Short-term progress plan for TTT

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In hand are simulations for single- and multi-locus Wright-Fisher and non-Wright Fisher models (summarized in table below).

To address comments from Stephen Keller et al. :

We also have a multi-locus common garden simulation, replicating the “instantaneous” change that Keller et al. believes will allow for GF to do a better job of serving as a predictive tool of fitness.

Concerns regarding new emerging environments (environmental values outside historical exposure) being included in the simulation don’t make sense when the goal is addressing the efficacy of GF’s predictive potential when it comes to climate change. Quite easy to implement a scenario where the only environmental shifts occur towards values that are not “new” (say, set a maximum) but seems like this concern is more readily addressed by the common garden simulation.

Need to write out a clear rational for the environmental rate of change – the biological idea behind the single environmental variable is a thermocline: a rate of 0.1 per generation rate increase is arguably high. NASA Earth Observatory reports a global temperature increase of 0.0075 degrees celsius per year, but localized increases can be much faster. Look climate change projections for reasonable rates.

To address comments from Exposito-Alonso (time points too far apart):

Look at smaller time intervals. Can we detect anything when looking at a smaller generational scale?

Proposed time interval comparisons:

* Per generation (for first five after environment begins to shift, five generations in the middle of environmental shift, and last five before end of simulation). Each group of five allows for four sequential GF comparisons.
* Every 10 generations (5 early, 5 middle, 5 late samples)
* Every 100 generations (T1, T1.5, T2) – assuming total of 300 generation env. shift time
* Every 300 generations (T1, T2) – assuming total of 300 generation env. shift time

- output at beginning of climate change as "baseline" for gradient forests

- Q1) Does pre-CC baseline predict results common garden (instantaneous shift)? (within historical climate envelope)

- Q2) Does pre-CC baseline predict short shift (10 generations)? (wouldn't any change take would us outside historical, but a short shift could be before the environment that causes a fitness decline)

- Q3) Does pre-CC baseline long shift (300 generations)?

- ~~Does mid-CC baseline predict X?~~

Q2 Q3 - Make sure to output summary statistics for interpolated vs. extrapolated (output you have now) populations with GF

Still need specifics - number of replications - aim 20-100 reps for each scenario

- what kinds of changes will we make from the base? Change fitness fnction? Change envi rate?

Write up methods before, then all authors approve plan

Effects of these will obviously change given the Env. Rate. and selection coefficient.

To address comments from Lasky "find with patterns of covariance among loci identified by gradient forest

Box 2 of Le Corre & Kremer "The genetic differentiation at quantitative trait loci under local adaptation" 2012.

I'm wondering if the different causal loci show negative covariation locally within populations because of stabilizing selection. I saw in Arabidopsis (with putative causal loci) that they did, compared to random pairs of loci as a null.":

From outputs from the multi-locus model we can readily construct within and between population variance-covariance matrices. Definitely more of a back-burner implementation.

- For all causal SNPs that underly a trait, calculate the covariance in allele frequency

Moving forward:

* Get simulations running on cluster (have contacted Discovery regarding installation of all python packages necessary)
* Run five replicates of single- and multi-locus Wright-Fisher and non-Wright Fisher models (common garden fitness matrix can be output during regular simulation; will compare to make sure it’s not affecting regular output results) – That’s 20 runs total.
* Recombination and mutation rate justifications have solid justifications; write out justifications for environmental shift rate, and selection coefficient. Migration rate is explored at multiple levels.
* Run a Wright-Fisher model (single and multi) with varying population sizes (Column 1 = 100, Column 2 = 50, Column 3 = 100, etc.) and no selection (no M2/QTNs). Also, generate a SLiM code with similarly no selection where initial population size is randomly drawn from a uniform distribution from 10 to 100.
* Verify R script is outputting correct data summaries (individual loci summaries, population level summaries, whole simulation summaries; see https://github.com/TestTheTests/TTT\_Offset\_Vulnerability\_GF\_Sims/blob/master/Notebook/2019\_06\_notes.md)