How do linked deleterious mutations restrict adaptation and adaptedness?

Is there a threshold where the number of mutations and the strength of their deleterious effects halts adaptation, or is it more of a curve?

How effective is recombination at reducing these effects?

Inversions – could interpret large blocks between recombination

The three above questions, but in regards to the maintenance of variation: how is genetic variation maintained when linked deleterious mutations inhibit adaptation, and what does that curve look like? Does recombination reverse these effects somewhat?

Does this matter differently in highly polygenic systems vs oligogenic/monogenic?

The backbone: number of loci and size effects: affecting the evolution of that with recombination and del mut

Be careful with fitness function -> need to make sure it is used in quantitative models, has backing

Make diagram to clarify

Implications of each parameter on what will happen (predictions)

Shiny app for different pop gen concepts used – used to quickly get an idea of figures

Dist of size effects: have a few of them: needs to be empirically anchored

Phil trans recent issue – all about recombination

Del mut rates literature – to define ranges

What will the diagram provide us? What predictions?

Need to match theory to the diagram

Check Charlesworth and Walsh and Lynch

Quantitative models: HoC vs Gaussian – do they respond differently?

Maintenance of variation is the focus, so need to compare VA probably. Perhaps it’s different after extended periods of adaptation (i.e. further distance from new optimum).

Perhaps makes sense to look at just one trait for this? Yes

First, will need to adjust the script – think about fixing deleterious mutation implementation: sliding scale has to go, will need to have fixed positions that are chosen to be deleterious non-QTL, so if they get a mutation, they are definitely deleterious. In that case we will need to increase the size of the genome to accommodate for that.

Also need to adjust distance to the optimum so there is a decent adaptive walk period that we can separate from the maintenance period: we can detect when a population reaches the optimum and then run for a further 50,000 generations or so.

We can fix Mutation rate and selection strength at certain points to define as HoC and Gaussian, and recover quantitative genetics expectations as a starting point

LHC is a key novelty for this paper – we can use it for deleterious mutation strength, ‘rate’ (being the number of potentially deleterious loci), nloci, recombination rate.

Pop size we also may be able to adjust as well –although there we are changing the effective mutation rate, so maybe we want to keep it fixed.

Change it: a few sizes, do tests on how fast/slow it is

Mutation rate must vary across loci due to rate of molecular evolution: some are constrained, other fast evolving

Very relaxed GA vs very conserved GA – how to model?

Look at ranges of conservation in existing networks – levels of lambda

Look at centrality and connectivity of network – modelling that (central nodes are conserved) – highly connected ones will evolve slower

Distribution of pathways that can produce a trait that can be neutral or selected etc.

Reading into pathways – intro to developmental systems biology

Flowering time – complex

Idea of how to deal with deleterious background selections –mutation rate

Implementing pleiotropy/multiple traits: how to define traits? Some multiplier to their effect on fitness so they aren’t all the same? Will need to think about treating traits as non-arbitrary to do this.