



## EVOLTREE TRAINING EVENT

### NGS data analysis: from Hell to Heaven

2<sup>nd</sup> – 4<sup>th</sup> July 2014

Organized by University of Udine (Dr. G. Zaina and Prof. M. Morgante),  
with the collaboration of  
the Applied Genomic Institute (IGA)  
and IGA Technology Services (IGA-TS). Udine, Italy.



UNIVERSITÀ  
DEGLI STUDI  
DI UDINE



**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. Deadline: 16<sup>th</sup> June 2014. No registration fee requested.

Number of participants is limited to 25.

#### **EVOLTREE participants**

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

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

## Program - **NGS data analysis: from Hell to Heaven**

### Day 1 - 2<sup>nd</sup> 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 – 3<sup>rd</sup> 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 – 4<sup>th</sup> 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