# Possible future research topics

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### Extending the theoretical results

- What is the effect of adaptive resampling?
- Corollaries also for residual-multinomial and stratified resampling.
- Rates of convergence (modifying more of Möhle's work).
- Could badly-behaved potentials produce a non-Kingman Lambda-coalescent? For example, use for potentials some heavy-tailed fitnesses like in Schweinsberg model. This is probably not interesting from an SMC point of view.
- A way to estimate coalescent rates a priori for some specific tractable class of models, say.
- Do our results apply to cloning models, or other continuous-time models?

### Resampling

- Compare residual-stratified vs. stratified resampling (and residual-systematic vs systematic): are they equivalent? What if the weights are sorted? Maybe start by coding up an exploratory experiment.
- Explore more generally the effect of pre-sorting the weights. How does this link with results of Gerber Chopin Whiteley (where they sort by particle position, if I remember rightly)?
- Compare theoretical computation/storage costs and parallelisability between the different resampling schemes.
- Is there a nice set of weights that will nicely illustrate all the points I want to make about resampling schemes?
- Can the comparison of time-scales for different schemes be wrangled into/ related to a direct comparison of the variances? Is this even useful?
- Don't forget the resampling scheme that's even worse than multinomial: sampling once from Categorical and replicating it N times. This leads to a star-shaped coalescent, which sets a precedent for non-Kingman Lambda coalescents from SMC genealogies.
- (See marked notebook 3 page circa Jun/Jul 2020 for some more thoughts/ideas.)
- Does residual-systematic share the same pathological behaviour as systematic resampling? E.g. try plugging it into the pathoglogical example from Douc Cappe Moulines.
- (Just for fun:) in stochastic rounding, how many possible ways are there to assign the offspring counts? Consider that each of the N counts takes one of two possible values, but this will overcount a lot because we are also constrained by offspring counts summing to N.
- (Conjecture:) pre-sorting of weights reduces resampling variance, but increases the coalescence rate. Intuition: when weights are sorted, small weights that sum to less than 1/N are grouped together so only one of them can have a child. (It may be that this effect is entirely cancelled by the reduction in variance elsewhere.)

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## Simulation experiments

- Now we (almost?) have weak convergence, redo similar experiments to those at end of KJJS, but without having to fudge the argument in order to apply FDD convergence.
- Code up all the different sampling schemes (and sorted/unsorted variants etc.) and come up with some useful (if only illustrative) experiments comparing them.
- Decide which functions would be most interesting to illustrate the performance of resampling schemes, say using ternary diagrams. (See marked notebook 3 page at 8/7/20.)
- Explore pre-asymptotic behaviour of CSMC for example. I did some work on this previously.
- Make edits to my ternary plot "library" (see notebook 3 marked page at 8/7/20).

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