

# Advanced Bioinformatics Workshop

**Date:** Monday, August 20<sup>th</sup> – Friday, August 24<sup>th</sup>, 2018

**Venue:** Adriatico Guest House - Denardo Lecture Hall

International Centre for Theoretical Physics

Trieste, Italy

**Course URL:** <http://www.codata.org/datatrieste2018>

**Material:** <https://codata-rda-advanced-bioinformatics-2018.readthedocs.io>

## Description

This advanced bioinformatics course will provide an overview of the current status of different NGS workflows (variant calling, RNA-Seq, ChIP-Seq, etc), and combine them with the appropriate Machine Learning and Data Mining approaches. The course will heavily rely on hand-on exercises and tutorials, and attempt to provide a strong foundation on the underlying theory.

## Instructors

- **Fotis Psomopoulos**, Institute of Applied Biosciences (INAB|CERTH) / ELIXIR GR  
Contact details: [email](#), [website](#), [twitter](#)
- **Amel Ghouila**, Institut Pasteur de Tunis / H3Bionet
- **Gabriele Schweikert**, Cyber Valley Initiative, University of Tuebingen, DE /  
Computational Biology, University of Dundee, UK

## Course Schedule

	Topic
<i>Day 1</i>	
11:30 – 12:30	Experiments: Design and Analysis
14:00 – 15:00	Components of an Experiment. What is a good experiment design?
15:00 – 16:00	Data Distributions and Multiple Hypotheses Adjustment Methods
16:15 – 18:00	Introduction to basic NGS pipelines
<i>Day 2</i>	
09:00 – 10:00	Introduction to basic NGS pipelines
10:00 – 11:00	Short read quality and trimming (part 1)
11:30 – 12:30	Short read quality and trimming (part 2)
14:00 – 15:00	Mapping
15:00 – 16:00	Variant calling (part 1)
16:15 – 18:00	Variant calling (part 2)
<i>Day 3</i>	
09:00 – 10:00	Introduction to DM and ML, Machine Learning basic concepts
10:00 – 11:00	Taxonomy of ML and examples of algorithms
11:30 – 12:30	Applications of ML in Bioinformatics
14:00 – 15:00	RNASeq analysis in R
15:00 – 16:00	RNASeq analysis in R to be continued
16:15 – 18:00	RNASeq analysis in R to be continued

<i>Day 4</i>	
<b>09:00 – 10:00</b>	Introduction to ChIP-Seq, ATAC-Seq, BS-Seq
<b>10:00 – 11:00</b>	Hands-on application: ChIP-Seq workflow (part 1)
<b>11:30 – 12:30</b>	Hands-on application: ChIP-Seq workflow (part 2)
<b>14:00 – 15:00</b>	Hands-on application: ATAC-Seq
<b>15:00 – 16:00</b>	Hands-on – Apply algorithms to own dataset
<b>16:15 – 18:00</b>	Hands-on
<i>Day 5</i>	
<b>09:00 – 10:00</b>	Introduction to Regression
<b>10:00 – 11:00</b>	Hands-on application: regression algorithms - pros and cons
<b>11:30 – 12:30</b>	Closing, Final Remarks, Post-workshop survey