Appendix 1 – Population Genetics and Colony Assignments

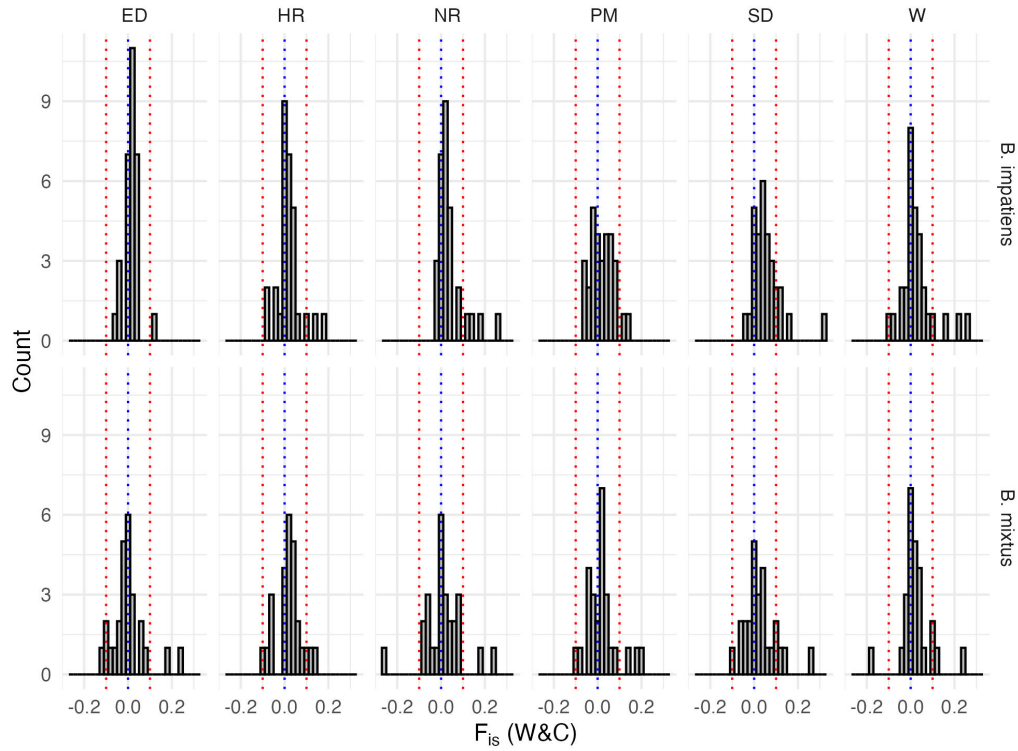## 1 Assessing locus F_{is}, F_{st} and linkage disequilibrium

Figure A1: Estimates of F_{is} for each locus in each subpopulation. Estimates from 2022 and 2023 were calculated separately but are shown together for each site x species combination. Blue dotted lines indicates $F_{is} = 0$ and red dotted lines indicate $F_{is} = \pm 0.1$.
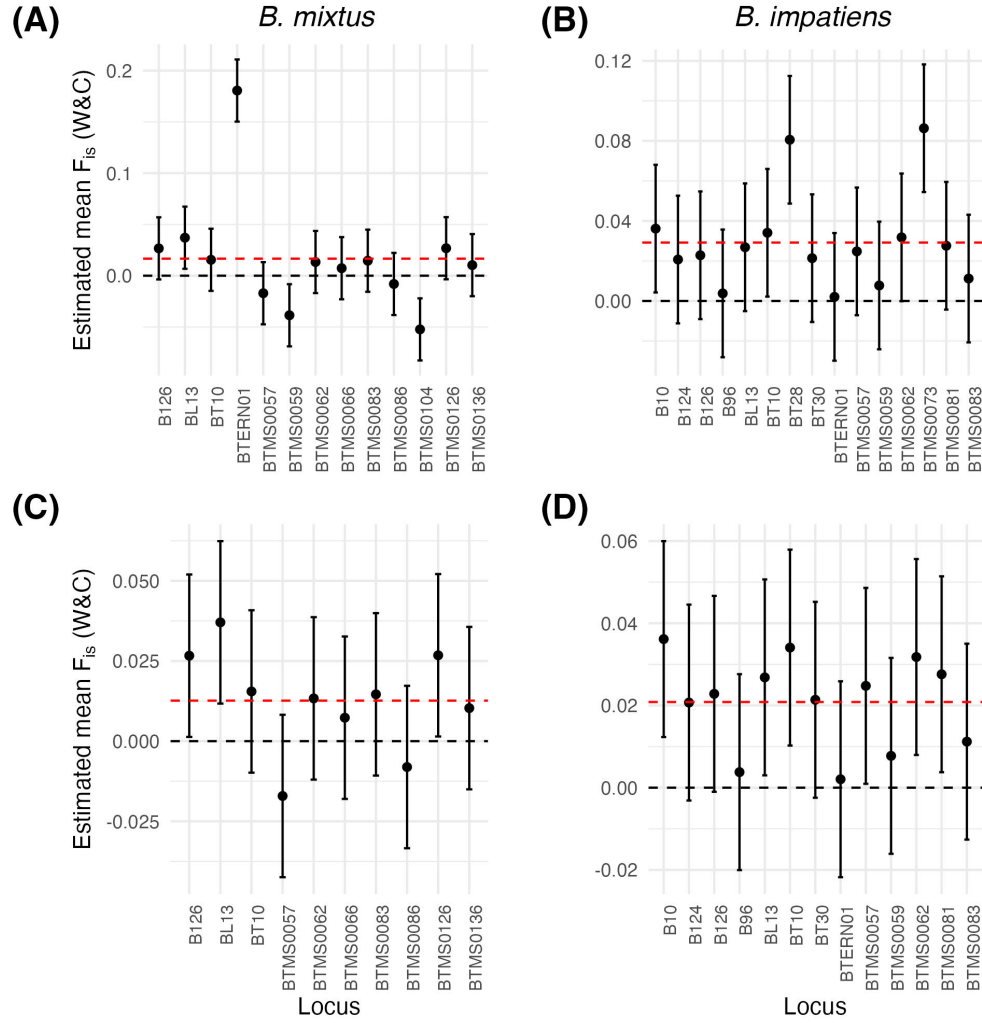
Figure A2: Locus-specific F_{is} marginal means. A) *B. mixtus* all loci; B) *B. impatiens* all loci; C) *B. mixtus* loci following iterative removal of loci which differed significantly from global mean F_{is}; D) *B. impatiens* loci following iterative removal of loci which differed significantly from global mean F_{is}. Dashed black line denotes $F_{is} = 0$, dashed red line denotes global mean F_{is} for each species.
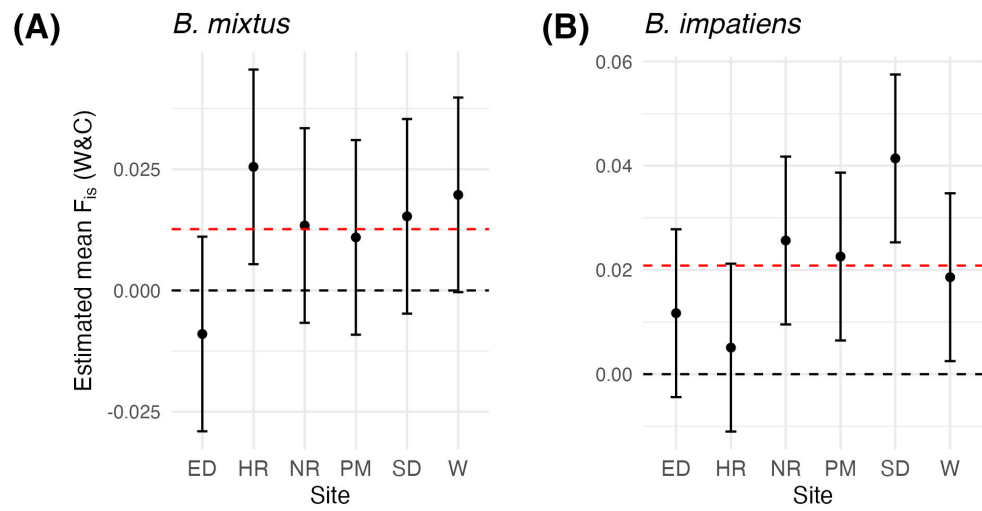
Figure A3: Site-specific F_{is} marginal means following removal of low-quality loci for A) *B. mixtus* and B) *B. impatiens*. Dashed black line denotes $F_{is} = 0$, dashed red line denotes global mean F_{is} for each species.

2 Testing COLONY on simulated data

3 Observing colonymates at multiple sites