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Is the Ewens Sampling formula valid for Oysters?

Kingman's coalescent is a process which describes how ancestral lineages merge when one goes backward in time into the past. Since its introduction in the 80's, it has become the standard genealogy model in population genetics. One of the main question in this field is to try to detect the trace of natural selection's action in today's genomes. One of the main tool for doing so is the celebrated Ewens sampling formula which describes the expected genetic diversity in a neutral, constant-size population (for which Kingman's coalescent accurately describes the genealogy). As such, it gives the nil hypothesis for statistical tests designed to detect selection.

However, it is now known that for many species (particularly in marine biology) in which there is a strong variance of the reproductive success, other coalescents are better suited to model neutral genealogies. The purpose of the work presented here is to obtain an asymptotic analogue of Ewens formula in this framework. This requires studying some of the deep connections which links coalescence and branching processes.

Based on joint works with Nathanaël Berestycki and Jason Schweinsberg.