

plotsims

```
plot_grid(pretreat, thinning, single_locus, twofoci, labels = c('A', 'B', 'C', 'D'), align = 'v', ncol = 2)
```

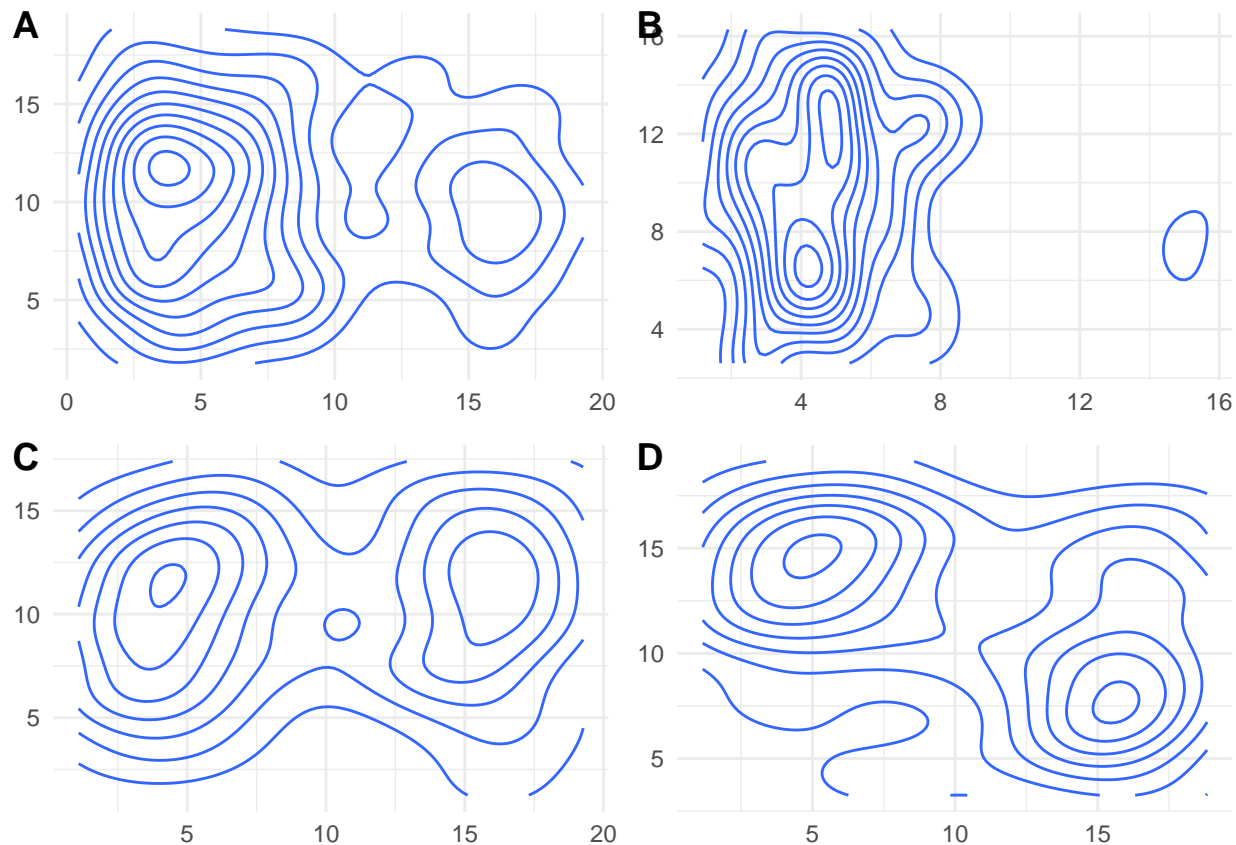


Figure 1 Output of present states of forward genetic simulations in SLiM. Contours represent KDE.

A: No treatment. **B:** Landscape reduces fitness by 2X 30 generations ago (ga) **C:** Left focus reduces fitness by 2X 30ga **D:** Bottom half of LHS focus fitness reduced by 2X 30ga

```
plot_grid(ptpretreat, ptthinning, ptsingle_locus, pttwofoci, labels = c('A', 'B', 'C', 'D'), align = 'v', ncol = 2)
```

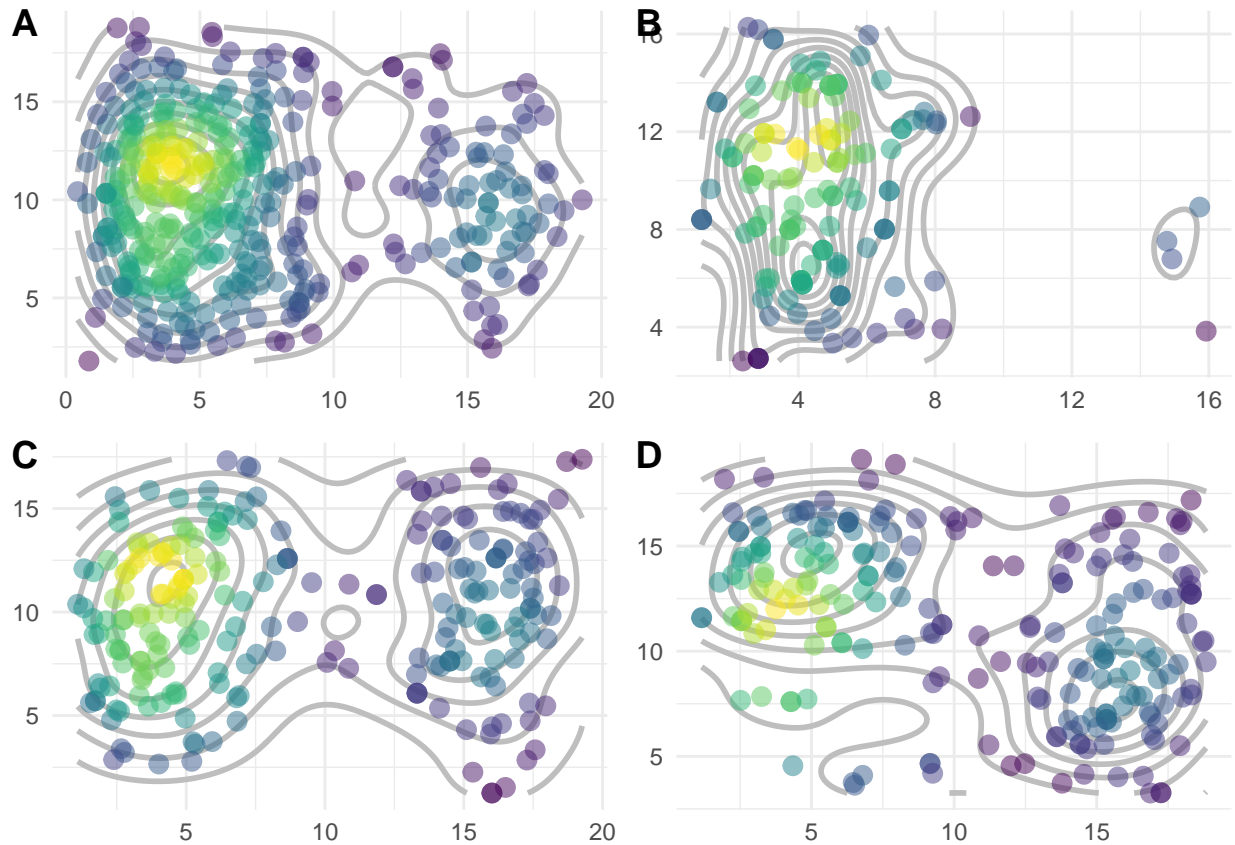


Figure 2 As above but with points for individuals - ‘heat’ = KDE.

A: No treatment. **B:** Landscape reduces fitness by 2X 30 generations ago (ga) **C:** Left focus reduces fitness by 2X 30ga, continued to present. **D:** Bottom half of LHS focus fitness reduced by 2X 30ga

Simulation produced in SLiM (Haller *et al*, 2019). SLiM output recorded as a tree sequence parsed in tskit, Kelleher, *et al*, 2018 and pySLiM Haller *et al*, 2019