

List of works published by Dario Gasbarra (December 2007)

Publications in university series

[1]. Ph.D. dissertation: 'Bayesian inference for models based on point processes, by using Markov chain methods'(1997). *Acta Universitatis Ouluensis* **A 302**.

Publications in international refereed journals

[2]. Arjas E. & Gasbarra D. (1994) 'Nonparametric Bayesian inference from right censored survival data using the Gibbs sampler'. *Statistica Sinica* **4** 505-524.

[3]. Arjas E. & Gasbarra D. (1996) 'Bayesian inference of Survival probabilities under stochastic ordering constraints'. *JASA* **91** 1101-1109.

[4]. Arjas E. & Gasbarra D. (1997) 'On prequential model assessment in life history analysis'. *Biometrika* **84** 505-522.

[5]. Gasbarra D. & Karia S. (2000) 'Analysis of competing risks by using Bayesian smoothing'. *Scandinavian Journal of Statistics* **27** 605-617.

[6]. Kulathinal S. B. , Kuulasmaa K., & Gasbarra D. , (2002) 'Estimation of association between trends in event rates and trends in risk factors in the presence of measurement errors using EM-algorithm'. *Statistics in Medicine*, 21(8) 1089-1101 .

[7]. Kulathinal S. & Gasbarra D. (2002) 'Testing equality of cause-specific hazard rates corresponding to m competing risks among K groups'. *Lifetime Data Analysis* 8(2), 147-161.

[8]. Eerola, M., Gasbarra, D., Mäkelä, P.H., Linden, H, Andreev, A. (2003):' Joint modelling of recurrent infections and antibody response by Bayesian data augmentation'. *Scandinavian Journal of Statistics* 30 (4) 677-698.

[9]. Gasbarra D. & Valkeila E. (2004) Initial Enlargement: a Bayesian approach. *Theory of Probability and Mathematical Statistics* Vol. 9 (25), no. 3-4, pp 26-37.

[10]. Gasbarra D., Mikko J. Sillänpää and Elja Arjas (2005). Backward simulation of ancestors of sampled individuals *Theoretical Population Biology* 67:75-83).

[11]. Gasbarra D. Kulathinal S.B., Dewan I and Nissinen A. (2006) Testing dependence between the failure time and failure modes: An application of enlarged filtration. *Journal of statistical planning and inference*, 136, 1669-1686.

[12]. Gasbarra D. & Sillanpää M. (2006) Constructing parental linkage phase and genetic map over distances $< 1\text{cM}$ using Pooled Haploid DNA. *Genetics* 172 (2) 1325-1335.

[13]. Pirinen M. & Gasbarra D. (2006) Finding Consistent Gene Transmission Patterns on Large and Complex Pedigrees. *IEEE Transactions in Computational Biology and Bioinformatics* 3 (3) 252-261.

[14]. Gasbarra D., Pirinen M., Sillanpää M., Salmela E. and Elja Arjas (2007). Estimating genealogies from unlinked marker data: a Bayesian approach. *Theoretical Population Biology* 72, 305-322.

[15]. Gasbarra D., Pirinen M., Sillanpää M. and Elja Arjas (2007). Estimating genealogies from marker data: a Bayesian approach. *BMC Bioinformatics* 8:411.

Publications in refereed conference proceedings

[16]. Gasbarra D. Esko Valkeila and Lioudmila Vostrikova (2006). Enlargement of filtration and additional information in pricing models: A Bayesian approach. In *The Shiryaev Festschrift, from Stochastic Calculus to Mathematical Finance*, edited by Kabanov Liptser and Stoyanov, pp 257-285, Springer Berlin.

[17]. Gasbarra D. Tommi Sottinen and Esko Valkeila (2007). Gaussian bridges. in *Stochastic Analysis and Applications, Proceedings of the Abel symposium 2005 in honour of Kiyosi Ito*, pp 361-381, Springer.

Unpublished manuscripts, available at <http://www.RNI.Helsinki.FI/~dag/>

[18]. Gasbarra D. (2000) 'Particle filters for counting process observations' (under revision).

[19] Kulathinal S., Gasbarra D., Kinra S., Ebrahim S., and Sillanpää M.J. (2007) *Estimation of additive genetic and environmental sources of quantitative trait variation using data on married couples and their siblings*. (Communicated).

[20] Karvanen J., Kulathinal S., Gasbarra D. (2007) *D-optimal Designs for Collecting Genetic Information in Follow-up Studies*. (Communicated).

Short communcations in refereed journals

[21]. Sillapää, M. J., D. Gasbarra, and E. Arjas (2004): Comment on the "On the Metropolis-Hastings acceptance probability to add or drop a quantitative trait locus in Markov Chain Monte Carlo-based Bayesian analyses". *Genetics* 167: 1037-1037.