

## ANDREA RIEBLER: PUBLICATIONS

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### PUBLICATIONS IN INTERNATIONAL JOURNALS WITH PEER-REVIEW

1. Simpson, D., Rue, H., Riebler, A., Martins, T. G., and Sørbye, S. H. (2017). Penalised model component complexity: A principled, practical approach to constructing priors (with discussion). *Statistical Science*. **32**(1): 1–28.
2. Guo, J., Riebler, A. and Rue, H. (2017). Bayesian bivariate meta-analysis with interpretable priors. *Statistics in Medicine*. Online first.
3. Etxeberria, J., Goicoa, T., López-Abente, G., Riebler, A., and Ugarte, M.D. (2017) Spatial gender-age-period-cohort analysis of pancreatic cancer mortality in Spain (1990-2013). *PLOS ONE*. **12**(2). e0169751.
4. Riebler, A. and Held, L. (2017). Projecting the future burden of cancer: Bayesian age-period-cohort analysis with integrated nested Laplace approximations. *Biometrical Journal*. **59**(3): 531–549.
5. Rue, H., Riebler, A., Sørbye, S. H., Illian, J. B., Simpson, D. P., Lindgren, F. K. (2017). Bayesian computing with INLA: A review. *Annual Review of Statistics and Its Application*. Volume 4.
6. Guo, J. and Riebler, A. (2016). meta4diag: Bayesian bivariate meta-analysis of diagnostic test studies for routine practice. *Journal of Statistical Software*. Accepted. Former version available here: <http://arxiv.org/abs/1512.06220>.
7. Riebler, A., Sørbye, S. H., Simpson, D. P. and Rue, H. (2016). An intuitive Bayesian spatial model for disease mapping that accounts for scaling. *Statistical Methods in Medical Research*. **25**(4): 1145-1165.
8. Muff\*, S., Riebler\*, A., Rue, H., Saner, P. and Held, L. (2015). Bayesian analysis of measurement error models using integrated nested Laplace approximations. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*. **64**(2): 231–252. \*These authors contributed equally.  
Paper has been invited to be presented at Royal Statistical Society (RSS) 2015 conference in Exeter, UK.
9. Riebler, A., Menigatti, M., Song, J.Z., Statham, A. L., Stirzaker, C., Mahmud, N., Mein, C. A., Clark, S. J. and Robinson, M. D. (2014). BayMeth: Improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach. *Genome Biology*. **15**(2): R35.
10. Papoila, A. L., Riebler, A., Amaral-Turkman, A. São-João, R., Ribeiro, C., Geraldes, C. and Miranda, A. (2014). Stomach cancer incidence in Southern Portugal 1998–2006: a spatio-temporal analysis. *Biometrical Journal*. **56**(3): 403–415.
11. Held L. and Riebler, A. (2013). Comment on “Assessing validity and application scope of the intrinsic estimator approach to the age-period-cohort (APC) problem”. *Demography*. <http://dx.doi.org/10.1007/s13524-013-0255-8>
12. Riebler, A., Held, L. and Rue, H. (2012). Estimation and extrapolation of time trends in registry data – Borrowing strength from related populations. *Annals of Applied Statistics*. **6**(1): 304–333.
13. Riebler, A., Held, L., Rue, H. and Bopp, M. (2012). Gender-specific differences and the impact of family integration on time trends in age-stratified Swiss suicide rates. *Journal of the Royal Statistical Society: Series A (Statistics in Society)*. **175**(2): 473–490.
14. Held, L. and Riebler, A. (2012). A conditional approach for inference in multivariate age-period-cohort models. *Statistical Methods in Medical Research*. **21**(4): 311–329.
15. Schrödle, B., Held, L., Riebler, A. and Danuser, J. (2011). Using INLA for the evaluation of veterinary surveillance data from Switzerland: A case study. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*. **60**(2): 261–279.

16. Paul, M., Riebler, A., Bachmann, L., Rue, H. and Held, L. (2010). Bayesian bivariate meta-analysis of diagnostic test studies using integrated nested Laplace approximations. *Statistics in Medicine*. **29**(12): 1325–1339.
17. Riebler, A. and Held, L. (2010). The analysis of heterogeneous time trends in multivariate age-period-cohort models. *Biostatistics*. **11**(1): 57–69.
18. Gautier, M., Flori, L., Riebler, A., Jaffrézic, F., Laloé, D., Gut, I., Moazami-Goudarzi, K. and Foulley, J. L. (2009). A whole genome Bayesian scan for adaptive genetic divergence in West African cattle. *BMC Genomics*. **10**(1): 550+.
19. Held, L. and Riebler, A. (2009). Discussion of Rue et al. (2009). *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*. **71**(2): 357–358.
20. Riebler A., Held L. and Stephan W. (2008). Bayesian variable selection for detecting adaptive genomic differences among populations. *Genetics*. **178**(3): 1817–1829.

#### BOOK CHAPTER IN AN INTERNATIONAL BOOK WITH PEER-REVIEW

Riebler, A., Robinson, M. D., and van de Wiel, M. A. (2014). Analysis of Next Generation Sequencing Data Using Integrated Nested Laplace Approximation (INLA). In “Statistical Analysis of Next Generation Sequencing Data” (pp. 75-91). Springer International Publishing.

#### TECHNICAL REPORTS

1. Höhle, M. and Riebler, A. (2005). The R-Package ‘surveillance’. Discussion Paper No. 422, SFB 386. University of Munich, Department of Statistics.

#### CONFERENCE PROCEEDINGS WITHOUT PEER-REVIEW

Guo, J., Riebler, A., and Rue, H. (2015). Making Bayesian bivariate meta-analysis practice friendly. In: *Proceedings of the 30th International Workshop on Statistical Modelling*, H. Friedl and H. Wagner, Editors.

Riebler, A., Held, L. and Rue, H. (2011). Modelling seasonal patterns in longitudinal profiles with correlated circular random walks. In: *Proceedings of the 26th International Workshop on Statistical Modelling*, D. Conesa, A. Forte, A. López-Quílez and F. Muñoz, Editors. 503–508.

Riebler, A., Held, L. and Rue, H. (2010). Correlated GMRF priors for multivariate age-period-cohort models. In: *Proceedings of the 25th International Workshop on Statistical Modelling*, A. Bowman, Editor. 455–460. (Awarded as best student paper of the IWSM 2010.)

#### REFEREEING

**Reviewer of journal articles:** *Annals of Applied Statistics* (2012:1), *Australian and New Zealand Journal of Statistics* (2014:2), *Bayesian Analysis* (2015:2), *Bioinformatics* (2011:1), *Biometrical Journal* (2014: 1, 2015:1), *Biometrics* (2012:2), *Demographic Research* (2015:1), *Environmetrics* (2013:2), *JAIDS* (2014:1), *Journal of the Royal Statistical Society—Series B* (2013: 1), *Journal of the Royal Statistical Society—Series C* (2014: 1), *PLOS Computational Biology* (2014:1), *Stat* (2014:1), *Statistical Science* (2016:1), *Statistics in Medicine* (2010:1, 2011:4).

**Reviewer of book proposals for:** Chapman & Hall/CRC

## SOFTWARE

- Since 2015 **Author of the R-forge R-package** `BAPC`  
Implements Bayesian age-period-cohort models with the focus on projections.  
BAPC uses integrated nested Laplace approximations (INLA) for full Bayesian inference.  
Hosted on: [https://r-forge.r-project.org/R/?group\\_id=2054](https://r-forge.r-project.org/R/?group_id=2054)
- Since 2015 **Co-author of the CRAN R-package** `meta4diag`  
Bayesian inference analysis for bivariate meta-analysis of diagnostic test studies using INLA.  
A purpose built graphic user interface based on shiny is available.  
Hosted on: <https://cran.r-project.org/web/packages/meta4diag/index.html>
- Since 2009 **Committer/maintainer of the project** `R-INLA`  
Implements approximate Bayesian inference using integrated nested Laplace approximations.  
Hosted on: <http://www.r-inla.org>, <https://bitbucket.org/hrue/r-inla>
- 2012–2013 **Co-author of the Bioconductor R-package** `Repitools`  
Implements tools for the analysis of enrichment-based epigenomic data.  
Including a novel empirical Bayes model called BayMeth to quantify DNA methylation.  
Hosted on: <http://bioconductor.org/packages/release/bioc/html/Repitools.html>
- 2004 **Co-author of the CRAN R-package** `surveillance`  
Implements statistical tools for outbreak detection in routinely collected surveillance data.  
Assisted in development and implementation.  
Hosted on: <https://cran.r-project.org/web/packages/surveillance/index.html>

## INVITED TALKS

- 11/05/2016 *Bayesian hierarchical models for routine use: What do we need?*  
ZüKoSt: Seminar for Applied Statistics, ETH Zurich and University of Zurich, Switzerland.
- 31/03/2016 *Estimation and extrapolation of time trends in registry data using Bayesian age-period-cohort models*  
Statistics Seminar Series, University of Toronto, Canada.
- 04/11/2015 *An intuitive Bayesian spatial model for disease mapping that accounts for scaling*  
Scaling Problems in Statistics Seminar, Georg-August-Universität Göttingen, Germany.
- 03/06/2015 *Invited discussion of “A Few Priors of Computational Convenience” by Yee Whye Teh*  
O’Bayes 15, Valencia, Spain.
- 15/05/2015 *Projecting cancer incidence and mortality: Bayesian APC models ready for routine use*  
CRiSM seminar series, Warwick, UK.
- 02/12/2014 *Projecting the future burden of cancer: Bayesian APC analysis made simple*  
Statistics Seminar, Oslo, Norway.
- 06/11/2014 *BayMeth: Improved DNA methylation quantification for affinity capture sequencing data*  
Oslo, Norway.
- 20/06/2014 *Bayesian projections: routine analysis without Markov chain Monte Carlo*  
Workshop on Spatial-temporal Models in Epidemiology and Health, Lisbon, Portugal.
- 12/12/2013 *BayMeth: Improved DNA methylation quantification for affinity capture sequencing data*  
University of Bergen, Norway.
- 07/10/2013 *BayMeth: Improved DNA methylation quantification for affinity capture sequencing data*  
VU University medical center, The Netherlands.
- 12/06/2013 *Measurement error in GL(M)Ms using INLA*  
17th Norwegian Statistical meeting, Halden, Norway.
- 07/02/2013 *Measurement error in GL(M)Ms using INLA*  
NTNU, Department of Mathematical Sciences, Trondheim, Norway.

- 13/12/2012 *BayMeth: Improved DNA methylation quantification for affinity capture sequencing data*  
Bioconductor European Developers' Workshop 2012, Zurich, Switzerland.
- 23/11/2012 *Estimation and extrapolation of time trends in multivariate registry data using Bayesian age-period-cohort models*  
Research Seminar, Vienna University of Economics and Business, Austria.
- 14/11/2012 *A flexible Bayesian approach for improved DNA methylation quantification from genome-scale count data*  
Institute of Statistics, Ludwig-Maximilians-Universität München, Munich, Germany.
- 26/06/2012 *A novel empirical Bayes approach for profiling immunoprecipitation-based DNA methylation*  
ISBA 2012 conference, Kyoto, Japan.
- 18/06/2012 *Statistical methods for epidemiological and genome-scale count data*  
NTNU, Department of Mathematical Sciences, Trondheim, Norway.
- 26/05/2011 *Gaussian Kronecker product Markov random fields (with INLA)*  
INLA discussion meeting, Trondheim, Norway.
- 20/07/2009 *Latent Gaussian Markov Random Field Models: A Case Study*  
European Meeting of Statisticians 2009 (EMS 2009), Toulouse, France.
- 14/05/2009 *Performance of INLA analysing bivariate meta-regression and age-period-cohort models*  
INLA user workshop, Trondheim, Norway.
- 05/10/2007 *Bayesian Methods for Detecting Selection in the Genome*  
EES Conference 2007, Munich, Germany. (Winner of the EES prize.)

#### CONTRIBUTED TALKS

- 11/09/2015 *Choosing sensible priors for Bayesian spatial analysis in epidemiology*  
GEOMED 2015, Florence, Italy.
- 04/07/2014 *Penalising model component complexity: A principled, practical approach for constructing priors*  
Bayesian Biostatistics 2014, Zurich, Switzerland.
- 11/07/2011 *Modelling seasonal patterns in longitudinal profiles with correlated circular random walks*  
26th International Workshop on Statistical Modelling (IWSM2011), Valencia, Spain.
- 03/02/2011 *Gaussian Kronecker product Markov random fields*  
Workshop on Bayesian Inference for Latent Gaussian Models with Applications, Zurich, Switzerland.
- 05/06/2010 *Correlated GMRF priors for multivariate age-period-cohort models*  
25th International Workshop on Statistical Modelling (IWSM2010), Glasgow, Scotland.
- 21/10/2009 *Correlated Gaussian Markov Random Field Models: A Case Study*  
Norwegian University of Science and Technology (NTNU),  
Department of Mathematical Sciences, Trondheim, Norway.
- 20/10/2009 *Correlated Gaussian Markov Random Field Models: A Case Study*  
University of Tromsø, Norwegian Centre for Integrated Care and Telemedicine,  
Tromsø, Norway.
- 17/07/2008 *Modelling of Heterogeneous Time Trends in Bayesian Age-Period-Cohort Models*  
XXIVth International Biometric Conference, Dublin, Ireland.  
(Awarded as best student oral presentation of the IBC 2008.)
- 09/04/2008 *Bayesian Analysis of Multivariate Age-Period-Cohort Models*  
Norwegian University of Science and Technology (NTNU),  
Department of Mathematical Sciences, Trondheim, Norway.

- 12/03/2008 *Bayesian Age-Period-Cohort Models for Detecting Temporal Patterns in Multivariate Mortality Data*  
LIFESTAT 2008: "Statistics and Life Sciences: Perspectives and Challenges", Munich, Germany.
- 10/01/2008 *Auxiliary Mixture Sampling for Bayesian Age-Period-Cohort Models*  
Leopoldina Symposium "Recent Challenges for Statistics in the Biosciences – 100 Years after Gustav Zeuner", Freiberg, Germany.
- 16/11/2007 *Auxiliary Mixture Sampling for Age-Period-Cohort Models*  
Schweizer Statistiktage 2007, Lucerne, Switzerland.
- 29/09/2007 *Auxiliary Mixture Sampling for Age-Period-Cohort Models*  
Gemeinsame Arbeitstagung der Arbeitsgruppen Bayes-Methodik, Räumliche Statistik und Ökologie und Umwelt, Schloss Reisenburg (Günzburg), Germany
- 11/09/2007 *Bayesian Variable Selection for Detecting Adaptive Genomic Differences among Populations*  
Seminar 2007 der Internationalen Biometrischen Gesellschaft Region Österreich-Schweiz (ROeS), Berne, Switzerland.
- 02/07/2007 *Bayesian Variable Selection for Detecting Adaptive Genomic Differences among Populations*  
Statistical Computing 2007, Schloss Reisenburg (Günzburg), Germany.
- 27/03/2007 *Bayesian Methods for Detecting Selection in the Genome*  
Conference 2007: "Statistics under one Umbrella", Bielefeld, Germany.

#### POSTER PRESENTATIONS

- 16/06/2016 *A computationally efficient model to account for space-time variation in disease risk*  
ISBA 2016, Sardinia, Italy.
- 13/07/2014 *Adjusting for spatial misalignment in the analysis of seedfall and seedling recruitment data*  
Satellite workshop of the IBC 2014 on Spatio-Temporal Statistics, Valencia, Spain.
- 13/09/2013 *Bayesian projections: Routine analysis without Markov chain Monte Carlo*  
The Third Workshop on Bayesian Inference for Latent Gaussian Models with Applications, University of Iceland, Iceland.
- 28/06/2012 *A novel empirical Bayes approach for profiling immunoprecipitation-based DNA methylation*  
ISBA 2012 Conference, Kyoto, Japan.
- 14/09/2011 *Bayesian multiple changepoint models with dependence within segments for detecting epigenetic patterns*, Statistical Modelling for Biological and Environmental Systems, Venice, Italy.
- 07/06/2011 *Changepoint models with dependence within segments for detecting epigenetic patterns*  
Ascona Workshop 2011: Statistical Challenges and Biomedical Applications of Deep Sequencing Data, Ascona, Switzerland.
- 06/06/2010 *Correlated GMRF priors and INLA*  
Ninth Valencia International Meeting on Bayesian Statistics, Benidorm, Spain.