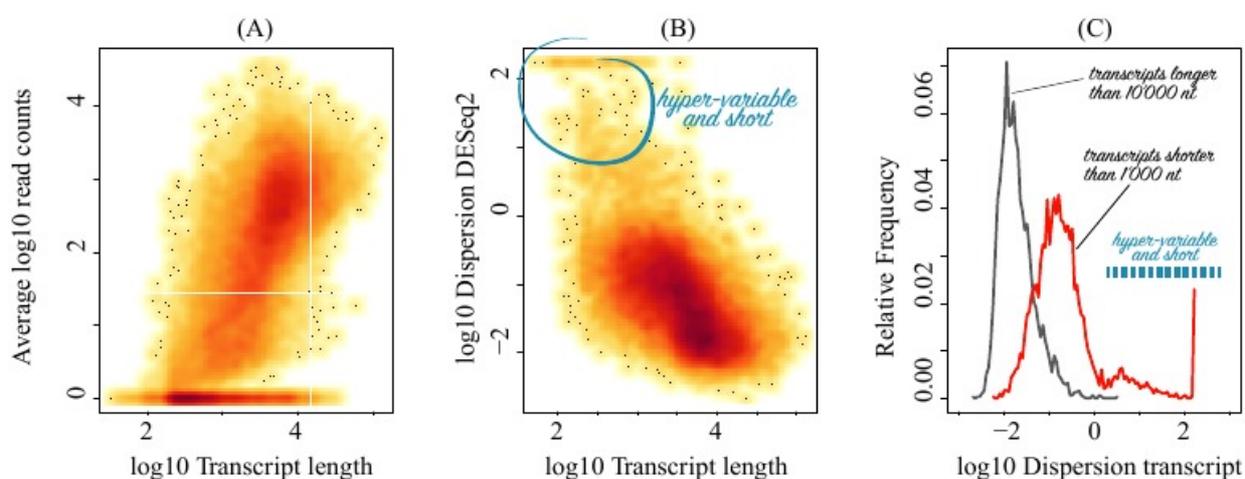


# NGS Bioinformatics seminars and training

## *A workflow for RNAseq analysis*

by

**Dr. Matteo Brilli**



## Final programme

**15<sup>th</sup> March 2019, 14:00-18:00 – Theory (4 hrs)**

**Room 11P (Pentagono, Agripolis – Legnaro, PD)**

- Gene expression regulation
- RNA-seq library preparation, strand-specific protocols
- Illumina sequencing basics, single-end and paired-end
- Sequencing output, quality check and adapter trimming
- Merging overlapping reads
- Short read aligners, basics
- Gene expression quantification: raw counts and normalizations (rpkm, fpkm, tpm ecc)
- Differential gene expression analysis, the importance of replicates and transcript dispersion modeling, multiple test problem
- Functional enrichments in non-model species, multiple test problem
- From gene expression to networks, reverse engineering of regulatory networks

## 22<sup>nd</sup> March 2019, 10:00-13:00 – Practice (3 hrs)

### Room 22P (Pentagono, Agripolis – Legnaro, PD)

- Quality Control
- Adapter trimming
- Merging overlapping reads
- Transcript abundance quantification
- Differential Gene Expression analysis

## 29<sup>th</sup> March 2019, 10:00-13:00 – Practice (3 hrs)

### Room 22P (Pentagono, Agripolis – Legnaro, PD)

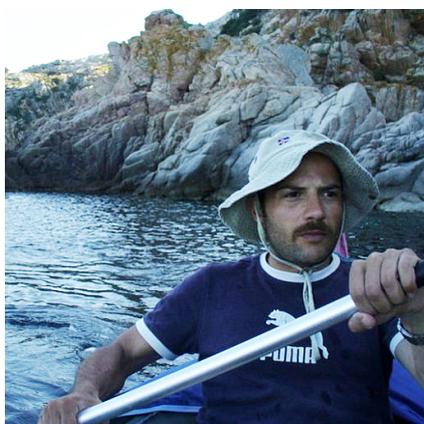
- Representing gene expression data, heatmap, dimensionality reduction (umap and PCA) [with good chart practices!]
- Functional enrichments for non-model organisms: enrichments using user-defined GO annotations
- Co-expression network reconstruction
- Reverse engineering of gene regulatory networks

**Please note that a minimum knowledge of both R fundamentals and command line running is suggested for a fruitful participation.**

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## Dr. Matteo Brilli - Curriculum vitae

Matteo Brilli graduated in Biological Sciences at the University of Florence in 2002, with a thesis focused on bioinformatics for studying the origin and evolution of metabolic pathways. During his PhD, he passed some time abroad at the University of Cambridge, at Pietro Liò's lab, where he refined his skills in bioinformatics and biostatistics. Matteo got his PhD in 2007 at the University of Florence with a dissertation titled "Origin and evolution of metabolic pathways - developing bioinformatics tools for functional genomics". He started his post-doc at the same university working for one year on bioinformatics analysis of cell cycle genes in alpha-proteobacteria and then he moved to the University of Lyon, first under the supervision of Dr. Daniel Kahn, to work on the mathematical modeling of the diauxic shift in *Escherichia coli*, and then under the supervision of Marie-France Sagot to focus on comparative genomics, metabolic and regulatory network modeling in symbiotic bacteria. He passed three years (2013-2016) as a researcher at the Edmund Mach Foundation of San Michele all'Adige, where he was involved in the genome sequencing and multi-omics analysis of the grape pathogen *Plasmopara viticola*, and more than one year at the University of Padova working on genomics of fruit crop pathogens (*Phytoplasma mali*, *Plasmopara viticola*, *Botrytis cinerea*) and NGS analysis of fruit ripening and maturation. After one year of post-doc at the University of Milan, he finally got a position there as Assistant Professor in the scientific sector BIO/19 (General microbiology).



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