RAD-seq in Roscoff

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Mini-workshop about ddRAD

Introduction about RAD-seq

- RAD? RAD-seq? ddRAD?
- Applications
- Workflow

Practicals

- One complete project, from raw reads to final results
- Cherry-picking of some analysis steps
- Open questions

Objectives

- Overview of RAD-seq
- Arouse curiosity
- Give useful pointers

Disclaimer about the speaker

- Not a population geneticist, not a bioinformatician
- Evolutionary biologist who dropped into a RAD-seq project when he was post-doc
- Some things are probably wrong!

What are RAD markers?

Miller et al. 2007 restriction site polymorphism

RAD-seq

Single read vs. paired ends

Examples, applications

ddRAD

Examples, applications (population genomics, mapping, QTL, phylogeography, . . .) or put those appplications in more general context? nonmodel species, marker discovery anything that needs lots of markers in lots of individuals or pools

Other flavours

Typical analysis

Depends on the question and objectives! Experimental/sampling design DNA extraction, library preps Barcoding? pooling? Sequencing (service?) Reads cleaning demultiplexing assembly or alignment (mapping if reference available) genotype calling RAD stops here (i.e. lots of markers and allele frequencies for different populations or genotypes for individuals) Downstream analysis:

- genome scan
- Fst, Gst, outlier detection
- Phylogeography
- Parallel evolution
- and many other things. . .

General workflow scheme

One complete project

Tour of other tools and specific analyses

To illustrate some specific points (e.g. likelihood or bayesian based genotyping or allele frequency estimates or Fst calculations, . . .)