NBBC09: conference program

Tuesday, 9th June
14:00 – 18:00 Pre-conference course (day 1)

Wednesday, 10th June

9:00 – 13:00	Pre-conference course (day 2)
14:00 – 14:30	**Opening plenary**, chair: Krista Fischer – L111
	Kristjan Haller (Vice-Rector of the University of Tartu), Geir Egil Eide (President of the IBS Nordic Region)
14:30 – 15:30	**Keynote lecture:**
	Nanny Wermuth, *What does indirect confounding imply for meta-analyses?*
15:30 – 16:00	Coffee break

	I1: **Statistics in demography** (chair: Esa Läärä)	C1: **Bioinformatics I** (chair: Marijus Radavičius)	C2: **Spatio-temporal modeling** (chair: Eric Renshaw)
16:00 – 17:30	16:00 Ene-Margit Tiit, *Census – the first step in the history of (bio-) statistics*	16:00 Jukka Corander, *Bayesian clustering and feature selection for cancer tissue samples*	16:00 Juha Heikkinen, *Assessing the uncertainty of the polygonal declustering estimator of a spatial mean*
	16:35 Juha Alho, *Dual System Estimation of Drug Abuse*	16:22 Jukka Sirén, *Reconstructing Population Histories from Single-Nucleotide Polymorphism Data*	16:22 Laura Saltyte, *Spatial-temporal modeling of Baltic Sea coastal zone parameters*
	17:10 Discussion (discussant Niels Keiding)	16:44 Jüri Lember, *Measuring goodness of segmentation performed with hidden Markov models*	16:44 Ottmar Cronie, *Improved estimation in a spatio-temporal growth-interaction model*
		17:06 Rimantas Eidukevičius, *A Simple Stochastic Cell Cycle Model with Application to Cytometry Data*	17:06 Jaan Liira, *European biodiversity is still impacted by nature – spatial autocorrelation in mixed models*

18:30 – 21:00	**Welcome reception at the University History Museum, Toome Hill**

Thursday, 11th June

9:00 – 10:00	**Keynote lecture** (chair: Bendix Carstensen)
	Martyn Plummer, *Bayesian hierarchical modelling with JAGS*
10:00 – 10:30	Coffee break

	I2: **Bioinformatics** (chair: Jüri Lember)	C3: **Causal inference** (chair: Carlo Berzuini)	C4: **Statistics in epidemiology** (chair: Juha Karvanen)
10:30 – 12:00	10:30 Timo Koski, *De Novo Detection of DNA: Regulatory Binding Regions Using a Bayesian Random Frame Model*	10:30 Olli Saarela, *Bayesian nonparametric monotonic regression*	10:30 Elina Parviainen, *Feature extraction in visualizing and describing a predictive classifier: A case study*
	11:05 Daniel Gudbjartsson, *Learning from the results of genome-wide association studies*	10:52 Elja Arjas, *Predictive Bayesian inference and dynamic treatment regimes: the MACS data revisited*	10:52 Jurate Saltyte Benth, *Modelling and prediction of weekly influenza A specimens in England and Wales*
	11:40 Discussion (discussant Jukka Corander)	11:14 Peter Jakobs, *Major treatment incompliance (including unplanned "cross-over" of study treatment): structural nested failure time model as an alternative analysis method?*	11:14 Nora Fenske, *Boosting Additive Quantile Regression for Investigating Childhood Malnutrition*
		11:36 Krista Fischer, *The role of baseline covariates in the causal inference of randomized clinical trials*	11:36 John Öhrvik, *Factor Analysis of the Metabolic Syndrome Identifies two Factors with Different Survival Patterns in Elderly*

12:00 – 13:30	Lunch at restaurant *Püssirohukelder*, Lossi 28

13:30 – 15:00	I3: **Causal inference in genetics** (chair: Jukka Corander) 13:30 Stijn Vansteelandt, *Semiparametric tests for sufficient cause interactions* 14:05 Carlo Berzuini, *Causal inference in genetic epidemiology* 14:40 Discussion (discussant Claus Ekstrøm)	C5: **Statistics in ecology and forestry** (chair: Jaan Liira) 13:30 Birgir Hrafnkelsson, *Estimation of discharge rating curves with B-splines* 13:52 Mark Brewer, *A Temporal Compositional Analysis of Water Quality Monitoring Data* 14:14 Artur Nilson, *Test of the Family of rth-functions for Growth and Distribution Models* 14:36 Crispin Mutshinda, *Teasing out the workings of community dynamics*	C6: **Clinical tests and measurement** (chair: Nora Fenske) 13:30 Rima Kregzdyte, *Statistical detection of cut-off cadmium concentration in breast cancer etiopathogenesis study* 13:52 Rossana Moroni, *Statistical modelling of measurement errors in gas chromatographic analyses of blood alcohol content* 14:14 Bendix Carstensen, *Practical aspects of assessing agreement of clinical measurement methods* 14:36 Kristi Kuljus, *Comparing Experimental Designs for Benchmark Dose Calculations for Continuous Endpoints*
15:00 – 15:30	**Poster session with coffee** (L-111 and Foyer)		
15:30 – 17:00	I4:**Life course epidemiology** (chair: Thor Aspelund) 15:30 Mervi Eerola, *Comparing methods for life-course analysis – an example: pathways to adulthood* 16:00 Sven Ove Samuelsen, *Case-cohort and nested case-control studies: Differences and similarities* 16:30 Kristiina Rajaleid, *Size at birth, adult body mass index, and risk of myocardial infarction in the SHEEP study*	C7: **Bioinformatics** II (chair: Jukka Sirén) 15:30 Marijus Radavičius, *Local reverse-complement symmetry of DNA sequences* 15:52 Tomas Rekašius, *A method of visualization of DNA sequences* 16:14 Erinija Pranckeviciene, *Elucidating predictably different phenotypes by multiclass classification and clustering*	C8: **Statistical modeling** (chair: Mark Brewer) 15:30 Søren Højsgaard, *Where are the cows and what are they doing* 15:52 Lauri Jauhiainen, *Effect of a pen in group feeding trials: modeling data from suckler cows* 16:14 Johannes Forkman, *The performance of best linear unbiased prediction in small randomised complete block experiments* 16:36 Peter Dalgaard, *Ideas about likelihood-based data analysis in R*
17:30 – 19:00	**Guided walks in Tartu** (see the social programme section for options)		
20:00 – 22:00	**Conference dinner at the restaurant "Atlantis"**		

Friday, 12th June

9:00 – 10:00	**Keynote lecture:** (chair: Jun Yu) Eric Renshaw, *Stochastic Growth/Interaction Strategies for Simulating Spatial-Temporal Marked Point Processes*		
10:00 – 10:30	Coffee break		
10:30 – 12:00	I5: **Spatial statistics** (chair: Juha Heikkinen) 10:30 Geir Aamodt, *Cluster of disease: making or solving problems* 11:05 Aki Vehtari, *Advances in Gaussian processes for spatial epidemiology* 11:40 Discussion (discussant Jun Yu)	C9: **Statistical genetics** (chair: Tanel Kaart) 10:30 Matti Pirinen, *Bayesian QTL mapping based on reconstruction of recent genetic histories* 10:52 Bob O'Hara, *Estimating heritability of fluctuating asymmetry in Sticklebacks* 11:14 Klara Verbyla, *Comparison of Bayesian models for genomic selection using real dairy data*	C10 **Survival analysis** (chair: Peter Dalgaard) 10:30 Karri Seppä, *Mean and median survival times of cancer patients should account for informative censoring and general mortality predictions* 10:52 Juha Karvanen, *Visualizing covariates in proportional hazards model* 11:14 Priyantha Wijayatunga, *Asymptotic properties of collective conditional likelihood estimators for Bayesian network classifiers with censored data* 11:36 Szilard Nemes, *Bootstrap confidence intervals for dynamic path models*
12:00 – 12:30	**Closing** – L-111		