional factorial design offers a particularly efficient method for vertex selection.

References:

- [1] A. Nogales Gómez, L. Pronzato, and M.-J. Rendas. Incremental space-filling design based on coverings and spacings: improving upon low discrepancy sequences. *Journal of Statistical Theory and Practice*, 15(4):77, 2021.
 - [2] L. Pronzato and A.A. Zhigljavsky. Quasi-uniform designs with asymptotically optimal and near-optimal uniformity constant. *Journal of Approximation Theory*, 294(105931), 2023.
 - [3] P.L. Zador. Asymptotic quantization error of continuous signals and the quantization dimension. *IEEE Trans. Inform. Theory*, 28:139–149, 1982.
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Thursday 4
09:00-10:30
Lecture room F3020

Optimal designs for discrete choice models via graph Laplacians

Frank Röttger
University of Twente

In this talk, we connect design theory for discrete choice experiments with Laplacian matrices of connected graphs. We rewrite the D -optimality criterion in terms of Laplacians via Kirchhoff's matrix tree theorem, and show that its dual has a simple description via the Cayley–Menger determinant of the Farris transform of the Laplacian matrix. This results in a drastic reduction of complexity and allows us to implement a gradient descent algorithm to find locally D -optimal designs. For the subclass of Bradley–Terry paired comparison models, we find a direct link to maximum likelihood estimation for Laplacian-constrained Gaussian graphical models. This implies that every locally D -optimal design is a rational function in the parameter when the design is supported on a chordal graph. Finally, we study the performance of our algorithm and demonstrate its application on real data.

Joint work with Thomas Kahle¹ and Rainer Schwabe¹
¹ University of Magdeburg, Germany

Thursday 4
09:00-10:30
Lecture room F3020

Optimal allocation of trials to sub-regions in crop variety testing with multiple years and correlated genotype effects

Maryna Prus
University of Hohenheim

New crop varieties are extensively tested in multi-environment trials in order to obtain a solid basis for recommendations to farmers. When the target population of environments is large, a division into sub-regions is often advantageous. If the same set of genotypes is tested in each of the sub-regions, a linear mixed model (LMM) may be fitted with random genotype-within-sub-region effects. The first analytical results to optimizing allocation of trials (designs) to sub-regions have been obtained in Prus and Piepho (2021). In that paper *one-year* experiments, in which the genotype effects for different genotypes were assumed to be *uncorrelated* with each other, were considered. Prus and Piepho (2024) extended the results from Prus and Piepho (2021) to *multi-year* experiments. In Prus (2025) a solution is proposed for *one-year* experiments with *correlated* genotype effects. The present work generalizes the results obtained so far to *multi-year* experiments models with *correlated* genotype effects.

Joint work with Lenka Filová¹, Hans-Peter Piepho², and Waqas Malik²
¹ Comenius University of Bratislava, Slovakia
² University of Hohenheim, Germany

References:

Prus, M. and Piepho, H.-P. (2021). Optimizing the allocation of trials to sub-regions in multi-environment crop variety testing. *Journal of Agricultural, Biological and Environmental Statistics*, 26, 267–288.

Prus, M. and Piepho, H.-P. (2024). Optimizing the allocation of trials to sub-regions in crop variety testing with multiple years and locations. *Journal of Agricultural, Biological and Environmental Statistics*.

Prus, M. (2025). Computing optimal allocation of trials to sub-regions in crop-variety testing in case of correlated genotype effects. *Statistica Neerlandica*

Spectral gap in parallel tempering: a variational analysis

Peter Rudzis
University of Gothenburg

Thursday 4
09:00-10:30
Lecture room F3005

Parallel tempering is a popular MCMC-based method for sampling from Gibbs measures, designed to avoid the pitfall of getting trapped in potential wells in the low-temperature regime. Previous mathematical work on the convergence of parallel tempering has focused on particular classes of potential functions, or to the extent that more general potentials are considered, the results are asymptotic or deal with convergence senses which are weaker than in total variation. In this talk, we present a spectral gap bound for parallel tempering which holds for general potential functions, in both discrete and diffusive settings. The bound provides insight into practical matters of implementation, confirming the near optimality of a geometric sequence of temperatures and also shedding light on the optimal number of chains at which to run the algorithm and the influence of dimension. The bound depends on the internal energy of the Gibbs ensemble, and when the temperatures are chosen near optimally, one obtains a relaxation time which is polynomial in the inverse lowest temperature. The proof of this result works directly with the variational characterization of the spectral gap and exploits the structure of the Dirichlet form associated with the parallel tempering process. This work is joint with Pierre Nyquist (Chalmers University of Technology and University of Gothenburg).

Parameter estimation in Conditional Sequential Monte Carlo algorithms through Particle Learning

Alfonso Diz-Lois Palomares, Geir Storvik
Department of Statistics and Data Science, University of Oslo (Norway)

Thursday 4
09:00-10:30
Lecture room F3005

In this work, we explore particle learning strategies for the joint estimation of static parameters and latent states within conditional sequential Monte Carlo (CSMC) algorithms. Building on this idea, we propose the p(parameter)-CSMC algorithm, which incorporates both parameter learning and ancestor sampling, leading to much better mixing properties compared to Gibbs sampling in settings where strong internal correlations may challenge effective exploration. We include an application to the estimation of weights in a branching process model against synthetic data and show that, in this setting, performance is dramatically enhanced, with substantially faster mixing and markedly reduced autocorrelation compared with standard particle Gibbs implementations.

Large Language Models as Tools for Statistics Education: Problem Generation and Mathematical Reasoning

Sigrún Helga Lund, Hafsteinn Einarsson, et al.
Department of Physical Sciences, University of Iceland

Thursday 4
09:00-10:30
Lecture room F3005

Large language models (LLMs) have rapidly become capable tools across scientific disciplines, and their integration into mathematics and statistics education raises both practical opportunities and important empirical questions. This talk examines two complementary aspects of LLM use in educational and assessment contexts.

The first concerns the use of LLMs as problem generators. Drawing on recent work demonstrating that ChatGPT can successfully reframe probability and statistics problems for students across diverse academic disciplines, preserving theoretical content in over 77% of cases and adding perceived educational value in the majority of expert-reviewed instances, we discuss the potential and current limitations of automated problem adaptation. We reflect on practical experience applying this approach in university-level statistics courses, including challenges related to mathematical precision, disciplinary appropriateness, and instructor oversight.

The second concerns the mathematical reasoning capabilities of current frontier LLMs. We present results from the Icelandic Math Eval benchmark, a dataset of 1,027 competition mathematics problems spanning 41 years (1984–2025) across four domains: algebra, number theory, geometry, and combinatorics. Three state-of-the-art models achieved 81-93% overall accuracy on these Icelandic-language problems, with performance declining sharply on image-containing geometry problems and at the highest difficulty levels. A dual evaluation design, presenting problems with and without multiple-choice options, revealed a systematic gap of 6.7 percentage points, suggesting that standard multiple-choice benchmarks overestimate genuine reasoning ability.

Together, these results inform how educators and statisticians can use LLMs productively while maintaining appropriate expectations about their limitations. We discuss implications for benchmark design, assessment integrity, and the use of AI tools in teaching quantitative reasoning.

Thursday 4
09:00-10:30

Lecture room F3017

Asymptotics of large-dimensional projection matrices

Stanislav Anatolyev

CERGE-EI (Prague)

We characterize the joint asymptotic behavior of diagonal and off-diagonal elements of projection matrices, whose underlying dimensionality (or rank) is asymptotically proportional to the sample size, with the aspect ratio in $(0,1)$, under the rotated i.i.d. assumption. The rate of convergence is a square root of the sample size, and the limiting distribution is multivariate centered Gaussian. The formulas for the asymptotic variances and covariances are expressed as functions of the aspect ratio and moments of data. The instrumental tools in deriving the asymptotic results are the Woodbury matrix identity, a central limit theorem for quadratic forms, and elements of the random matrix theory such as the Marchenko-Pastur law.

Thursday 4
09:00-10:30

Lecture room F3017

Hilbert space methods for approximating multi-output latent variable Gaussian processes

Soham Mukherjee

Aalto University (Finland)

Gaussian processes are a powerful class of non-linear models, but have limited applicability for larger datasets due to their high computational complexity. In such cases, approximate methods are required, for example, the recently developed class of Hilbert space Gaussian processes. They have been shown to significantly reduce computation time while retaining most of the favorable properties of exact Gaussian processes. However, Hilbert space approximations have so far only been developed for uni-dimensional outputs and manifest (known) inputs. Thus, we generalize Hilbert space methods to multi-output and latent input settings. Through extensive simulations, we show that the developed approximate Gaussian processes are indeed not only faster, but also provide similar or even better uncertainty calibration and accuracy of latent variable estimates compared to exact Gaussian processes. While not necessarily faster than alternative Gaussian process approximations, our new models provide better calibration and estimation accuracy, thus striking an excellent balance between trustworthiness and speed. We additionally illustrate our methods on a real-world case study from single cell biology.

Strang Splitting Parameter Estimator for Nonlinear Multivariate Pearson-Type Diffusions

Predrag Pilipović

University of Copenhagen (Denmark)

Thursday 4
09:00-10:30
Lecture room F3017

A nonlinear multivariate Pearson-type diffusion is a stochastic differential equation (SDE) with nonlinear drift and a state-dependent diffusion matrix whose entries are quadratic functions of the state. Statistical inference for such models is challenging due to the lack of tractable transition densities. The proposed Strang splitting (SS) estimator first splits the SDE into a deterministic nonlinear ordinary differential equation (ODE) and a linear multivariate Pearson diffusion. For the Pearson diffusion, we derive closed-form expressions for the conditional mean and covariance using results on matrix exponential integrals, and approximate its solution by a Gaussian transition density with these exact first two moments. The nonlinear ODE part is then solved or numerically approximated separately. The SS estimator is obtained by composing these two steps. As an example of this model class, the multivariate Wright–Fisher diffusion from population genetics is considered. In addition, we introduce a new model within the class, the Student Kramers oscillator with heavy-tailed noise, and establish the existence and uniqueness of its strong solution as well as the existence of an invariant measure. We assess the Strang splitting estimator in simulation studies for both this model and the multivariate Wright–Fisher diffusion, showing that it outperforms the Euler–Maruyama, Gaussian approximation, and local linearization estimators, particularly at coarser sampling intervals. Finally, an application to Greenland ice-core data demonstrates the practical applicability of the SS estimator and the Student Kramers oscillator in modeling real climate proxy series.

Integrated Joint Distribution Modeling to Estimate the Biomass of Commercial Fish in the Baltic Sea from Acoustic and Trawl Data.

Mikhail Shubin

University of Helsinki (Finland)

Thursday 4
09:00-10:30
Lecture room F3006

Integrated species distribution models (ISDMs) have seen rapid development in the recent years. By integrating multiple data sets under single hierarchical Bayesian model has been demonstrated to improve parameter identifiability and prediction in multiple works. However, applications of ISDMs to multispecies modeling are few. In this work, we developed an Integrated Joint species distribution model (IJSJM) for three commercially important fish in the Baltic Sea. We combine annual acoustic and trawl survey data on herring (*Clupea harengus*), sprat (*Sprattus Sprattus*) and stickleback (*Gasterosteus aculeatus*) within our IJSJM to provide estimates on the spatiotemporal distribution and trends in their biomasses. Herring, sprat and stickleback constitute a major part of the Baltic sea fish biomass so their biomass estimates are of great importance to fisheries management and assessment of the ecological status of the Baltic Sea. We compare our results to the results obtained with the current acoustic stock assessment method StoX, which approximates the fish stock by synthesizing data collected by Baltic International Acoustic Survey (BIAS). Unlike StoX, our IJSJM explicitly models fish abundance and its dependence on environmental covariates and provides uncertainty quantification for the estimates.

Diffusion limit for Markovian models of evolution in structured populations with migration

Thursday 4
09:00-10:30
Lecture room F3006

Celia García-Pareja

KTH Royal Institute of Technology

The evolution of microbial subpopulations that migrate within spatial structures has gained interest in recent years. Questions of relevance include, for instance, the ability of a migrant mutant to take over the population (fixate). Estimating fixation probabilities is, however, usually hindered by the lack of analytical formulas and by computational complexity of simulation-based strategies when considering large populations. In this work, we study several population genetics models where the population is divided into D subpopulations (called demes) consisting of two types of individuals, mutants and wild-types, that evolve through discrete Markovian updates. We prove that under certain assumptions all the considered models converge to the same diffusion approximation, which we call *universal*. This diffusion approximation is amenable to simulation strategies that underly methods of statistical inference while significantly reducing computational costs. In all models, each Markovian update follows two phases: First, a local growth phase in each subpopulation, where the growth of each type of individual depends on its fitness, and then a sampling phase that implements migration between subpopulations. Our proof relies on existing diffusion approximation results for degenerate diffusions but requires further technicalities due to fact that sample sizes in each deem are not necessarily fixed but change randomly with each update.

This is joint work with Alia Abbara and Anne-Florence Bitbol at EPF Lausanne.

Base rate problems in mapping rare ecological phenomena using remote sensing

Thursday 4
09:00-10:30
Lecture room F3006

Joel Kostensalo

Natural Resources Institute Finland, Luke (Finland)

Remote sensing data, e.g., in the form of airborne laser scanning (ALS) or aerial images, are widely in forestry and ecology for mapping various phenomena. A typical problem is that of classification, typically done using machine learning methods. While in typical machine learning applications sample sizes are large, ecological datasets tend to be much smaller, and the interest tends to be on rare phenomena, with base rates around one percent or even significantly lower.

Most current remote-sensing based ecological research is uses balanced samples with rare classes overrepresented, as some level of oversampling in the training data is generally known improve model performance. However, the widely used practice of using an unrepresentative test set leads to overconfident statements about model performance and suboptimal model transferability to actual mapping applications with low base rates.

As an example application, the mapping European aspen (*Populus Tremula*) in considered. We reanalyze the results of ten previously published aspen detection papers alongside original classification results from Norway using a Bayesian approach with realistic base rates. We show that in a realistic scenario the false detection rates are high, and that some studies have sample sizes so small that even a perfect confusion matrix would not be sufficient evidence of reasonable model performance. Optimal practices for oversampling, necessary sample sizes, and estimating base rates below which model performance degrades to an unacceptable level are discussed.

Abstracts of Posters

Comparing estimators in contaminated ARMA models

Kusti Aholainen, Leena Kalliovirta, Jyrki Möttönen
University of Helsinki (Finland)

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

We compare with simulations the performance of different estimators, when the nearly non-identifiable invertible stationary ARMA process has been contaminated with innovation outliers. The classical estimators are the OLS estimator and the ML estimator implemented with the Kalman filter as described by Harvey and Phillips (1979). The robust estimators are the filtered τ -estimator, as defined by Bianco et al. (1996), the S-estimator, the MM-estimator and the BIP-MM estimator proposed by Muler et al (2009). To standardize the effect of the starting value, the algorithm of Hannan and Rissanen (1982) was used for all the estimators. In our simulations, none of the estimators outperformed and depending on the type of contamination some estimators performed very poorly. An R package *RobARMA* is available on CRAN and Python package *RobARMA* in PyPI.

References:

- Bianco, A. M., E. J. Martinez, M.G. Ben and V.J. Yohai (1996): Robust Procedures for Regression Models with ARIMA Errors, *COMPSTAT*, pp. 27-38.
Hannan E.J. and J. Rissanen (1982): Recursive estimation of mixed autoregressive-moving average order, *Biometrika*, vol.69(1), pp. 81-94.
Harvey A.C. and G.D.A. Phillips (1979): Maximum Likelihood Estimation of Regression Models with Autoregressive- Moving Average Disturbances, *Biometrika*, vol.66(1), pp. 49-58.
Muler, N., D. Peña and V.J. Yohai (2009): Robust estimation for ARMA models, *The Annals of Statistics*, vol 37(2), pp. 816-840.

Efficient sampling of excursion trajectories for stationary Gaussian processes via Slepian models

Henrik Bengtsson
Chalmers University of Technology

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Characterizing the excursion behavior of stationary Gaussian processes is an important problem across many applications. Since it appears in several areas such as risk analysis, statistical physics, and extreme value theory. Despite the problem receiving considerable attention, several key analytical results are still missing. This is why substantial effort has been devoted to developing numerical and approximation methods.

One approach is to use Monte Carlo methods based on simulating trajectories of the process. However, obtaining a sufficient number of excursions above even a moderate level requires lengthy simulations. Despite the existence of efficient methods for simulating trajectories, there remains a need for a more computationally efficient approach. In particular for higher-level excursions.

Therefore, a more efficient way to obtain finite-dimensional samples from the excursion trajectories is proposed [1]. This method is based on the well-known Slepian model, which is the Palm version of the process, where an up-crossing is attached to the origin. This model has an explicit form that allows for direct simulation of a single excursion at a time.

This approach has two main advantages. The first is that since only the excursions are simulated, the total length of time needed to be simulated is reduced. The second is that since the trajectories are simulated, these can be used to study several aspects of the excursions, such as maxima and excursion lengths.

Several examples are studied. In particular, persistency coefficients for processes with oscillating covariance functions, which standard approximation methods such as the independent interval approximation method have had difficulty with [2].

References:

[1] Efficient sampling of excursion trajectories for stationary Gaussian processes via Slepian models. (2026). Manuscript in preparation.

[2] Wilson, L. R. M., & Hopcraft, K. I. (2017). Periodicity in the autocorrelation function as a mechanism for regularly occurring zero crossings or extreme values of a Gaussian process. *Physical Review E*, 96(6), 062129. <https://doi.org/10.1103/PhysRevE.96.062129>

Estimation of minimum VaR and minimum CVaR optimal portfolios for small samples and singular covariance matrices

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Svitlana Drin
Örebro University

We study estimation of minimum Value at Risk (VaR) and minimum Conditional Value at Risk (CVaR) portfolios when the covariance matrix is singular, a situation that often arises in high dimensional settings with small samples or strong multicollinearity. Working under multivariate normality and using the Moore Penrose inverse, we derive stochastic representations for the estimated expected return and variance of the minimum VaR and minimum CVaR portfolios. The results provide a finite sample characterization of these estimators conditional on their existence. We also obtain analytical expressions for the corresponding moments and show that, in this setting, the conditional variance of the estimated return and the conditional mean of the estimated variance are infinite. The study extends earlier results for non singular covariance structures and contributes to the understanding of risk based portfolio selection in small sample and high dimensional environments.

Modeling Spatially Obfuscated Street-Crime Data on Metric Graphs using a Log-Gaussian Cox Process

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Lulu Jiang, David Bolin
King Abdullah University of Science and Technology

We develop a log-Gaussian Cox process model for street-level crime data observed on a road network under spatial location obfuscation. Motivated by UK police crime data, we model crime intensity on a metric graph and account for the fact that released coordinates are anonymized proxies rather than exact event locations. To address the resulting support mismatch, each published record is represented by a local support region on the network, and the observations are modeled through an aggregated likelihood. The latent log-intensity is specified as a Whittle-Matérn Gaussian field on the metric graph via an SPDE representation, which enables efficient Bayesian inference. In an application to theft crimes in the City of London, we compare the proposed model with planar point model and planar aggregated model. The metric-graph model achieves a better fit and identifies positive associations between theft risk and amenities related to pedestrian flow and opportunity exposure, such as convenience stores, supermarkets, subway entrances, and nightlife venues. The proposed framework offers a principled approach for analyzing network-constrained spatial event data with privacy-protected and imprecise locations.

Hypothesis Testing for Shape Constraints in Generalized Functional Linear Models

Yuwei Jiang, Natalya Pya Arnqvist, Jun Yu
Umeå University

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Shape constraints on functional regression coefficients, such as monotonicity and convexity, are often motivated by structural prior knowledge. While these constraints improve interpretability, formally testing their validity remains a challenging problem. Existing approaches largely rely on bootstrap procedures, which can be computationally expensive in high-dimensional functional settings.

To address this issues, we propose a hypothesis testing procedure for shape constraints based on the shape-constrained functional regression framework introduced in Jiang and Pya Arnqvist(2025). Specifically, we develop an F-test statistics based on the deviances of the constrained and unconstrained models. The performance of the proposed test statistics is evaluated through extensive simulation studies. As an alternative approach for approximating the null distribution of the test statistic, we also consider a bootstrap procedure.

In addition, we derive an analytical expression for the degrees of freedom associated with smoothing parameters in the context of shape-constrained modelling. Using this result, we investigate a refined version of the F-test that incorporates these degrees of freedom into the calculation of the model degrees of freedom when computing the model deviances.

References:

Yuwei Jiang and Natalya Pya Arnqvist. Functional regression with shape constraints. In *International Workshop on Functional and Operatorial Statistics*, pages 277–284. Springer, 2025.

Forecasting maritime in-situ observations using satellite data in the Gulf of Finland

Henri Karttunen¹, Martin Härkönen¹, Leena Kalliovirta^{1,*}, Elina Miettunen², Laura Tuomi²

¹University of Helsinki. ²Finnish Meteorological Institute. *Presenter

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Having up to date knowledge of key maritime measurements can help understanding and preparing for changes in the environment, but measuring in-situ at sea is costly. Using satellite imaging to forecast variables such as temperature, turbidity and oxygen saturation could help by providing some insight at a lower cost and higher frequency. In this paper, we provide models for forecasting some of these variables in the Gulf of Finland based on satellite measurements and discuss the uncertainty related to the forecasting.

State space modelling of auditory attention using electroencephalography

Oskar Keding

Centre for Mathematical Sciences, Lund University, Sweden

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

In this work, we apply state-space modeling to decode auditory attention from electroencephalography (EEG) data. We consider a dataset in which participants listened to two simultaneous speakers and were instructed to attend to one of them. Each trial also includes an attention switch between speakers. The objective is to infer the attentional state of participants over time. This task is challenging due to the low signal-to-noise ratio of EEG measurements, the complexity of background neural activity, and the limited amount of available data, necessitating careful modeling. We adopt a two-step approach. First, attention-related observations are constructed from the EEG signals and the concurrent speech stimuli. These observations are then used in state-space models to decode the attended speaker.

Attention observations are generated in several ways to capture complementary aspects of attention. First, linear filters are used to model the relationship between EEG signals and the attended speech envelope. The resulting filter weights serve as features, as does the Pearson correlation between the reconstructed and measured speech envelopes. In addition, direction-specific neural activations are extracted from the EEG. In our approach, these are obtained using a common spatial pattern (CSP) algorithm combined with linear discriminant analysis (LDA) to discriminate between leftward and rightward attention states.

These observations are incorporated into state-space models in both filtering and smoothing settings. We compare different model formulations, including Kalman filters and hidden Markov models with sparsity constraints on the transition dynamics. Our results show that state-space models can reliably decode auditory attention, with smoothing consistently outperforming filtering. This improvement is observed for a subset of participants in the study. Overall, the findings suggest that state-space modeling is a promising framework for auditory attention decoding from EEG, with potential applications in brain-computer interfaces and auditory scene analysis for hearing aid systems.

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Conflict Forecasting via Conformal Prediction for Markov Processes

Emmett B. Kendall
The University of Texas at Dallas

Whether or not a country is at war, or experiencing escalating or deescalating levels of conflict, has massive ramifications on a country's national and foreign policy. Given a country's history of conflict, or lack thereof, future predictions about the war-status of a country is valuable information. In this paper, we present the use of conformal prediction on temporally-dependent data to obtain prediction sets of possible future conflict state-sequences. More specifically, we compare the results of conformal prediction to a likelihood-based prediction strategy when the data are assumed to come from a discrete-state Markov process. A point-prediction may not supply sufficient information because the penalty for a wrong prediction is extreme, and so we consider a machine learning alternative that gives valid uncertainty quantification and is robust to model misspecification. In the data analysis, we present real forecasts of conflict dynamics across multiple countries. Lastly, we comment on the possible limitations of existing approaches for applying conformal prediction to Markovian data, where the exchangeability assumption is violated.

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Uncertainty quantification for forest attribute maps with conformal prediction and k -Nearest Neighbor method

Mikko Kuronen
Natural Resources Institute Finland (Luke)

Forest attribute maps relying on remotely sensed data are increasingly required for local decision making related to the use of forest resources. Such maps always have uncertainty, which can be challenging to quantify. For example, the k -Nearest Neighbor (k -NN) method is a popular technique for producing forest attribute maps based on remote sensing and field data. However, it remains unclear how to best characterize the uncertainty related to the k -NN predictions. Prediction intervals based on heuristic uncertainties, such as the standard deviation of the k nearest neighbors, do not generally achieve the desired (e.g., 90%) coverage. That means that the prediction intervals will cover the ground truth value less or more often than desired, which can result in suboptimal decisions. Conformal prediction is a technique that can be used to adjust heuristic uncertainties (from k -NN or any other modelling technique), to obtain prediction intervals with predetermined coverage. Thus, the objective of this work is to introduce the conformal prediction methodology to forest attribute mapping, particularly for the k -NN method. We compare several conformal k -NN procedures for the mapping of total volume, broadleaved volume and Lorey's

height using Sentinel-2 satellite images and airborne laser scanning data. We use multiple measures to quantify how well the prediction intervals adapt to the difficulty of prediction in different forest strata. We conclude that conformal prediction intervals based on the standard deviation or quantiles of the k nearest neighbors usually work well. We present how to produce a forest attribute map with the proposed conformal prediction intervals. We show that jackknife conformal k -NN procedure using heuristic uncertainty measures produces valid prediction intervals. In conclusion, the k -NN maps can be conveniently accompanied with conformal prediction intervals. We recommend conformal prediction for unit-level uncertainty quantification of forest attribute maps.

Pivotal inference for linear predictions in stationary processes

Sebastian Kühnert

Ruhr University Bochum; Bochum (Germany)

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

We develop pivotal inference for the final (FPE) and relative final prediction error (RFPE) of linear forecasts in stationary processes. Our approach is based on a self-normalizing technique and avoids the estimation of the asymptotic variances of the empirical autocovariances. We provide pivotal confidence intervals for the (R)FPE, develop estimates for the minimal order of a linear prediction that is required to obtain a prespecified forecasting accuracy and also propose (pivotal) statistical tests for the hypotheses that the (R)FPE exceeds a given threshold. Additionally, we provide pivotal uncertainty quantification for the commonly used coefficient of determination R^2 obtained from a linear prediction based on the past $p \geq 1$ observations and develop new (pivotal) inference tools for the partial autocorrelation, which do not require the assumption of an autoregressive process.

Fast likelihood ratio testing for case control GWAS on GPU with direct modeling of imputed genotypes

Magnús Ingvi Magnússon

University of Iceland

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Genome-wide association studies (GWAS) at biobank scale require computationally efficient methods capable of analyzing millions of variants across large cohorts while preserving statistical accuracy. We present a GPU-accelerated framework for GWAS that enables rapid evaluation of regression models for both continuous and binary phenotypes, with a focus on case-control studies using imputed genotype data.

Our approach implements a likelihood-based method that explicitly accounts for genotype uncertainty by modeling probabilistic genotype distributions, rather than relying solely on dosage approximations. We derive analytic gradient and Hessian expressions for the resulting mixture likelihood and employ a Newton-Raphson optimization scheme with stabilization to ensure robust and efficient convergence. The framework is designed for parallel execution across multiple phenotypes, maximizing GPU utilization while minimizing memory overhead.

We evaluate the method using simulated and real datasets, benchmarking against established GWAS approaches. Our implementation achieves substantial computational speedups while maintaining well-calibrated test statistics. Across a range of minor allele frequencies, imputation qualities, and case-control ratios, the probabilistic approach demonstrates comparable or improved statistical power relative to standard dosage-based models.

These results show that combining probabilistic modeling with GPU acceleration provides an efficient and flexible approach for large-scale GWAS, offering a practical alternative for high-throughput genetic association analysis.

Statistical Modeling of Saturated BJT Circuits with Component Tolerances

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Leonardo Rodrigues Miranda¹, Hudson Vieira de Sousa^{1,2}, Pedro de Sousa Freitas¹

¹Federal Institute of Brasília (IFB), Brazil. ²University of Brasília (UnB), Brazil

The statistical modeling of electronic circuits under parametric uncertainty provides a consistent framework for integrating probability theory into technical education. This work considers a bipolar junction transistor (BJT) operating in the saturation region, where semiconductor voltages and passive components exhibit bounded variability. The electrical parameters are modeled as independent random variables with uniform distributions,

$$V_{BE} \sim U(0.7, 0.8), \quad V_{CE} \sim U(0.1, 0.2), \quad R \sim U(0.8R_0, 1.2R_0),$$

representing manufacturing tolerances and admissible operating ranges.

In a DC saturated configuration, the base and collector currents are given by

$$I_B = \frac{V_{in} - V_{BE}}{R_B}, \quad I_C = \frac{V_{CC} - V_{CE}}{R_C}.$$

Since these quantities depend on uniformly distributed inputs, the resulting outputs are also random variables defined through nonlinear transformations. Under independence assumptions, the expected values can be approximated analytically using first-order propagation,

$$\mathbb{E}[I_C] \approx \frac{V_{CC} - \mathbb{E}[V_{CE}]}{\mathbb{E}[R_C]},$$

with

$$\mathbb{E}[V_{CE}] = 0.15, \quad \mathbb{E}[R_C] = R_0.$$

Similarly, the variability can be expressed through finite variations,

$$\Delta I_C \approx \left| \frac{\Delta V_{CE}}{R_C} \right| + \left| \frac{(V_{CC} - V_{CE})}{R_C^2} \Delta R_C \right|.$$

Considering uniform distributions $U(a, b)$, the variation can be associated with the interval width,

$$\Delta X = b - a,$$

which provides a direct measure of uncertainty spread.

This formulation allows a direct analytical connection between circuit theory and statistical descriptors such as mean and variability, without relying on numerical simulation. The uniform distribution plays a central role as a non-informative model, assuming equal likelihood within tolerance intervals, which is particularly appropriate in early-stage engineering analysis.

From an educational perspective, this approach provides a clear and mathematically tractable framework for introducing uncertainty, variability, and sensitivity analysis in electronic systems. The results indicate that uniform modeling not only captures realistic component behavior at a first-order level but also serves as an effective pedagogical bridge between applied electronics and foundational statistics for technical-level students.

On the learnability and sample complexity of RL with recursive OCE preferences

Oliver Mortensen
University of Copenhagen

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

We study risk-sensitive reinforcement learning in finite discounted Markov decision processes (MDPs), where a generative model of the MDP is assumed to be available. We consider a family of risk measures derived from the optimized certainty equivalent (OCE) of a utility function u , which provides a unifying framework for a large class of risk measures which includes important risk measures such as entropic risk, CVaR, and mean-variance. Our focus is on the sample complexities of learning the optimal state-action value function (value learning) and an optimal policy (policy learning) when the objective is defined recursively with respect to an OCE-induced risk measure. We provide an exact characterization of utility functions u for which the corresponding OCE defines an objective that is PAC-learnable. We analyse a simple model-based approach and derive PAC sample complexity bounds that are polynomial and in fact optimal in the number of states S , the number of actions A and the PAC-parameters ε and δ . The dependence on the effective horizon $\frac{1}{1-\gamma}$, where $\gamma \in (0, 1)$ is the discount factor depends on the shape of the utility function and can thus yield exponential dependence on the effective horizon which is the case for the entropic risk measures. We establish that whenever u does not have full domain $\text{dom}(u) \neq \mathbb{R}$, the corresponding problem is not PAC learnable. Finally, we establish corresponding lower bounds for both value and policy learning, demonstrating tightness in $S, A, \varepsilon, \delta$, and for a more restricted class of utilities, we derive lower bounds that makes the dependence on the effective horizon $\frac{1}{1-\gamma}$ explicit, and which can be tighter than state-of-the-art for CVaR $_{\tau}$ in the $\tau \ll \frac{1}{1-\gamma}$ regime.

Adaptive-Bias Random Walk in Static and Dynamic Percolation

William Nordansjö
Lund University

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

We study how a simple agent moves through a changing and partially blocked environment. A random walker on a lattice repeatedly attempts to move to a randomly chosen neighboring site at rate one. If the chosen edge is open, the move succeeds. If it is closed, the walker remains in place until the next attempt. In the dynamic setting, the environment evolves as edges open and close randomly over time, governed by a refresh rate μ and openness parameter p , while in the static case the configuration is fixed.

Recent theoretical results show that in dimension $d \geq 2$, the long-term speed of a biased walker can behave differently depending on the environment. Increasing the bias may either improve or reduce the asymptotic speed. However, how this behavior appears at realistic parameter values and finite times remains less understood.

Using simulations in three dimensions, we investigate both average speed and the occurrence of “stall” events, defined as periods of repeated failed movement. We find that while mean speed often saturates as bias increases, stall events grow rapidly in both frequency and severity, particularly in slowly evolving environments. This indicates that rare but significant trapping events dominate the dynamics well before asymptotic effects become visible.

Motivated by this tradeoff, we introduce an adaptive walker that adjusts its bias based on recent failures. Our results suggest that while strong constant bias is near-optimal in open or fast dynamic environments, adaptive strategies reduce extreme stalls and can improve transport in more restrictive or static settings.

Poster
Wednesday 3
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Agora
(1st floor)

Time Reversibility Testing for Stochastic Processes

Hedvika Ranošová
Charles University

Time reversibility, or its absence, represents a fundamental property of stochastic processes. We introduce tests for the time reversibility of continuous-time stochastic processes. The Cramér-von Mises type test statistic is based on the distance between empirical characteristic functionals, which allows for testing equality of distributions. In addition to classical time reversibility, we explore several alternative formulations to include seemingly non-reversible processes, such as the standard Wiener process. We derive the asymptotic behavior of the test statistic given a sample of either independent or weakly dependent continuous functions. Due to the intricate asymptotic behavior of the test statistics, critical values are obtained through a resampling approach, via either a block bootstrap or a Bernoulli mixture. The effectiveness of the proposed tests is evaluated through simulation studies and further demonstrated using S&P 500 market data.

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Belyaev-Waiting model: From Waiting Times to Birth Control

Rebecca Schmitz^{1,2}, Per Arnqvist¹, Natalya Pya Arnqvist¹
¹Umeå University ²Otto-Friedrich University Bamberg

Understanding how the level of fertility control influences birth counts in a population is a highly relevant question, yet measuring it in a way that is comparable across time and countries remains difficult, especially if only aggregated data is available. Marital fertility has been studied using age-specific fertility rates, with models such as the Coale-Trussell fertility intensity specification. This model assumes that births within each age group follow a Poisson distribution. However, evidence shows systematic underdispersion in birth counts, which violates this assumption.

An alternative approach, the Belyaev-Waiting model, suggested by Arnqvist (2017), relies on individual fertility data and introduces the concept of waiting time between pregnancies. This model allows us to better understand fertility intensity as the intensity of a woman becoming pregnant. Simulation studies show that the Belyaev-Waiting model provides substantially more accurate parameter estimates in comparison to the classical Coale-Trussell model, when applied to data generated from the renewal process underlying the model. In this work, we apply the Belyaev-Waiting model in a cross-national setting to data from the Human Fertility Database at several time points to capture the level of birth control intensity and its change over time within and across populations. Additionally, we investigate potential drivers of the level of birth control in a population by analyzing the relationship between the estimated level of birth control and various sociodemographic and economic factors at the country-level.

References:

Arnqvist, P. (2017). Functional clustering methods and marital fertility modelling (Doctoral dissertation, Umeå universitet).

Neural Simulation-Based Inference for Earthquake Modeling in the North Atlantic

Øyvind H. Singsaas

Norwegian University of Science and Technology (Norway)

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

We consider statistical modeling of seismicity in the North Atlantic–Nordic region using a recently unified earthquake catalogue combining data from the International Seismological Centre (ISC), the Norwegian National Seismic Network (NNSN), the Icelandic Meteorological Office (IMO), and the NORSAR network. The merged dataset contains several hundred thousand events and provides unprecedented spatial and temporal coverage across Greenland, Iceland, Norway, and Svalbard. In this work, we focus on a seismically active region along the Norwegian coast.

To model clustering and triggering mechanisms in seismic activity, we adopt an Epidemic-Type Aftershock Sequence (ETAS) framework, extended to incorporate environmental covariates inspired Adelfio and M. Chiodi (2020). Classical likelihood-based inference for such models is computationally demanding, particularly in the presence of covariates and large datasets. We therefore explore neural simulation-based inference (SBI) methods such as SB-ETAS of Stockman et al. (2024), which replace the intractable likelihood with a learned neural approximation based on simulated data.

Building on recent developments in simulation-based ETAS modeling and neural likelihood estimation, we investigate approaches based on neural density estimation and classifier-based likelihood ratios. Particular emphasis is placed on scalable inference, the role of summary statistics, and the integration of covariates such as meteorological variables, fault lines, and sensor locations. The goal is to assess whether neural SBI methods can provide accurate and computationally efficient inference for complex marked space-time point process models in seismology. This work aims to contribute toward flexible and scalable tools for earthquake modeling, with potential applications in seismic hazard assessment.

References:

G. Adelfio and M. Chiodi. Including covariates in a space-time point process with application to seismicity. *Statistical Methods & Applications*, 30, July 2020. doi: 10.1007/s10260-020-00543-5.

S. Stockman, D. Lawson, and M. Werner. SB-ETAS: using simulation based inference for scalable, likelihood-free inference for the ETAS model of earthquake occurrences. *Statistics and Computing*, 34(5), Aug. 2024. ISSN 0960-3174. doi: 10.1007/s11222-024-10486-6.

Triply Scalable Equivariant GP modeling

Tim Steinert

University of Bern

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Gaussian process (GP) models offer a principled framework for probabilistic predictions and have been shown to allow enforcing prior knowledge including equivariances, but the use of equivariant GPs in large-scale scientific problems is limited by associated computational costs. While equivariant neural networks are commonly used in current practice, they typically do not come with the benefits of GPs concerning uncertainty quantification, that can be instrumental in support of predictions and scientific discovery in fields such as molecular research. Also, inputs can themselves be high-dimensional and/or with equivariances involving groups with high orders, called for scalability.

We introduce triply scalable equivariant Gaussian processes based on a flexible class of integration-free equivariant kernels that encode group actions directly at the level of the covariance structure. These kernels are straightforward to evaluate, avoid costly group integration, and naturally extend to vector-valued quantities and molecular systems with increasing numbers of atoms. Leveraging the stability of GP equivariance under conditioning, we construct equivariant sparse GPs via suitable mean functions and covariance kernels. We instantiate the framework using integration-free equivariant kernels, resulting in scalable and data-efficient GP inference schemes. We employ equivariant sparse variational Gaussian processes for $SO(2)$ -equivariant vector fields and for molecular

property prediction, and preconditioned conjugate gradient-based exact GP inference for large-scale molecular systems. We illustrate the approach on synthetic $SO(2)$ -equivariant fields and on the prediction of rotationally equivariant molecular electric dipole moments of N-Methylformamide, achieving accurate, uncertainty-aware predictions at a fraction of the computational cost of classical GP inference.

Gaussian Process Sound Field Reconstruction Under Finite-Window Observations

David Sundström

Centre for Mathematical Sciences, Lund University

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

We study the problem of reconstructing a sound field from distributed microphone measurements under causal, finite-window observations. Existing approaches are typically formulated in the frequency domain and rely on independence between frequency components. While this assumption yields tractable covariance models, it is no longer valid after causal finite-window truncation, which induces dependence across frequencies.

To address this issue, we formulate the reconstruction problem directly in the spatio-temporal domain. The sound field is modeled as the solution to the wave equation driven by a stationary stochastic spatio-temporal source distribution, which induces a covariance model for the observed field. Within this framework, we derive the optimal linear estimator of the sound field from causal finite-window microphone data.

A main practical challenge is that the computational cost grows rapidly with the number of microphones and time samples. We therefore introduce a budget-constrained spatio-temporal sampling problem: selecting an informative subset of spatio-temporal observations by minimizing the posterior reconstruction variance. This yields a principled criterion for trading reconstruction accuracy against computational complexity.

The proposed methodology is illustrated in numerical experiments with both simulated and measured data, showing how causal spatio-temporal estimation and optimized sample selection improve reconstruction in real-time settings.

Bayesian phenomenological modeling of the flight curve of a multi-voltine butterfly

Ilmari Talo

University of Helsinki

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Butterflies are widely considered as important indicators of environmental change and ecosystem health. Extensive longitudinal data of butterfly abundances is collected in *Butterfly Monitoring Schemes* (BMSs) in several European countries, including Finland. This data allows us to study the annual phenology of different butterfly species by estimating their *flight curve* (species abundance as a function of time within flying season).

A phenomenological model for estimating the flight curve using a sum of Gaussian functions with varying locations, scales and heights was introduced by Dennis et al. (2016). The model uses (a sum of) one or two Gaussian functions to estimate the flight curves of species with one or two distinct annual generations. This parametric representation of the flight curve allows for a straightforward analysis of species phenology.

I present a Bayesian extension of the model for the small tortoiseshell butterfly – a species exhibiting up to three distinct generations annually – tested with abundance data from the Finnish BMS. The Bayesian framework, combined with the interpretable parametrization of the flight curve, allows us to easily incorporate prior ecological knowledge in the form of prior distributions. The new model also incorporates ecologically motivated hierarchical structure between parameters of different years and sites.

References:

Dennis, E.B., Morgan, B.J.T., Freeman, S.N. et al. Dynamic Models for Longitudinal Butterfly Data. *JABES* 21, 1–21 (2016). <https://doi.org/10.1007/s13253-015-0216-3>

Variational Bayesian inference for a nonlinear ODE inverse problem

Maria Tirronen

Natural Resources Institute Finland (Luke)

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Parameter inference for nonlinear ordinary differential equation (ODE) models is computationally demanding and often ill-posed. We consider the inverse problem of the allometric trophic network (ATN) model, a high-dimensional ecological ODE system, and investigate recovery of functional response parameters from time-series data.

We develop a mean-field variational Bayesian approach in which the ODE solver is embedded in a Bayesian neural network formulation. To avoid costly gradient computation through the numerical solver, variational inference is combined with derivative-free evolutionary optimization (CMA-ES). The framework enables practical approximate Bayesian inference with constraints that regularize the inverse problem.

Using synthetic data, we evaluate parameter recovery, predictive performance, and indications of multimodality, and compare results with ordinary least squares (OLS). The variational approach yields parameter estimates comparable to OLS in accuracy and produces good predictive dynamics despite non-uniqueness in the inverse problem. These results highlight both the identifiability challenges of nonlinear ODE systems and the potential of variational Bayesian methods for approximate inference in complex dynamic models.

Disaggregation of residential building electricity consumption: Insights for energy efficiency and resilience

Denise Uwamariya

Swedish Defence University

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Geopolitical tensions and an increase in the number of sabotages have led to an increased need to understand where we can reduce electricity consumption in times of energy crisis. Smart energy meters are being deployed in residential buildings to monitor electricity consumption at a high temporal resolution, enabling electricity consumers to manage their consumption and suppliers to efficiently manage billing and supply. However, typical electricity meters installed in residential buildings only provide an aggregate of the household's consumption at the main fuse, not providing information about the consumption of individual appliances. This paper proposes a statistical method to disaggregate household's electricity consumption data from smart meters to understand how electricity is consumed at appliance-level. We demonstrate the method using a Swedish dataset containing smart meter data from 10,609 households. The results show that, throughout the week, the most electricity is consumed for heating and kitchen appliances. Comparing our results with previous literature, we see that lighting has become more efficient, while we see an increase in the use of electronic and entertainment appliances compared to previous years. The results of this study will help in targeted communication to citizens in time of an energy crisis, to effectively reduce electricity consumption in an effort to avoid large-scale blackouts. The results also give insight into the type of appliances where we can gain most in energy efficiency development.

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

A Bayesian regression framework for circular models with INLA

Xiang Ye^{*1}, Janet van Niekerk^{1,2}, Håvard Rue¹

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Advancements in computational power and methodologies have enabled research on massive datasets. However, tools for analyzing data with directional or periodic characteristics, such as wind directions, instrument turning angles and time-of-day effects, remain underdeveloped. While statisticians have proposed circular distributions for such analyses, significant challenges persist in constructing circular statistical models, particularly in the context of regression modeling, since the concept of building a linear predictor from linear combinations of covariates and various random effects, breaks the circular nature of the variable.

We developed a new Bayesian framework to rectify this issue, leading to well-defined regression models for circular responses when the data are concentrated. Our approach extends naturally to joint regression models where we can have several circular and non-circular responses, and allow us to handle a mix of linear covariates, circular covariates and various random effects. Our formulation aligns naturally with the integrated nested Laplace approximation (INLA), which provides fast and accurate Bayesian inference. Overall, the aim is to provide tools and guidance that make Bayesian methods more useful in circular statistics, both in methodology and in practice.

To select or not to select - predictively consistent priors instead of model selection

Poster
Wednesday 3
16:30-18:30
Agora
(1st floor)

Anna Elisabeth Riha
Aalto University (Finland)

Bayesian modelling workflows often require the consideration of different candidate models. Approaches for model selection in the Bayesian framework aim to support the modeller in navigating potential trade-offs between model complexity and generalisability of the results to yet unobserved data. In this work, we propose a change of perspective towards choosing predictively consistent priors, instead of relying on model selection after the fact. We revisit the issue of overfitting, and clarify why model selection is not necessarily needed and can even be harmful in case of finite data. When integrating over the posterior and using predictively consistent priors, even if those priors are considered weakly informative, we can often safely use flexible models with a large number of parameters. Using extensive numerical experiments, we illustrate the relevance of appropriate prior choices, as well as the limitations and alternatives for model selection in different modelling tasks, including forward variable selection and increasing the complexity of nonlinear models. We also investigate different implications for the predictive consistency of the priors depending on the chosen nonlinear model and provide detailed examples for adjusting R^2 -based priors for logistic regression models and models that include a known relevant treatment covariate in the analysis of randomised controlled trials.

Co-authors: Leevi Lindgren, David Kohns, Aki Vehtari

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