ForBio
Forskerskole i Biosystematikk
Research School in Biosystematics

Introduction to RADseq

Time: June 3-7, 2013
Place: The course will use the RADseq platform at Blindern, University of Oslo. (http://www.mn.uio.no/cees/english/research/groups/rad/index.html).
Course credits: 5 ECTS
Assessment: Written report summarizing the course content within two weeks after course is finished.
Registration: Register before May 5, 2013 at https://nettskjema.uio.no/answer/54325.html
Course fee: No course fee, ForBio covers the travel and accommodation costs for members, see more information at http://www.forbio.uio.no/membership/
Teachers: Emiliano Trucchi (emiliano.trucchi@ibv.uio.no)
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Magnus Popp (magnus.popp@nhm.uio.no)
Invited Speaker: Walter Salzburger

Prerequisites: All participants must have experience from basic laboratory work and be comfortable with lab techniques such as DNA extraction, PCR, and/or enzymatic reactions. Please describe your lab experience when you register for the course.

Maximum number of participants: For practical reasons the number of participants is limited to 16. If more students apply we will prioritize ForBio members having concrete plans to apply RADseq techniques in their research. Please describe how RADseq fits in your research plans and if/when you plan to start your RADseq work when you register for the course.

Course content: Restriction site Associated DNA (RAD) sequencing along with advances in sequencing technology is making it realistic to obtain genome scale data not only from model organisms, but also from species without available genomic resources. RADseq techniques have been used for SNP discovery and genotyping, genotype-phenotype association mapping, linkage mapping, QTL analysis, hybridization and gene flow analysis, and population genetics. More recently, RADseq data has also been used to address problems in phylogeographic and phylogenetic studies by utilizing information from linked SNPs in "mini-contigs" obtained from paired end sequencing. This is a flexible method for people looking to work on both model and non-model organisms.

Over the course of the week, each participant will construct a RAD tag library that will be sequenced on an Illumina HiSeq or MiSeq at the Norwegian Sequencing Centre. The samples will be chosen to address a research question in an ongoing project that will be planned in collaboration with our invited speaker, Walter Salzburger. After the libraries have been sequenced, there will be a second RADseq course where the topic will cover data handling and analysis. The second course is preliminary scheduled for October 2013. Participants from the first (lab) course will have priority in if the second (analysis) course fills up.

The participants will use the Etter protocol for library preparation (available here: https://www.wiki.ed.ac.uk/display/RADSequencing/Home;jsessionid=A1374CCB24452859AF755FF98A140BC4) with some modifications developed by the RADseq platform. Other RADseq protocols will also be presented and their advantages and disadvantages discussed.

TENTATIVE COURSE SCHEDULE:

Monday June 3:

09:00 – 10:00: Introduction to RADseq
10:00 – 12:00: **Sample quality check**
12:00 – 13:00: Lunch
13:00 – 15:00: **Sample normalization and Digestion**
15:00 – 16:00: *LECTURE*: *Research presentations, teachers*
16:00 – 17:00: Take out from PCR samples after digestion (4 student presentations)
17:00 – 18:00: Optional mingling hour

Tuesday June 4:

09:00 – 12:00: **P1 Ligation** (2 student presentations)
12:00 – 13:00: Lunch
13:00 – 14:00: **Sample pooling**
14:00 – 15:00: **Sonication**
15:00 – 16:00: **Run gels etc.**
16:00 – 17:00: **QIAquick**
17:00 – 18:00: Optional mingling hour

Wednesday June 5:

09:00 – 10:00: **Run gel** (2 student presentations while gel runs)
10:00 – 12:00: **Cut out band, set gel to melt**
12:00 – 13:00: Lunch
13:00 – 14:00: **Gel extraction**
14:00 – 15:00: *LECTURE: Sequencing technologies*
15:00 – 16:00: (4 student presentations)
16:00 – 17:00: *LECTURE*: *Other RADseq methodologies: Pros and Cons*
17:00 – 18:00: Optional mingling hour

Thursday June 6:

09:00 – 10:00: **Blunting** (2 student presentations)
10:00 – 11:00: **Klenow** (2 student presentations)
11:00 – 12:00: **Beads into P2** (2 student presentations)
12:00 – 13:00: Lunch
13:00 – 14:00: **Bead purification**
14:00 – 15:00: **Test amplification**
15:00 – 16:00: **Run gel**
16:00 – 17:00: *LECTURE: Walter Salzburger on our cichlid RADseq question(s)*
17:00 – 18:00: Optional mingling hour
18:00 Course Dinner

Friday June 7:

09:00 – 11:00: **Real amplification and set gel**
11:00 – 12:00: **run gel**
12:00 – 13:00: Lunch
13:00 – 15:00: **Bead purification and quantification (Qubit, Bioanalyzer)**
15:00 – 16:00: *LECTURE*: TBA
16:00 – 17:00: Discussion, wrap-up