

# *Working Notes: Single-celled bottlenecks, germlines and the evolution of complex multi-cellularity*

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## 1 Data Collection

Data were collected by...

Phylogeny was constructed by

## 2 Statistical Analyses

All analyses were conducted in R (R Core Team 2021) using the package MCMCglmm [MCMCglmm], while documents were produced using [RMarkdown]. All data and code are accessible at [github].

Model parameters were optimised using the first model described in our results, for which we ran a total of 38 MCMCglmm chains of varying lengths (500000 - 10000000 iterations), with varying warm-ups (100000 - 1000000, and with thinning of either 100 or 1000 fold, see Figure S1. All subsequent models were then fit using the combination of these parameters where the autocorrelation in the sampled mean and variance were minimal: [X] iterations, a warm-up of [Y] iterations and thinning by a factor of [Z]. In all fitted models, the autocorrelation was well below the suggested tolerable maximum of 0.1 (**hadfield?**). For each model, [n\_chains] chains were run. These were visually inspected for chain convergence, and the Gelman-Rubin (**Gelman-Rubin?**) convergence diagnostic approximated 1 (<1.05) in all cases—these are reported in the summary of each model below.

### 2.1 Testing for a correlation between reproductive biology and multicellular complexity

### 2.2 Phylogenetically Informed Tests

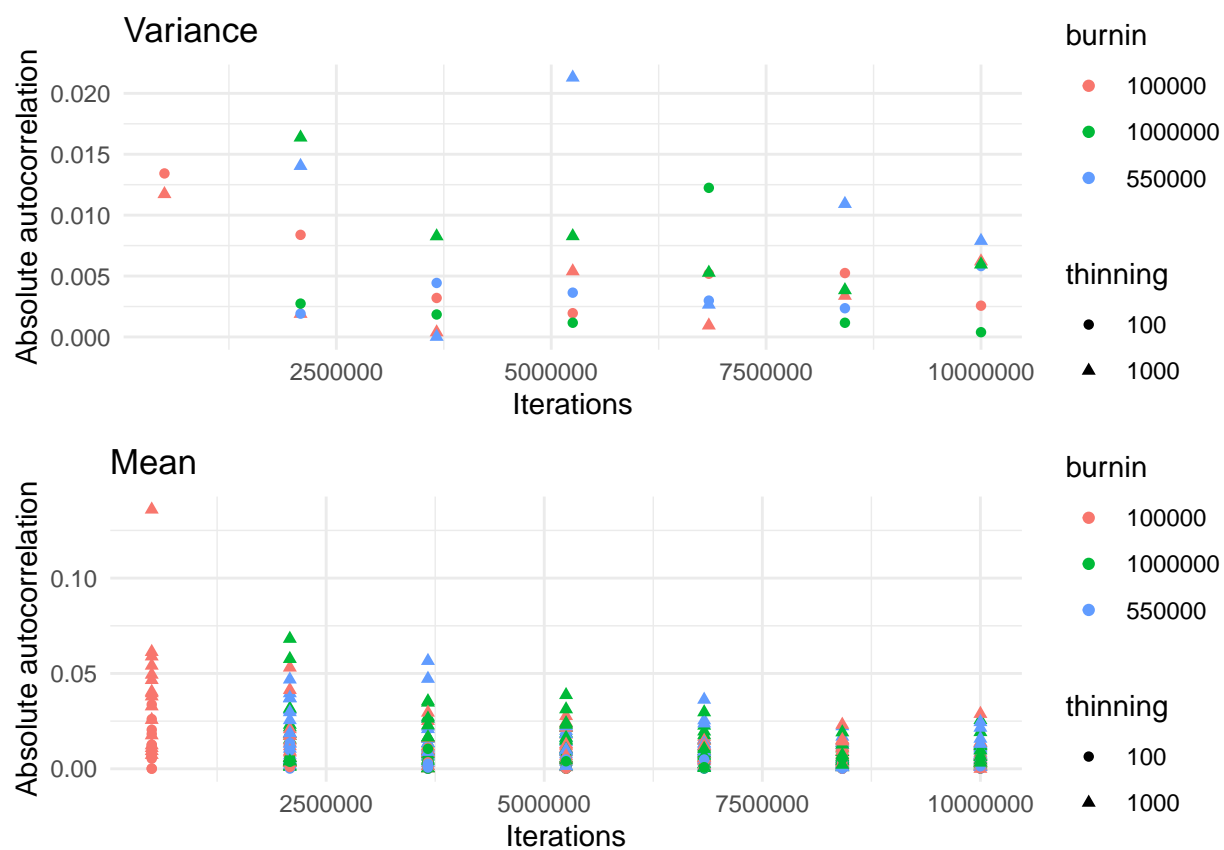


Figure 1: Fig S1: Autocorrelation of successively sampled mean and variance values from posterior distribution

### 3 References

R Core Team. 2021. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.