Motivation
Identifying regions with high amounts of consistent differences across populations has proven useful for identifying evolutionary divergence. Studies on drosophila melanogaster and marine-freshwater stickleback fish have been performed measuring such consistent differences across groups, but none have to my knowledge been made available online.

I implemented two algorithms for such measurements as tools in the Genomic HyperBrowser.

Implemented as Galaxy tools

Methods
Two algorithms measuring genomic divergence have been implemented:

- **Cluster separation scoring** of sliding windows based on two-dimensional scaling of the pairwise differences between individuals in the groups
- Performing **Fisher’s exact test** on 2x2 contingency table on each SNP in a sliding window of the genome

The algorithms are visualized below. For the cluster separation scores significance is measured through random permutation testing. Scores for windows based on Fisher’s exact score is meanwhile found by taking the upper 5% threshold of all scores obtained for the window.

Results
The figure shows the cluster separation scores and corresponding p-values for the EDA locus in chromosome IV of the stickleback genome, known for marine-freshwater divergence.

With the correct parameter choices the results from my tools reproduce earlier published results.

References and Acknowledgements
Stickleback study which was reproduced and methods figure was adapted from is published in “The genomic basis of adaptive evolution in threespine sticklebacks”. Jones et al. Nature 484.7392 (Apr. 2012), pp. 55–61.

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