

Analysis of genealogies induced by sequential Monte Carlo algorithms

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1 Introduction

- what is SMC and what is it used for?
- basic SMC algorithm
- the three main tasks: prediction, filtering, smoothing
- the problem with smoothing: ancestral vs. weight degeneracy
- motivating plots
- organisation of the report

2 SMC as a coalescent

- k-coalescent & Kingman coalescent
- pop gen literature about large population cts time limits of various models
- resampling viewed backwards in time: branching process -> coalescent process
- asymptotic properties of SMC lit review: CLT, path storage, coalescence etc.
- the gap in knowledge that we aim to fill
- (remark: although SMC has other problems in high dimension, the coalescence rate doesn't depend on the dimension...)

3 Conditional SMC

- motivation: particle MCMC, need for multiple lineages
- conditional (multinomial) SMC algorithm and its context within particle Gibbs
- result: coalescence rate etc in terms of standard multinomial one; verification of assumptions of KJJS theorem (but exile horrible calculations to appendix)
- simulations & conclusions thence

4 Alternative resampling schemes

- multinomial not really used in practice, but other schemes hard to analyse
- overview of the main variance-reducing schemes
- results: theorem for residual resampling (hopefully)
- maybe results for other schemes
- simulation comparing all of them, and conclusions thence

5 Discussion

- results so far
- impact of this work: to practitioners, to enriching the SMC literature, interpretation within pop gen.
- future directions