

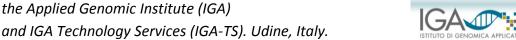
EVOLTREE TRAINING EVENT

NGS data analysis: from Hell to Heaven

2nd – 4th July 2014

Organized by University of Udine (Dr. G. Zaina and Prof. M. Morgante), with the collaboration of







Venue. University of Udine, via delle Scienze 206, 33100 Udine, Italy.

Event type. Three-day course with lectures and practical sessions at the bioinfo. lab. Beta 3.

Next Generation Sequencing (NGS) has recently revolutionized the approach to genomic studies enabling the sequencing of billions of bases in massively parallel reactions. These new sequencing technologies collectively referred to as "ultra-deep" sequencing or "massively parallel" sequencing are currently used for SNP discovery, detection of structural variants, genome-wide measurement of transcript levels and a number of other applications, and are revolutionizing biological research.

Speakers and Tutors

Federica Cattonaro CEO and NGS Lab. Manager IGA Technology Services and Istituto di Genomica Applicata Cristian Del Fabbro Senior Scientist Università degli Studi di Udine
Gabriele Magris Junior Scientist Università degli Studi di Udine
Fabio Marroni Senior Scientist Università degli Studi di Udine
Sara Pinosio Senior Scientist Consiglio Nazionale per le Ricerche and Istituto di Genomica Applicata
Nicola Prezza Junior Scientist Università degli Studi di Udine
Davide Scaglione Senior Scientist IGA Technology Services
Simone Scalabrin Senior Scientist IGA Technology Services
Ettore Zapparoli Junior Scientist Università degli Studi di Udine

REGISTRATION OPEN. <u>Deadline: 16th June 2014</u>. No registration fee requested. Number of participants is limited to 25.

EVOLTREE participants

Contact for registration and logistics: Giusi Zaina (giusi.zaina@uniud.it)

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Contact for reimbursements: Claudia Antoniotti (Claudia.antoniotti@efi.int)

Participants from Evoltree will get reimbursed for travel, accommodation and meals. Procedure at (http://www.evoltree.eu/index.php/summer-schools).



Program - NGS data analysis: from Hell to Heaven

Day 1 - 2nd July 2014: Welcome to the jungle

- 09.00 Registration (All, 15')
 - 09.15 Introduction to NGS sequencing focus on the Illumina platform (Cattonaro, 45')
 - 10.00 Introduction to Linux operating system (Del Fabbro, 30')
 - 10.30 Welcome to SHELL (Del Fabbro, 150')
- 11.00 Coffee Break
 - 11.15 Welcome to SHELL (continuation)
- 13.15 Lunch
 - 14.30 Welcome to SHELL /You are not alone: how to get info on the web (Del Fabbro, 30')
 - 15.00 Overview of the Illumina pipeline (Del Fabbro, 30')
 - 15.30 Raw sequence file format (Del Fabbro, 15')
 - 15.45 Get summary statistics before alignment (Scalabrin, 45')
- 16.00 Coffee Break
 - 16.30 Get summary statistics before alignment (continuation)
 - 17.00 Data cleaning: trimming and filtering (also practical exercises) (Scalabrin, 30')

Day 2 - 3rd July 2014: Patience

- 09.00 Overview of alignment software (with a practical session) (Pinosio, 60')
- 10.00 SAM and BAM alignment format (Scalabrin, 30')
- 10.30 Use of shell scripts to perform basic tasks (Del Fabbro, 150')
- 11.00 Coffee Break
 - 11.15 Use of shell scripts to perform basic tasks (continuation)
- 13.15 Lunch
 - 14.30 Viewing alignments: tablet (with a practical session) (Scalabrin, 30')
 - 15.00 Get alignment statistics (Scalabrin, 60')
- 16.00 Coffee Break
 - 16.30 SNP calling and viewing on alignments (with a practical session) (Pinosio, 90')

20.00 Social Dinner

Day 3 – 4th July 2014: Paradise City

- 09.00 Introduction to RNA-seq (Marroni, 30')
- 09.30 Analysis of RNA-seq data (Marroni, 90')
- 11.00 Coffee Break
 - 11.15 Genotyping by sequencing (Scaglione, 135')
- 13.30 Lunch & Departures