Discovering non-standard RNA transcripts
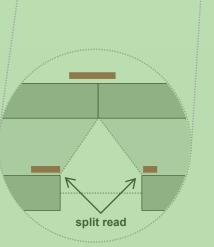
ECSEQ BIOINFORMATICS

How to detect canonical splicing, circular RNAs, trans-splicing, and fusion transcripts.

Workshop

split read

23rd - 24th October 2014
8:00 am - 17:00pm
Leipzig, Germany

Join this hands-on workshop taught by experts in the field. Learn how to use split-read mapping to detect not only canonical splice sites, but also circularized RNAs, trans- and fusion-splicing.

SCOPE AND TOPICS

- Discuss methods of mapping NGS data
- Understand the advantages and limitations of split-read mapping
- Use bioinformatics software and tools to undertake analysis of different splice events
- Learn how to predict/quantify isoforms using split-read information
- Interpret the results and extract scientific valuable findings

ENROLL TODAY

1. Visit www.ecseq.com/training.html
2. Choose from our list of upcoming workshops
   'Discovering standard and non-standard RNA transcripts'
3. Click 'Register'

Workshop Cost:

industry rate: 850EUR
   early-bird: 750EUR

academic rate: 600 EUR
   early-bird: 500 EUR

Travel expenses and accommodation are not covered by the registration fee.

Course materials, conference dinner and catering included!

SPEAKERS

- **Gero Doose (Universität Leipzig)**
  Expert in analyzing and interpreting split-reads in NGS experiments

- **Christian Otto (Universität Leipzig)**
  Developer of segemehl, a software suite for mapping NGS reads allowing split-reads

- **David Langenberger (ecSeq Bioinformatics)**
  Expert in NGS data analysis