

# Publication list 2012-2022, Statistics and Data Science group, Department of Mathematics, University of Bergen.

The list includes all articles and monographs published by permanent staff, emeriti, temporary staff (e.g. postdocs and phd-students) and adjunct professors (with publications with affiliation to UiB listed and during the given period).

1. Fournier, D.A., **H. J. Skaug**, et al. (2012). AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optimization Methods & Software* 27(2): 233-249.
2. Okamura, H., Minamikawa, S., **Skaug, H.J.**, and Kishiro, T. (2012). Abundance Estimation of Long-Diving Animals Using Line Transect Methods. *Biometrics* 68(2): 504-513.
3. Stordal, A.S., Karlsen, H.A., Nævdal, G., Oliver, D.S., & **Skaug, H.J.** (2012). Filtering with state space localized Kalman gain. *Physica D-Nonlinear Phenomena* 241(13): 1123-1135.
4. Stordal, A. S., Valestrand, R., Karlsen, H.A., Nævdal, G., **Skaug, H.J.** (2012). Comparing the adaptive Gaussian mixture filter with the ensemble Kalman filter on synthetic reservoir models. *Computational Geosciences* 16(2): 467-482.
5. Kleppe, T.S., Yu, J., **Skaug, H.J.** (2012) Fitting general stochastic volatility models using Laplace accelerated sequential importance sampling. *Computational Stat. and Data Analysis* 56 (11), 3105–3119.
6. Glover K.A., Haag T., Oien N., Walloe L., Lindblom L., Seluussen B.B., **Skaug H.J.** (2012) The Norwegian minke whale DNA register: a database monitoring commercial harvest and trade of whale products. *Fish and Fisheries* 13, 313-332.
7. Haaland, O.A., **Skaug, H.J.** (2013) Estimating genotyping error rates from parent-offspring dyads. *Statistics and Probability letters*. 83, 3, 812-819.
8. **Skaug, H.J.**, Yu, J. (2014) A flexible and automated likelihood based framework for inference in stochastic volatility models. *Comp. Stat. Data Analysis*, 76, 642-654.
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10. Langrock, R., Borchers, D.L., **Skaug, H.J.** (2013) Markov-Modulated Nonhomogeneous Poisson Processes for Modeling Detections in Surveys of Marine Mammal Abundance. *Journal of the American Statistical Association*. 108 (503) 840-851.
11. Anderson, E.C., **Skaug, H.J.**, Barshis, D.J. (2014) Next-generation sequencing for molecular ecology: a caveat regarding pooled samples. *Molecular Ecology* 23 (3) 502-512.
12. Kleppe, T.S., Yu, J., **Skaug, H.J.** (2014). Maximum likelihood estimation of partially observed diffusion models. *Journal of Econometrics* 180 (1) 73-80.
13. Quintela, M., **Skaug, H.J.**, Oien, N., Haug T., Seluussen, B.B., Solvang, H.K., Pampoulie, C., Kanda, N., Pastene, L.A., Glover, K.A. (2014). Investigating Population Genetic Structure in a Highly Mobile Marine Organism: The Minke Whale Balaenoptera acutorostrata acutorostrata in the North East Atlantic. *Plos One* 9(9): p. 15.
14. Vincenzi, S., Mangel, M., Crivelli, A.J., Munch, S., **Skaug, H.J.** (2014). Determining Individual Variation in Growth and Its Implication for Life-History and Population Processes Using the Empirical Bayes Method. *PLOS Computational Biology* 10(9).
15. Zhang, Y.H., Oliver, D.S., Chen, Y., **Skaug, H.J.** Data (2015). Assimilation by Use of the Iterative Ensemble Smoother for 2D Facies Models *SPE Journal* 20 p. 169-185.
16. Bravington, M.V., **Skaug, H.J.**, Anderson, E.C. (2016). Close-kin Mark-Recapture. *Statistical Science* 31, p. 259-274.
17. Kleppe, T.S., **Skaug, H.J.** (2016) Bandwidth selection in pre-smoothed particle filters. *Statistics and Computing* 26, p. 1009-1024.

18. Kristensen, K., Nielsen. A., Berg C.W., **Skaug, H.**, Bell, B. (2016) TMB: Automatic Differentiation and Laplace approximation. *Journal of Statistical Software* **70** p. 1-21.
19. Vincenzi, S., Mangel, M., Crivelli, A.J., Munch, S., **Skaug, H.J.** (2016). Trade-offs between accuracy and interpretability in von Bertalanffy random-effects models of growth. *Ecological Applications* **26** p. 1535-1552.
20. Brooks M.E., Kristensen K., Van Benthem K.J., Magnusson A., Berg C.W., Nielsen A., **Skaug H.J.**, Machler M., Bolker B.M. (2017). glmmTMB Balances Speed and Flexibility Among Packages for Zero-inflated Generalized Linear Mixed Modeling. *R Journal* **9**(2): p. 378-400.
21. Malde, K., Seliussen, B.B., Quintela, M., Dahle, G., Besnier, F., **Skaug, H.J.**, Øien, N., Solvang, H.K., Haug, T., Skern-Mauritzen, R. and Kanda, N. (2017). Whole genome resequencing reveals diagnostic markers for investigating global migration and hybridization between minke whale species. *BMC Genomics* **18**.
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26. Fallahi, S., **Skaug, H.J.**, & Alendal, G. (2020). A comparison of Monte Carlo sampling methods for metabolic network models. *Plos one*, **15**(7), e0235393.
27. Frøysa, H.G., **Skaug, H.J.**, & Alendal, G. (2020). Experimental design for parameter estimation in steady-state linear models of metabolic networks. *Mathematical Biosciences*, **319**, 108291.
28. Wacker, S., **Skaug, H.J.**, Forseth, T., Solem, Ø., Ulvan, E.M., Fiske, P., & Karlsson, S. (2021). Considering sampling bias in close-kin mark-recapture abundance estimates of Atlantic salmon. *Ecology and Evolution*, **11**(9), 3917-3932.
29. Mannseth, J., Berentsen, G.D., **Skaug, H.J.**, Lie, R.T., & Moster, D. (2021). Variation in use of Caesarean section in Norway: An application of spatio-temporal Gaussian random fields. *Scandinavian Journal of Public Health*, **49**(8), 891-898.
30. Berentsen, G.D., Azzolini, F., **Skaug, H.J.**, Lie, R.T., & Gjessing, H.K. (2021). Heritability curves: A local measure of heritability in family models. *Statistics in Medicine*, **40**(6), 1357-1382.
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32. Solvang, H.K., **Skaug, H.J.**, Øien, N. (2021). Measurement error model for the Norwegian common minke whale (*Balaenoptera acutorostrata acutorostrata*) surveys 2008-2013. *J. Cetacean Res. Manage.*, **22**(1), 01-16.
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35. Delaval, A., Bendall, V., Hetherington, S.J., **Skaug, H.J.**, Frost, M., Jones, C.S., Noble, L.R. (2022). Evaluating the suitability of close-kin mark-recapture as a demographic modelling tool for a critically endangered elasmobranch population. *Evolutionary Applications*, **16**(2), 461-473.
36. Azzolini, F., Berentsen, G.D., **Skaug, H.J.**, Hjelmborg, J.V., Kaprio, J.A. (2022). The heritability of BMI varies across the range of BMI—a heritability curve analysis in a twin cohort. *International Journal of Obesity*, **46**(10), 1786-1791.

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79. Chapon P.A., **Bulla J.**, Gauthier A., Moussay S. (2014), ‘On the importance of telemetric temperature sensor location during intraperitoneal implantation in rats’, *Laboratory animals* 48 (2), 114-123, <https://doi.org/10.1177/0023677214522035>
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