Recommended links and literature

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PhD course: High throughput sequencing of non-model organisms

The following sections list relevant literature, links to analysis pipelines, as well as to tutorials and learning environments that get you closer to become bioinformatics-experts.

1 Recommended Reading for RAD sequencing

- The Molecular Ecologist article: To RADseq or not to RADseq?
- Andrews, Kimberly R., et al. "Harnessing the power of RADseq for ecological and evolutionary genomics." Nature Reviews Genetics 17.2 (2016): 81-92.
- Baird, Nathan A., et al. "Rapid SNP discovery and genetic mapping using sequenced RAD markers." PloS one 3.10 (2008): e3376.
- Baker, Monya. "De novo genome assembly: what every biologist should know." Nature methods 9.4 (2012): 333-337
- Catchen, Julian, et al. "Stacks: an analysis tool set for population genomics." Molecular ecology 22.11 (2013): 3124-3140.
- Catchen, Julian M., et al. "Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations." Molecular Ecology Resources (2017).
- DaCosta, Jeffrey M., and Michael D. Sorenson. "Amplification biases and consistent recovery of loci in a double-digest RAD-seq protocol." PloS one 9.9 (2014): e106713.
- Davey, John W., and Mark L. Blaxter. "RADSeq: next-generation population genetics." Briefings in Functional Genomics 9.5-6 (2010): 416-423.
- Hohenlohe, Paul A., et al. "Population genomics of parallel adaptation in threespine stickleback using sequenced RAD tags." PLoS genetics 6.2 (2010): e1000862.
- Hohenlohe, Paul A., et al. "Nextgeneration RAD sequencing identifies thousands of SNPs for assessing hybridization between rainbow and westslope cutthroat trout." Molecular ecology resources 11.s1 (2011): 117-122.

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- Lowry, David B., et al. "Breaking RAD: an evaluation of the utility of restriction siteassociated DNA sequencing for genome scans of adaptation." Molecular ecology resources 17.2 (2017): 142-152.

- Lowry, David B., et al. "Responsible RAD: Striving for best practices in population genomic studies of adaptation." Molecular Ecology Resources (2017).

- McKinney, Garrett J., et al. "RADseq provides unprecedented insights into molecular ecology and evolutionary genetics: comment on Breaking RAD by Lowry et al.(2016)." Molecular Ecology Resources (2017).

- Peterson, Brant K., et al. "Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species." PloS one 7.5 (2012): e37135.

- Rasic, Gordana, et al. "Genome-wide SNPs lead to strong signals of geographic structure and relatedness patterns in the major arbovirus vector, Aedes aegypti." BMC genomics 15.1 (2014): 275.

- Schweyen, Hannah, Andrey Rozenberg, and Florian Leese. "Detection and Removal of PCR Duplicates in Population Genomic ddRAD Studies by Addition of a Degenerate Base Region (DBR) in Sequencing Adapters." The Biological Bulletin 227.2 (2014): 146-160.

- Puritz, Jonathan B., Christopher M. Hollenbeck, and John R. Gold. "dDocent: a RADseq, variant-calling pipeline designed for population genomics of non-model organisms." PeerJ 2 (2014): e431.

- Puritz, Jonathan B., et al. "Demystifying the RAD fad." Molecular ecology 23.24 (2014): 5937-5942.

- Blog on RAD seq

2 Guidelines for pooled sequencing data

- Schlötterer, Christian, et al. "Sequencing pools of individuals - mining genome-wide polymorphism data without big funding." Nature Reviews Genetics (2014).

3 Useful programs and analysis pipelines

- *Molecular Ecology Resources* Jan 2017; Special Issue: Population Genomics with R

- Popoolation: Population genomic analysis of pooled samples, see also this presentation

- Popoolation 2: allows comparison of allele frequencies between two or more populaitons

- The Simple Fool's Guide to Population Genomics via RNA-Seq

- Bioconductor: R packages for genomic data analysis
- Rosalind: Learning python
- Biopython
- BioPerl
- STACKS: building loci from short sequences and analyzing RADseq data
- Ddocent: ddRAD analysis pipeline

4 Recommended books

- Unix and Perl to the Rescue
- Computational Biology
- Primer to Analysis of Genomic Data Using R (Use R!)
- Bioinformatics Data Skills: Reproducible and Robust Research with Open Source Tools
- Practical Computing for Biologists

5 Upcoming Coursera courses

- R programming
- Algorithms, Biology, and Programming for Beginners
- Epigenetic Control of Gene Expression
- Bioconductor for Genomic Data Science
- Statistics for Genomic Data Science
- Comparing Genes, Proteins, and Genomes (Bioinformatics III)
- Python for Genomic Data Science
- Command Line Tools for Genomic Data Science

Emacs 24.5.1 (Org mode 8.3beta)