Annotated Bibliography

Suzie Brown

SEQUENTIAL MONTE CARLO

Gordon, Salmond, and Smith, 1993, "Novel Approach to Nonlinear/Non-Gaussian Bayesian State Estimation"

Original reference for SMC.

Kitagawa, 1996, "Monte Carlo Filter and Smoother for Non-Gaussian Nonlinear State Space Models"

Nice introduction to SMC. Review of other nonlinear filtering techniques: extensions to Kalman filtering.

Del Moral, 2013, *Mean Field Simulation for Monte Carlo Integration*

Loads of rigorous results about SMC e.g. convergence, rates, CLTs.

Doucet and Johansen, 2011, "A Tutorial on Particle Filtering and Smoothing: Fifteen Years Later"

Andrieu, Doucet, and Holenstein, 2010, "Particle Markov Chain Monte Carlo Methods"

Introduces particle MCMC methods, including particle Gibbs with conditional SMC.

RESAMPLING

Kitagawa, 1996, "Monte Carlo Filter and Smoother for Non-Gaussian Nonlinear State Space Models"

Comparison of multinomial, stratified & systematic resampling. And the effect of presorting. [in appendix]

Douc, Cappé, and Moulines, 2005, "Comparison of Resampling Schemes for Particle Filtering"

Comparison of Monte Carlo variance between mutli, res-multi, strat, syst. CLTs for resampled particles.

Lee, Murray, and Johansen, 2019, "Resampling in Conditional SMC Algorithms"

Implementation of lowvariance resampling within conditional SMC.

Murray, Lee, and Jacob, 2016, "Parallel Resampling in the Particle Filter"

Whitley, 1994, "A Genetic Algorithm Tutorial"

Carpenter, Clifford, and Fearnhead, 1999, "Improved Particle Filter for Nonlinear Problems"

Gerber, Chopin, and Whiteley, 2019, "Negative Association, Ordering and Convergence of Resampling Methods"

Li et al., 2020, *Stratification and Optimal Resampling for Sequential Monte Carlo*

Del Moral, Doucet, and Jasra, 2012, "On Adaptive Resampling Strategies for Sequential Monte Carlo Methods"

BACKWARD SIMULATION

Kitagawa, 1996, "Monte Carlo Filter and Smoother for Non-Gaussian Nonlinear State Space Models"

Some solutions to ancestral degeneracy: fixed lag smoother, forward-backward-type algorithm.

Doucet and Johansen, 2011, "A Tutorial on Particle Filtering and Smoothing: Fifteen Years Later"

Lindsten and Schön, 2013, "Backward Simulation Methods for Monte Carlo Statistical Inference"

A whole book on backward simulation. [Chapter 5] describes backward simulation and ancestor sampling in particle MCMC.

Whiteley, 2010, "Discussion on 'Particle Markov Chain Monte Carlo Methods'"

In the discussion, Nick Whiteley introduces (remarkably briefly) the idea of ancestor sampling in particle Gibbs.

CONVERGENCE OF GENEALOGIES

Also consider looking at: Tavaré 1984 "Line-of-descent and genealogical processes, and their applications in population genetics models"; Donnelly 1991 "Weak convergence to a Markov chain with an entrance boundary: ancestral processes in population genetics"; Donnelly Tavaré 1995 "Coalescents and genealogical structure under neutrality"; Griffiths Tavaré 1994 "Sampling theory for neutral alleles in a varying environment"; Marjoram 1992 "Correlation structures in applied probability" (PhD thesis, UCL); Schweinsberg 2003 "Coalescent processes obtained from supercritical Galton-Watson processes"

Kingman, 1982, "On the Genealogy of Large Populations"

- Introduces the n-coalescent (in a very nice clear way) with the same notation we still use

- **Theorem:** suppose $\nu_{1:N}$ are exchangeable and independent across generations and $\mathrm{Var}[\nu_1] \to \sigma^2 \in (0, \infty)$ and $\mathbb{E}[\nu_1^m] \leq M_m$ for all $m \in \mathbb{N}$. Then the n-genealogies scaled by $\lfloor N\sigma^{-2}t \rfloor$ converge to the n-coalescent in the sense of FDDs.

- n-coalescent also applies for models where ν_j are not exchangeable or independent across generations, as long as the genealogies are Markov at least up to error $O(N^{-1})$ and the transitions satisfy $p_{\xi\eta} = q_{\xi\eta}\sigma^2 N^{-1} + o(N^{-1})$, where q's are transition probs of n-coalescent

- The n-coalescent is a good robust model for *large neutral* populations

- Genealogy decouples into a jump chain and a pure death process

- There exists the Kingman coalescent as infinite-dimensional embedding of the n-coalescents

Kingman, 1982, "The Coalescent"

Broadly, this paper introduces the Kingman coalescent (as opposed to n-coalescent) and proves some properties

Tavaré, 1984, "Line-of-Descent and Genealogical Processes, and Their Applications in Population Genetics Models"

- Review article on genealogical models and their application to population genetics

Möhle, 1998, "Robustness Results for the Coalescent"

Necessary & sufficient conditions for convergence of Cannings model to a coalescent process more general than Kingman. Allowing large mergers but not simultaneous mergers.

- Population size can vary over time, but only deterministically

- Offspring counts must be independent but not necessarily identically distributed across generations

- This means time scale must be allowed to vary over time: τ_N becomes $\tau_N(t)$ and c_N becomes $c_N(t)$, or $c(t)$ in Möhle's notation

- Only proves convergence of FDDs

- Conditions of theorem are still very strong, requiring infinitely many moments to be bounded. There is now a condition on one mixed moment that wasn't needed in Kingman1982.

- The conditions are sufficient but not necessary

- Time scale $\tau_N(t)$ is allowed to be chosen freely, but the theorem only holds when it is an appropriate function (i.e. an inverse of c_N similar to the usual) so this is not a very great generalisation over defining τ in the usual way.

Möhle and Sagitov, 1998, "A Characterization of Ancestral Limit Processes Arising in Haploid Population Genetics Models"

- Assume $\nu_{1:N}$ are exchangeable, and i.i.d. across generations, and the population size N is constant

- Necessary & sufficient conditions are given for (FDD) convergence of the genealogies to a Λ-coalescent, and the correct measure Λ is uniquely constructed from infinitely many moment limits. (Note: Möhle's notation uses μ for the measure rather than Λ.)

- The conditions are: (I) infinitely many pure moment limits exist, slightly different from the condition 2a of Möhle1998; (II) the exchangeable version of the mixed moment condition 2b of Möhle1998.

- Under the additional condition $c_N \to 0$ we also get weak convergence to the Λ-coalescent, although the proof is not explicit in this paper (it just refers to the methods of another work).

Sagitov, 1999, "The General Coalescent with Asynchronous Mergers of Ancestral Lines"

- Assume $\nu_{1:N}$ are exchangeable, and i.i.d. across generations, and the population size N is constant

- k-mergers (but not simultaneous mergers) are allowed

- 3 necessary conditions are given for FDD convergence to some limit of the form $p_{\xi\eta} = \delta_{\xi\eta} + V_N q_{\xi\eta} + o(V_N)$, where $Q = (q_{\xi\eta})$ is some Markov generator, and $V_N \to 0$.

- Additionally, a subset of the necessary conditions are shown to be sufficient for the above asymptotic relation to hold with specific Q corresponding to a Λ-coalescent, on the (constant, deterministic) time scale $T_N^{-1} \sim V_N$.

- Unfortunately I didn't really understand the second and third conditions...

- As one would expect, the necessary conditions can be shown to hold when Kingman's condition $\sup_N \mathbb{E}[\nu_1^k] < \infty \forall k \geq 2$ applies (see Remark 1)

Pitman, 1999, "Coalescents with Multiple Collisions"

- Defines Λ-coalescents in the notation still used, proves its existence.

- Notes how Kingman coalescent and Bolthausen-Sznitman coalescent (indeed the whole class of β-coalescents) can be seen as special cases

- Properties: exchangeable random partition; Exponential waiting times with parameter determined by Λ; criterion for coming down from infinity; restriction to $[n]$

- This paper studies the Λ-coalescents from the point of view of coalescent theory / exchangeable random partitions. It doesn't make any reference to population dynamics that might lead to such a limit. That angle was covered in Sagitov1999 (who independently discovered the Λ-coalescents).

Möhle, 1999, "Weak Convergence to the Coalescent in Neutral Population Models"

- Population size can vary over time, but only deterministically

- Offspring counts must be independent but not necessarily identically distributed across generations — this ensures the genealogical process is Markovian, but not time-homogeneous

- Individuals are not necessarily exchangeable, but our standing assumption (here called the "random assignment condition") is assumed

- Time scale $\tau_N(t)$ is allowed to be chosen freely, but the theorem only holds when it is an appropriate function (i.e. an inverse of c_N similar to the usual) so this is not a very great generalisation over defining τ in the usual way.

- Theorem conditions are exactly the same as in Möhle1998

- Convergence is now proved additionally in the weak sense, as opposed to just FDDs

- Proof technique is overall the one I used for weak convergence of SMC genealogies, except Möhle's doesn't have the external expectations. These expectations appear in my proof because the coupled process can only be defined conditionally on $\mathcal{F}_\infty$, because the generations are not independent

Möhle, 2000, "Total Variation Distances and Rates of Convergence for Ancestral Coalescent Processes in Exchangeable Population Models"

- Fixed population size N

- Offspring counts are exchangeable and i.i.d. across generations

- Treats full characterisation of possible limiting coalescents (I think the class is known as Ξ-coalescents), where there are possibly simultaneous and/or multiple mergers. The particular limiting coalescent can be characterised by (mixed) factorial moments, here denoted $\Phi_a(b_1, \ldots, b_a)$. These quantities are central to the analysis, and results are given in terms of them, so can be applied to any exchangeable model.

- It is shown that the Kingman coalescent appears as the limit if and only if $\lim \frac{\mathbb{E}[(\nu_1)_3]}{N\mathbb{E}[(\nu_1)_2]} = 0$. (See equation (14) or (16).) This is the exchangeable version of the main theorem condition I use in my SMC genealogies work. I think this work is the earliest use of this simplified condition.

- Total variation bounds are proved in the general case, left in terms of the particular transition probabilities of the model (see Thm 1).

- More specific bounds are calculated for the case where the model is in the domain of attraction of Kingman's coalescent (i.e. second moments dominate third moments, as above / in equation (14)). The bounds have a simple form and are left in terms of c_N and some Φ functions which correspond to $\mathbb{E}[(\nu_1)_3]$ and $\mathbb{E}[(\nu_1)_2(\nu_2)_2]$, which could easily be computed for a given model. It is clear that under the conditions of convergence to KC, the given TV bound converges to zero, as expected.

Möhle and Sagitov, 2001, "A Classification of Coalescent Processes for Haploid Exchangeable Population Models"

- Constant population size N

- Offspring counts are exchangeable within generations and i.i.d. between generations — implies the genealogical process is a time-homogeneous Markov chain

- Treats full variety of possible limits for exchangeable models (again, I think the family is Ξ-coalescents)

- Presents necessary and sufficient conditions for weak convergence to an appropriate Ξ-coalescent, and the particular Ξ is uniquely determined by moments of the offspring distribution

- A proof of FDD convergence is given. When $c_N \to c \neq 0$ the limiting process is discrete and weak convergence follows immediately from FDDs. When $c_N \to 0$ the limit is continuous and tightness is needed for weak comvergence; the proof is not presented, just a reference to Möhle1999.

- Since the conditions given are necessary and sufficient, and can be applied to any exchangeable (Cannings-type) model, this constitutes a complete characterisation of the limiting genealogies for this class of models.

- Section 6 gives a cute bit of history of coalescent theory

Möhle and Sagitov, 2003, "Coalescent Patterns in Exchangeable Diploid Population Models"

SMC GENEALOGIES

Jacob, Murray, and Rubenthaler, 2015, "Path Storage in the Particle Filter"

Description of ancestries as trunk+crown. Upper bound on storage cost via an approximate multinomial resampling scheme that is independent of weights. Numerical simulations suggesting similar results for stratified and systematic resampling (including an ordering on the schemes?).

Koskela et al., 2018, *Asymptotic genealogies of interacting particle systems with an application to sequential Monte Carlo*

VARIANCE ESTIMATION

Chan and Lai, 2013, "A General Theory of Particle Filters in Hidden Markov Models and some Applications"

Lee and Whiteley, 2018, "Variance Estimation in the Particle Filter"

Olsson and Douc, 2019, "Numerically Stable Online Estimation of Variance in Particle Filters"