Asymptotic genealogies of sequential Monte Carlo algorithms
Thesis outline at 36 months

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1 Introduction

2 Background

2.1 State space models

Introduction of state space models: target tracking example (1D train); modelling assumptions for this example; why Bayesian? Scenarios where model is tractable: Kalman filter, extended KF, etc.

2.2 Interacting particle systems / sequential Monte Carlo

General description of what an IPS is, what they are useful for, and how to simulate one. SMC as a specific class of IPS. Relevant literature about SMC (e.g. convergence results).

2.3 Coalescent theory

Review of literature from population genetics, introducing the relevant population models (Wright–Fisher, Moran, Cannings) and Kingman's coalescent / n-coalescent. Domain of attraction of Kingman's coalescent, as far as previous works have shown. Properties of such models (neutrality, Markov property) that may be violated by SMC systems.

2.4 SMC genealogies

Description of how genealogies are induced by SMC algorithms and how this is related to the performance of the algorithms (ancestral degeneracy, variance estimation). Existing results characterising these genealogies.

2.5 Resampling

Definition of a 'valid' resampling scheme and justification for these restrictions. Tour of key resampling schemes (multinomial, residual, stratified, systematic, ...), with discussion of their properties, implementation and usage in practice. Idea of 'optimality' in resampling, description of so-called optimal schemes. Existing results and conjectures comparing the performance of different schemes. Introduction of stochastic rounding as a class of resampling schemes. Adaptive resampling.

3 Limiting coalescents for SMC genealogies (done)

3.1 General result for IPSs

Definition of the relevant quantities. Proof that finite-dimensional distributions of the rescaled genealogies converge to the n-coalescent (a refinement of Koskela et al. (2018, Theorem 1) with more tractable conditions). Interpretation of the conditions.

3.2 Application to multinomial resampling

Proof of corollary for multinomial resampling, the simplest/most tractable case. This was already proved in Koskela et al. (2018) but having simplified conditions for the main theorem, the proof is made briefer and more elegant.

3.3 Application to stochastic rounding

Proof of corollary for SMC with any stochastic rounding-based resampling. Comparison of time scale versus multinomial resampling.

4 Conditional SMC (done)

Introduction of conditional SMC as key component of particle MCMC / particle Gibbs, and what type of problem this is useful for. Proof of corollary for conditional SMC. Discussion of pre-limiting behaviour (possibly with simulation study).

4.1 Ancestor sampling

Motivation for ancestor sampling within particle Gibbs. Description of algorithm. Conditions under which it is possible. Effect of ancestor sampling on asymptotic genealogies.

5 Weak convergence (in progress)

Weak convergence result under the same conditions as the convergence in finite-dimensional distributions. I am currently working on the required tightness argument, somewhat following Möhle's proof in the neutral case (Möhle, 1999), but with non-trivial adjustments because our process is not Markovian.

6 Conclusions / discussion

References

Koskela, J., Jenkins, P. A., Johansen, A. M. and Spanò, D. (2018), 'Asymptotic genealogies of interacting particle systems with an application to sequential Monte Carlo', *arXiv preprint arXiv:1804.01811* .

Möhle, M. (1999), 'Weak convergence to the coalescent in neutral population models', *Journal of Applied Probability* **36**(2), 446–460.