talking points

Bob Week

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- what are the goals, questions, and/or problems that are motivating this project?
    - methods: correlation-based methods for detecting loci involved w coev may always struggle to deal with other processes that create correlations
        - things that lead to correlation: correlation by chance (drift), spatial autocorrelation (limited dispersal), sampling error
    - theoretical: what are some interesting quantities we can develop predictions for?
        - what is distr of ild as fct of relative disp abilities, eff densities, selection strengths, etc…
        - what is the spatial scale of ild?
- slim considerations
    - parameters:
        - size of genome relative to recomb rate
        - number of causal loci relative to number of neutral loci
    - boundary conditions:
        - currently coded as periodic, which is nice
        - other option is to make boundaries absorbing and cut out edges
    - how to measure ild
        - discretize space: results may depend on resolution. we might want to evaluate results at a fine-grain, medium-grain and coarse-grain
        - have parasites move to host:
            - advantage: this avoids the need to discretize space and therefore side-steps any issues with spatial resolution of discretization
            - aside: the sim allows multiple parasites per host.
            - aside: total parasite movement includes dispersal and movement to host
    - spatial variation in population density
        - i think we should aim to make these as homogeneous as possible: as fluctuations in densities can significantly alter conclusions
        - strong selection, which may be more bio realistic and lead to stronger ild, may cause significant fluctuations
        - depends on average abundance density. the larger the abund density the stronger selection can be without causing significant fluctuations. what is the optimal abund density to use?
    - genetic architecture of quant traits

        - biallelic causal loci with value zero or norm distr rv?
        - same fixed effect size for each locus?
    - debugging
        - use pairwise pi to check if distant spatial regions are genetically differentiated?
        - how to quantify if abund density is suff homogeneous? coefficient of variation?
    - downstream analysis
        - should we filter out intraspecific ld? (i've been doing this using `allel.locate_unlinked`)
        - alternatively, should we downsample loci by a fixed number of bp's? downsample at random?
        - alternatively, should we compute the ild matrix for all loci?
        - selection can lead to intraspp ld. is it then possible to find part of the coev signature in patterns of intraspp ld?
        - previously we saw fst carried a significant signal. should we continue to look at this statistic? what other statistics should we consider?