Daily Records

Caccone PostDoc

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1.1 Finding interesting regions from the ddRAD data

We may not need to treat the sequence data as continuous at first.

Can we:

- treat each RAD contig as a random sample of the genome and ignore the adjacency relationships while generating the Fst/SNP comparisons
- identify intersting RADs
- map them back to their loacations
- ask whether there are clusters of “interesting” RADs