

Notes

This repository contains raw data (and some processed output) used for the analyses contained in:

Gonçalves da Silva et al. Genomic data suggest environmental drivers of fish population structure in the deep sea; a case study for the orange roughy (*Hoplostethus atlanticus*). Journal of Applied Ecology. *in press*

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Please note that the population referred to as `North Rockall` in the manuscript is variously coded as `Fran` and `Scotland` in the data below.

Raw data

- `Genotyping_17mar14_Atlantic_FinalReport.txt` : Raw SNP calls produced with Illumina GenomeStudio

Data tables

- `orpg_hwe_le_raw_data.csv` : Data frame of SNP data and samples for loci found to be in HWE and LE
- `orpg_locus_status.csv` : Outlier status call for each locus and method used
- `orpg_atlantic_location.csv` : Population locations and provenance.

Genepop formatted files

All loci in HEW and LE

- `orpg_all_hwe_le.gen` : All loci found to be in HWE and LE across all sampled populations

Neutral loci

- `any_four_neutral.gen` : Loci identified as neutral in at least one of the four methods to detect selection

Outlier loci

- `pcadapt_southatlantic_outliers.gen` : Outlier loci identified with PCAdapt for the SA populations
- `pcadapt_northatlantic_outliers.gen` : Outlier loci identified with PCAdapt for the NA populations
- `pcadapt_all_outliers.gen` : Outlier loci identified with PCAdapt for the both NA and SA populations
- `lositan_southatlantic_outliers.gen` : Outlier loci identified with Lositan for the SA populations
- `lositan_northatlantic_outliers.gen` : Outlier loci identified with Lositan for the NA populations
- `lositan_all_outliers.gen` : Outlier loci identified with Lositan for the both NA and SA populations
- `bayescan_southatlantic_outliers.gen` : Outlier loci identified with BayeScan for the SA populations
- `bayescan_northatlantic_outliers.gen` : Outlier loci identified with BayeScan for the NA populations
- `bayescan_all_outliers.gen` : Outlier loci identified with BayeScan for the both NA and SA populations
- `bayenv2_southatlantic_outliers.gen` : Outlier loci identified with Bayenv2 for the SA populations
- `bayenv2_northatlantic_outliers.gen` : Outlier loci identified with BayeScan for the NA populations
- `bayenv2_all_outliers.gen` : Outlier loci identified with Bayenv2 for the both NA and SA populations