

# Scientific Programming

## Practical 1 (QCB)

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### Introduction

Luca Bianco - Academic Year 2020-21  
luca.bianco@fmach.it

# Outline

- ❖ Personal introduction
- ❖ Introduction to the practical
- ❖ Hands-on practical

# About me

## **Computer Science**

Ph.D. at the University of Verona, Italy, with thesis on Simulation of Biological Systems

## **Research Fellow at Cranfield University - UK**

Three years at Cranfield University working at proteomics projects (GAPP, MRMAid, X-Tracker...)

Module manager and lecturer in several courses of the MSc in Bioinformatics

## **Bioinformatician at IASMA – FEM**

Currently bioinformatician in the Computational Biology Group at Istituto Agrario di San Michele all'Adige – Fondazione Edmund Mach, Trento, Italy

## **Collaborator uniTN - CiBio**

I ran the Scientific Programming Lab for QCB for the last four years

# Fondazione Edmund Mach

FEM – San Michele, Trento - Italy



Agricultural Institute

Research and Innovation Centre

Genomics, metabolomics wet labs on  
fruits (apple, grape, small fruits,... )

Bioinformatics and computational biology

# Bioinformatics @FEM (UBC)

## ❖ Genomics

- Assembly and annotation of complex genomes (plants, insects, etc.)
- Development of SNP Chips for genetic screening
- Resequencing of genomes / Variant discovery

## ❖ Metagenomics

- Targeted metagenomic data
- *Feature selection* algorithms
- Algorithms for strain-level identification from un-targeted metagenomics

## ❖ Transcriptomics

- RNA-seq data analysis, gene and pathway enrichment
- Data integration and compilation of expression atlases

## ❖ Metabolomics

- Data analysis pipelines for targeted and untargeted data
- Methods for MS imaging

## ❖ Statistical data analysis

- Integration of -omic data and analysis of correlation networks



# Bix @FEM - Examples

## Genome assembly

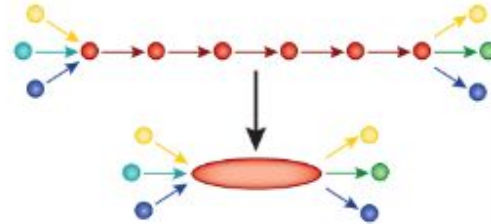
1. Fragment DNA and sequence



2. Find overlaps between reads

...AGCCTAGACCTACA**GGATGCGCGACACGT**  
**GGATGCGCGACACGT**CGCATATCCGGT

3. Assemble overlaps into contigs



4. Assemble contigs into scaffolds



In a nutshell... (Tunis' version...)



Reads

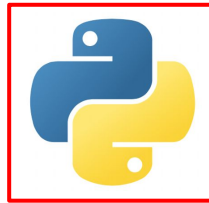


Assembled genome



[Virgil and the Muses, Bardo Museum, Tunis]

[from M. Baker, Nature Methods, 2014]



# Bix @FEM - Examples

## Genome assembly of DH of Pear and Apple

### Multiple sources of input data:

**Illumina:** ~ 100x PE information (mate pairs - in the past)

**Pacific Biosciences** > 50x

**Bionano optical maps:** ~ 600x

**Hi-C:** illumina sequencing of chromosome conformation capture libraries

**Genetic maps:** genetic information coming from mapping populations

### Output result (target):

Chromosome scale assembly

Ideally, we want to arrange all the sequences produced in  $N$  (= number of chromosomes) sequences





# Bix @FEM - Examples

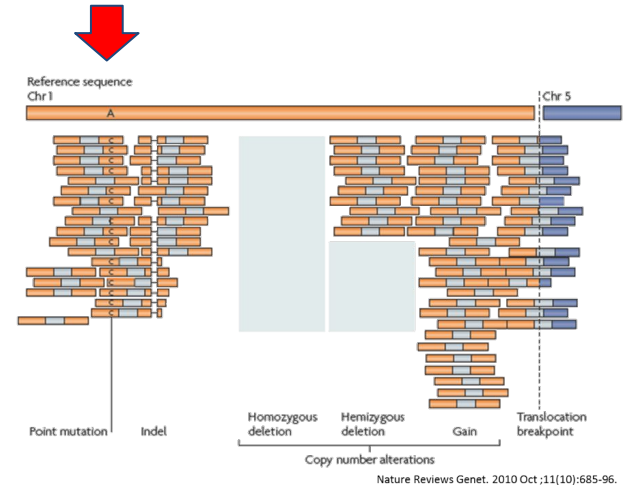
## SNP-Chips development for GWAS

20K SNP Illumina Infinium II Array (reseq of 16 Apple cultivars, Illumina 30x)  
487K SNP Affymetrix Axiom Array (reseq of 63 Apple cultivars, Illumina 20-30x)  
600K SNP Affymetrix Axiom Array Walnut (reseq. 18 cultivars, Illumina 80x)

1. Reads alignment and filtering
2. SNP calling
3. Identification of most reliable SNPs
4. Selection of (20K) 487K target SNPs

**Several Terabytes of data produced!!!!**

**Peach, pear and walnut done too!**







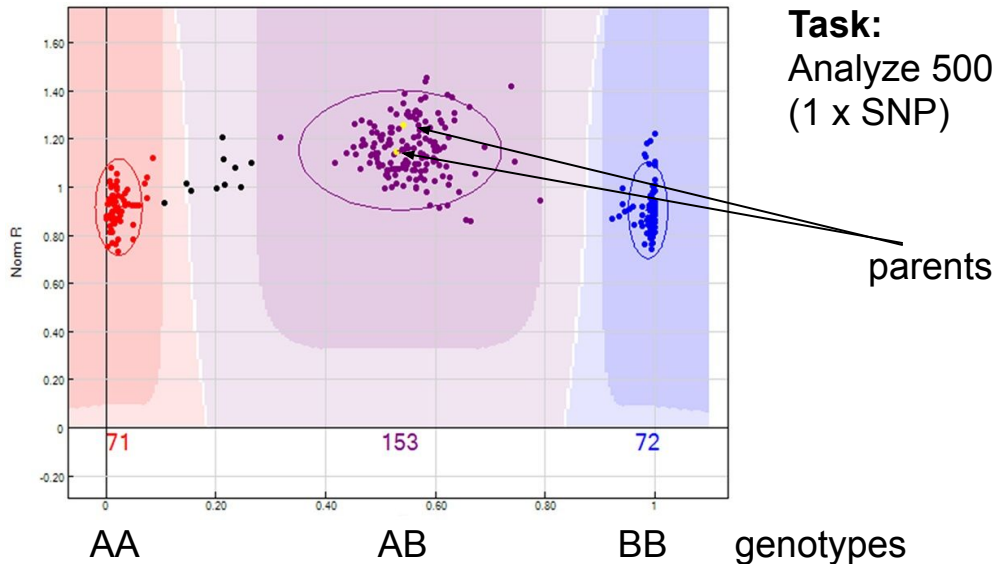
# Bix @FEM - Examples

## SNP-Chips development for GWAS

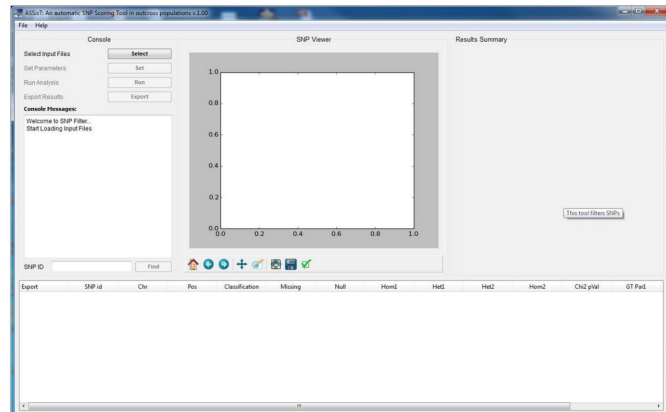
20K SNP Illumina Infinium II Array (reseq of 16 Apple cultivars, Illumina 30x)

487K SNP Affymetrix Axiom Array (reseq of 63 Apple cultivars, Illumina 20-30x)

600K SNP Affymetrix Axiom Array Walnut (reseq. 18 cultivars, Illumina 80x)



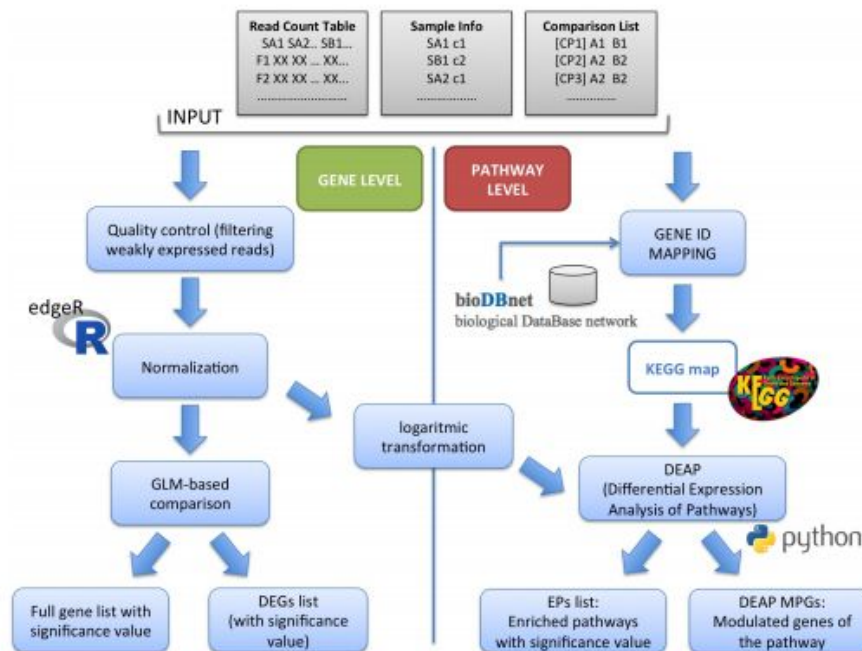
## ASSiST



[Di Guardo et al., Bioinformatics, 2015]

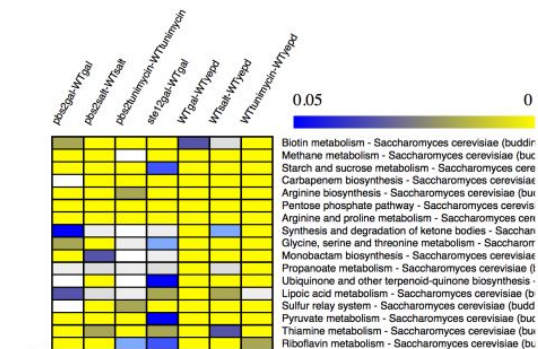
# Bix @FEM - Examples

## RNAseq data analysis with Pathway Inspector



# Bix @FEM - Examples

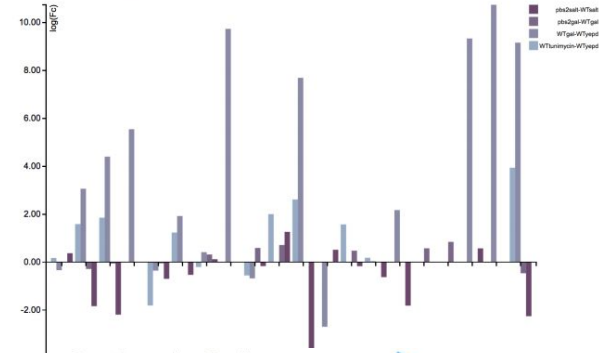
## RNAseq data analysis with Pathway Inspector



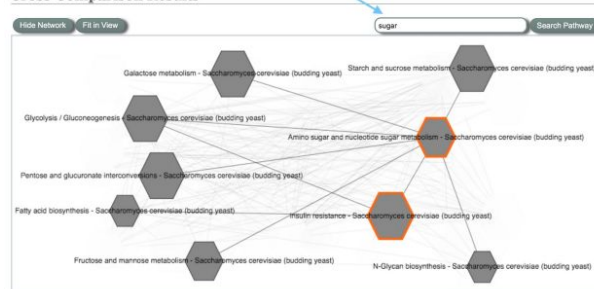
Intersection pbs2salt-WTsalt WTtunimycin-WTyeptd pbs2gal-WTgal WTgal-WTyeptd

Gene	Comparison	P-value	Fold Change	FDR
YOR04W	pbs2gal-WTsalt	0.028480382028946	0.2420311772254	0.0481361748189205
	WTtunimycin-WTyeptd	2.38460349315057e-07	0.524172138345184	4.474873128653e-07
	pbs2gal-WTgal	0.00087890548504029	-0.301105531814261	0.0207830810500887
	WTgal-WTyeptd	2.86788386434103e-15	0.83218803220708	7.1912488256014e-15
YIL140W	pbs2gal-WTsalt	3.85247940741733e-08	0.833589168058476	1.88548837803052e-07
	WTtunimycin-WTyeptd	1.58817870171733e-24	1.001609102893	5.8239103817754e-24
	pbs2gal-WTgal	1.87826251152733e-09	0.30764051192865	1.49862020134624e-08
	WTgal-WTyeptd	0.3034912842367044	0.276548277440217	0.0548210627860931
YLR130C	pbs2gal-WTsalt	0.301481010188815	0.31882150138088	0.0336287774872549
	WTtunimycin-WTyeptd	3.0140342077802e-06	-1.58765788614284	3.8332186378679e-05
	pbs2gal-WTgal	2.7870331888143e-09	0.488214138134541	2.3895374291845e-08
	WTgal-WTyeptd	8.80372033688032e-18	-0.8312188730247	1.8224549730366e-17
YOR011W	pbs2gal-WTsalt	1.00574728111917e-16	0.72183031688741	8.2817487473501e-16
	WTtunimycin-WTyeptd	0.010862387903186	0.21641810221331	0.014715787205527

Comparative analysis for Amino sugar and nucleotide sugar metabolism - Saccharomyces cerevisiae (budding yeast)



Cross-Comparison Results



# Bix @FEM - Examples

## Pedigree-based haplotype visualization

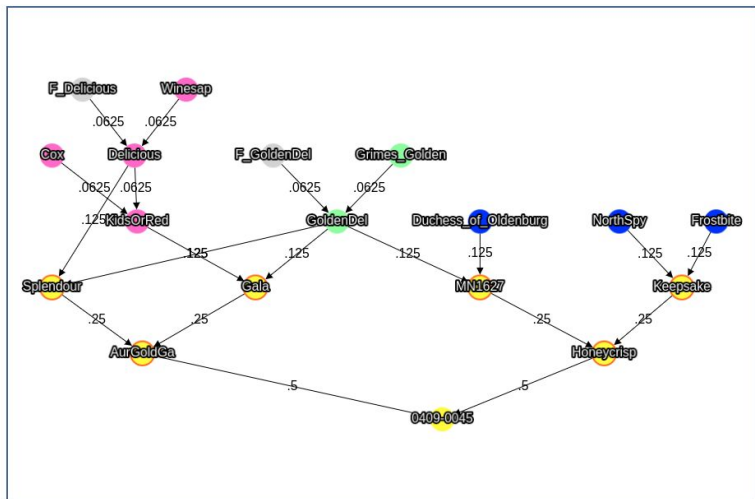
Family of sample: 0409-0045

0409-0045

Fit in View

View global stats

Pedigree browse



Legend  
Sample Mother Father Both No data

Choose one ancestor or other accessions

- Generation 1
  - ✓ Honeycrisp
  - ✓ AurGoldGa
- Generation 2
  - ✓ Keepsake
  - ✓ MN1627
  - ✓ Gala
  - ✓ Splendour
- Generation 3
  - Generation 4
  - Generation 5
- Relatedness 0-10% [2]
- Relatedness 10-20% [2]
- Relatedness 20-30% [17]
- Relatedness 30-40% [182]
- Relatedness 40-50% [183]
- Relatedness 50-60% [9]
- Relatedness 60-70% [0]
- Relatedness 70-80% [0]
- Relatedness 80-90% [0]
- Relatedness 90-100% [0]

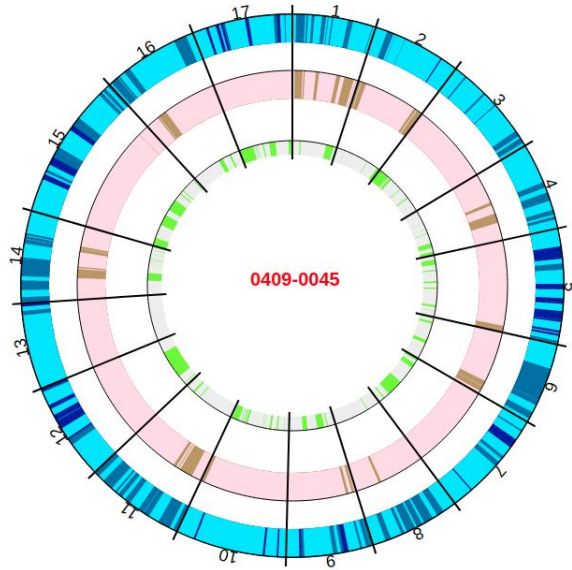
Comparison without pedigree check Comparison with pedigree check

Analyze

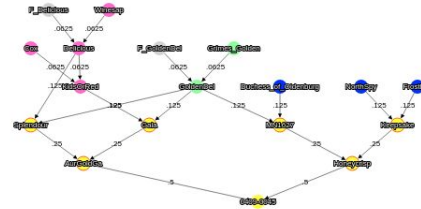
Relatedness

# Bix @FEM - Examples

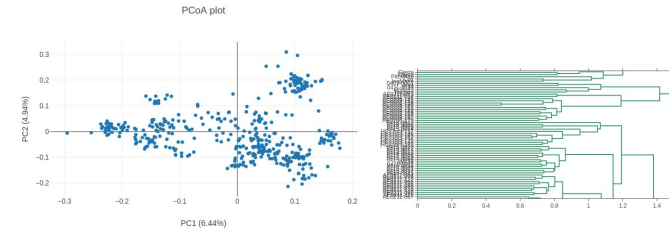
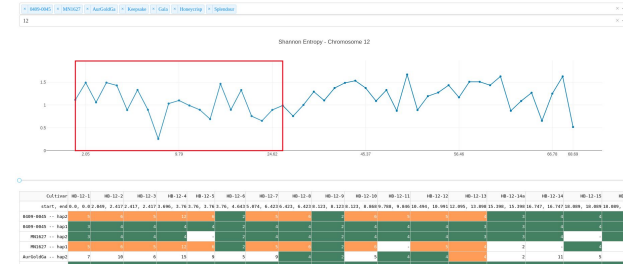
## Pedigree-based haplotype visualization



Pedigree of 0409-0045



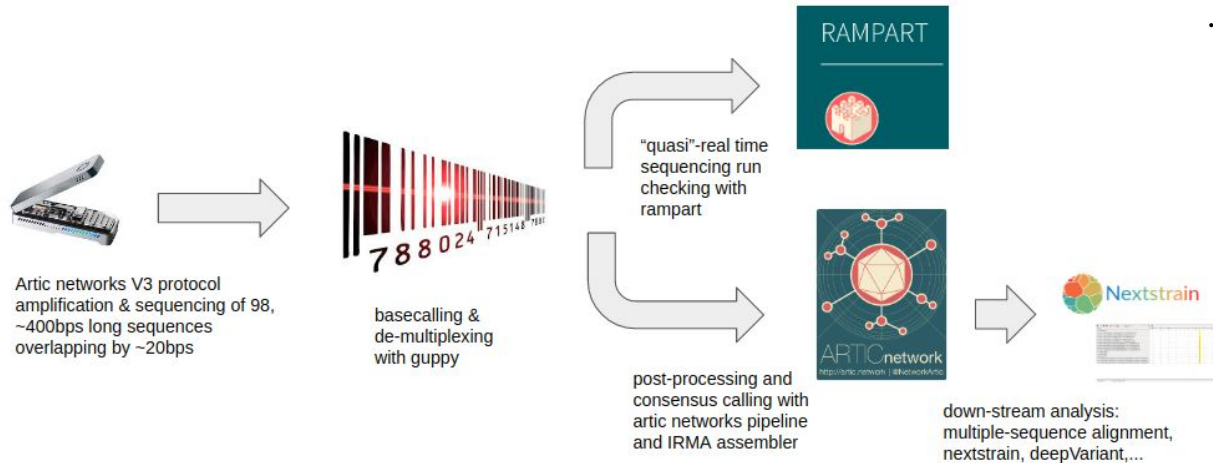
Cultivars	Relatedness	Color	
MN1627	0.39	1CE6FF	✓
AurGoldGa	0.55	FF4A46	✓
Keepsake	0.42	008FA6	✓
Gala	0.48	FFDBE5	✓
Honeycrisp	0.52	0000A6	✓
Splendour	0.48	B79762	✓



# Bix @FEM - Examples

## Sequencing and assembling of Sars-Cov-2 samples from the Province of Trento (sponsored by Fondazione VRT)

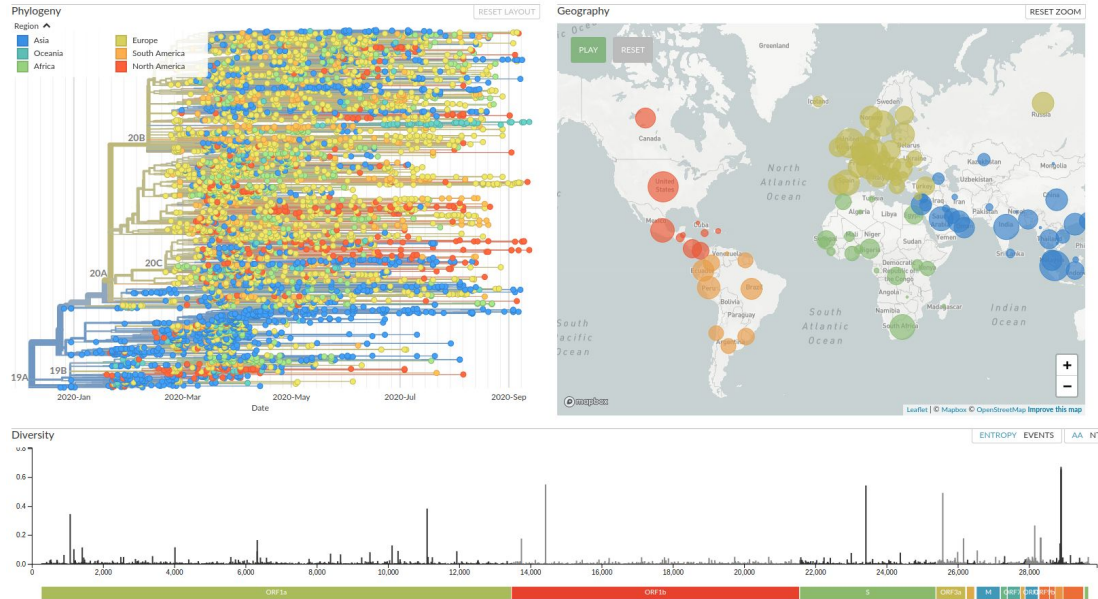
First 72 samples  
assembled...  
... 240 more to go!



# Bix @FEM - Examples

## Sequencing and assembling of Sars-Cov-2 samples from the Province of Trento (sponsored by Fondazione VRT)

Showing 4678 of 4678 genomes sampled between Dec 2019 and Sep 2020.



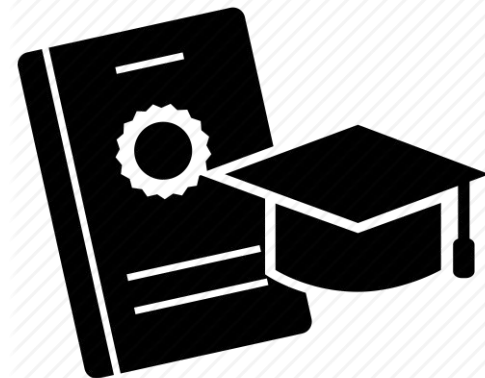
# Opportunities @FEM

## MSc External thesis

Are you interested in a bioinformatics project in NGS data analysis, RNA Seq, data integration?

Talk to me or email me at:

**[luca.bianco@fmach.it](mailto:luca.bianco@fmach.it)**





# Scientific Programming Practical

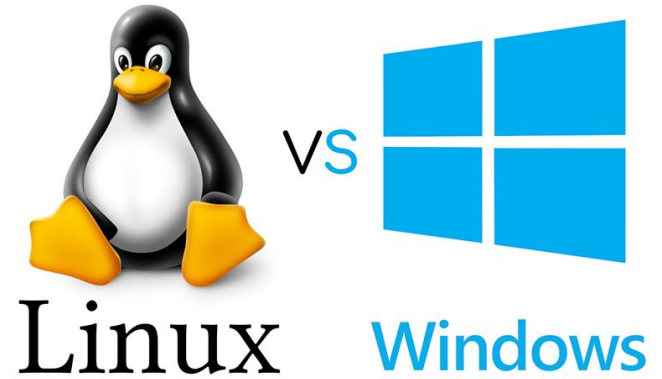
**Back to business now!**



# Linux or Windows?

Up to you, as far as this course is concerned...

but, if you are looking for a career in bioinformatics, I think it would be a good idea to get familiar with Linux



Two options:

- Linux on windows (via virtualization software)
- Dual boot system (decide which to use at boot)

In the description of the practical you have some instructions on how to do the two things.

**Think about the two options today and install Linux in the next few days...**

# Scientific Programming Practical

## In this practical you will

1. Install Python 3.x (and pip)
2. Install Visual Studio Code
3. Get familiar with the Python console
4. Start using Visual Studio Code and advanced features (like debugging)
5. End the session with some exercises

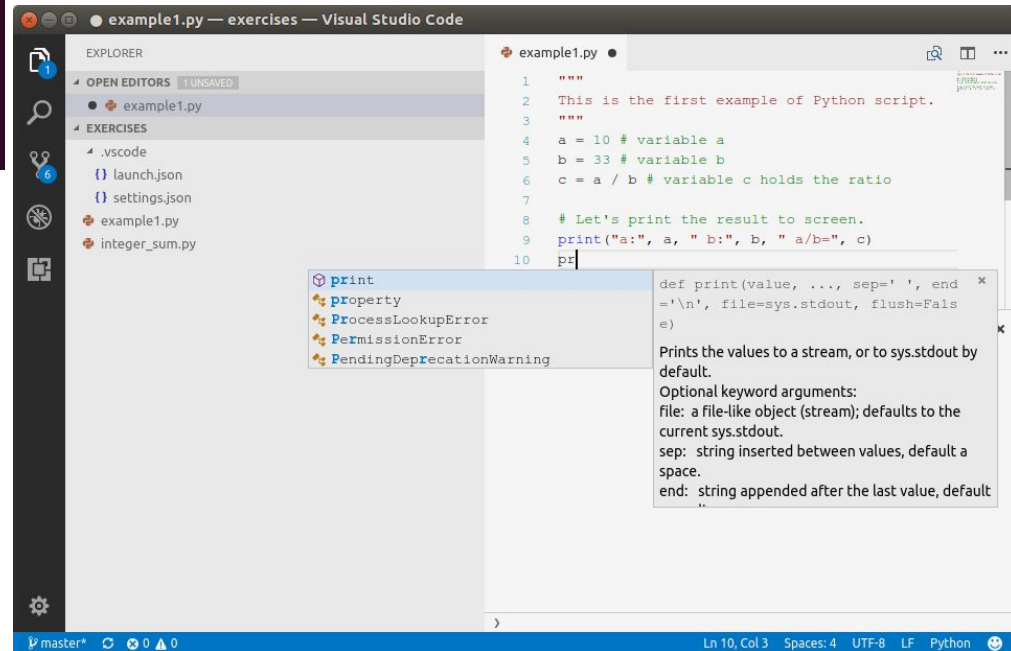


# Scientific Programming Practical

## Console VS. Integrated Development Environment (IDE)

```
biancol@bluhp:~$ python3
Python 3.5.2 (default, Aug 18 2017, 17:48:00)
[GCC 5.4.0 20160609] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>>
```

```
>>> print("Hi there")
Hi there
>>> print("{} + {} = {}".format(10,20, 10+20))
10 + 20 = 30
>>>
```



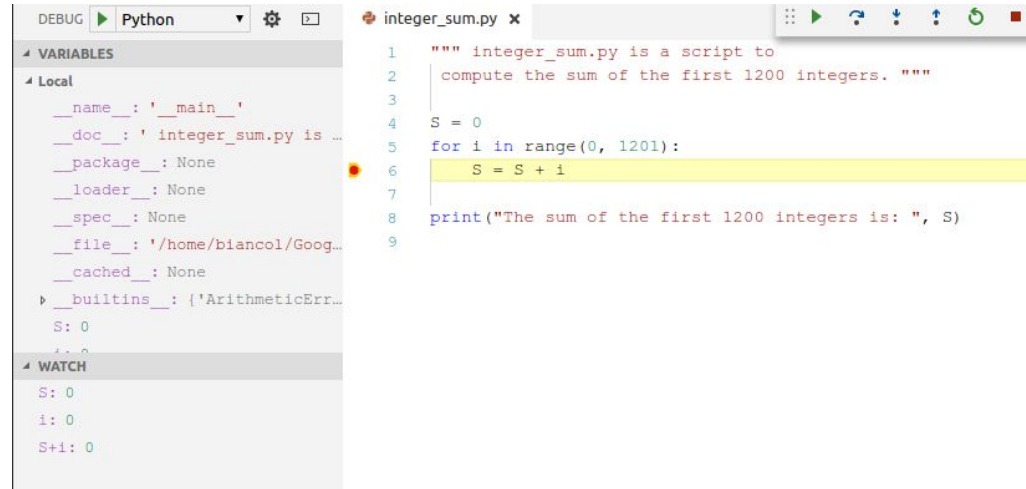
# Scientific Programming Practical

## Console VS. Integrated Development Environment (IDE)

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>>> 
```

```
>>> print("Hi there")
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10 + 20 = 30
>>> 
```

The debugger

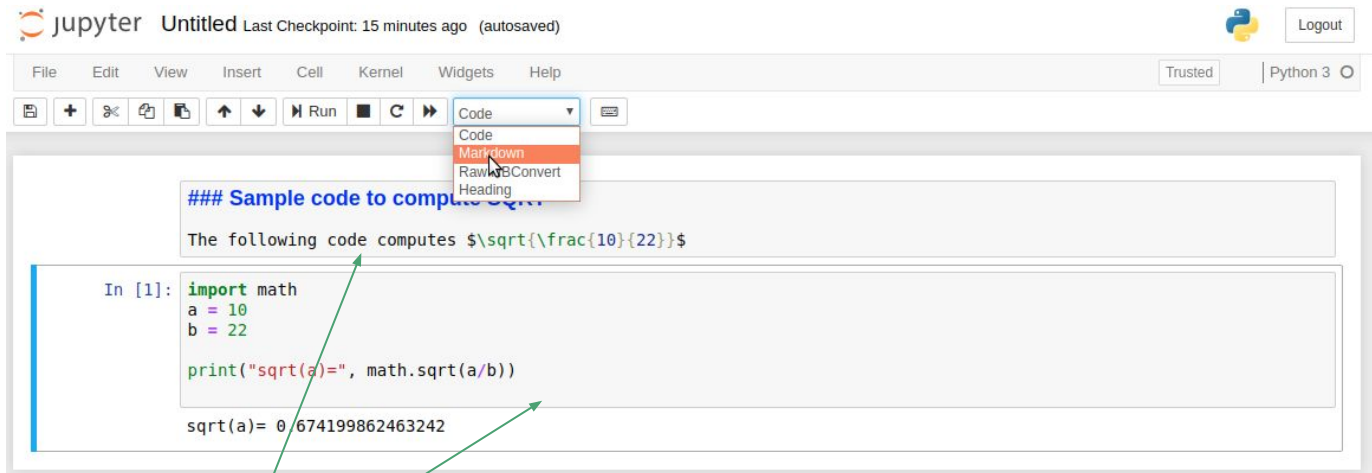


# Notebooks and Jupyter

“Jupyter is a web-based interactive development environment for python/R.. notebooks, code, and data.”

Notebooks contain both the **code**, some **text describing the code** and the **output of the code execution**,

*Jupyter is becoming the de-facto standard for writing technical documentation.*



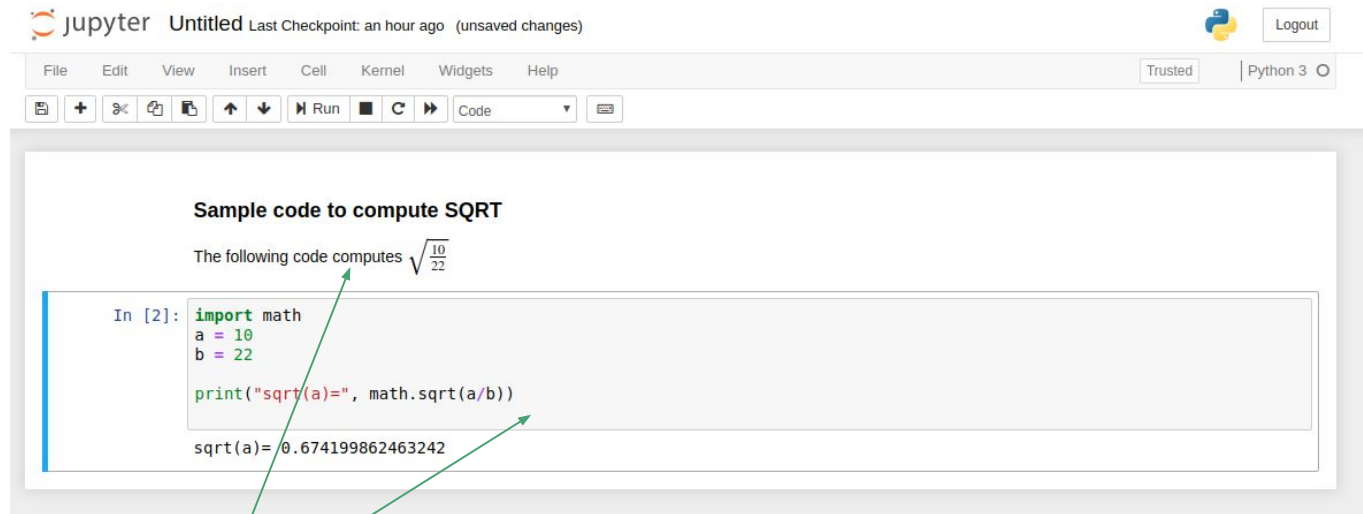
Cells

# Notebooks and Jupyter

Notebooks contain both the **code**, some **text describing the code** and the **output of the code execution**,

*Jupyter is becoming the de-facto standard for writing technical documentation.*

A cell can be executed by clicking on **Run**



Cells  
(after Run)

# Resources

All material regarding practicals will be found here:

<http://qcbsciprolab2020.readthedocs.io>



luca.bianco@fmach.it

## Scientific Programming for QCB

Download: [PDF](#) [EPUB](#) [HTML](#)

### General Info

The contacts to reach me can be found [at this page](#).

### Timetable and lecture rooms

Due to the current situation regarding the Covid-19 pandemic, Practicals will take place ONLINE this year. They will be held on **Mondays from 14:30 to 16:30** and on **Wednesdays from 11:30 to 12:30**.

Practicals will use the Zoom platform (<https://zoom.us/>) and the link for the connection will be published on the practical page available in this site a few minutes before the start of the session.

This first part of the course will tentatively run from **Wednesday, September 23rd, 2020 to Monday, November 2nd, 2020**.

### Moodle

In the moodle page of the course you can find announcements and videos of the lectures. It can be found [here](#).

### Zoom links

The zoom links for the practicals can be found in the Announcements section of the moodle web page. To get you started quickly, I report them here:

Join Zoom Meeting <https://unitn.zoom.us/j/97253388646>

Meeting ID: 972 5338 8646 Passcode: 794500

### Slides

Slides of the practicals will be available on the top part of each practical page.



# Timetable

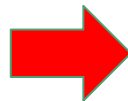
Mondays:

ONLINE: 15,30 - 17,30

Wednesdays:

ONLINE: 11,30 - 13,30

**!!! please write these details down,  
I will remove them from the site !!!  
(they will be on moodle)**



<http://qcbsciprolab2020.readthedocs.io>

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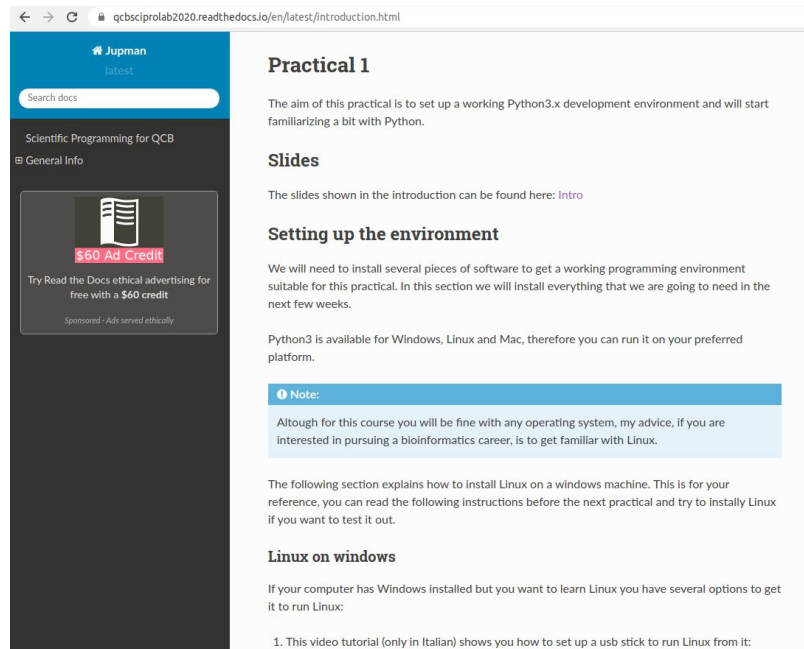


luca.bianco@fmach.it

# Any questions?

If not, please go to:

<https://qcbsciprolab2020.readthedocs.io/latest/introduction.html>



The screenshot shows a web browser displaying the introduction page of the qcbsciprolab2020.readthedocs.io website. The page has a dark blue sidebar on the left with the 'Jupman' logo and a search bar. The main content area is white and contains the following sections:

- Practical 1**: The aim of this practical is to set up a working Python3.x development environment and will start familiarizing a bit with Python.
- Slides**: The slides shown in the introduction can be found here: [Intro](#)
- Setting up the environment**: We will need to install several pieces of software to get a working programming environment suitable for this practical. In this section we will install everything that we are going to need in the next few weeks.
- Note**: Although for this course you will be fine with any operating system, my advice, if you are interested in pursuing a bioinformatics career, is to get familiar with Linux.
- Linux on windows**: The following section explains how to install Linux on a windows machine. This is for your reference, you can read the following instructions before the next practical and try to install Linux if you want to test it out.

At the bottom, there is a list of tasks, with the first one being: 1. This video tutorial (only in Italian) shows you how to set up a usb stick to run Linux from it:

@  
luca.bianco@fmach.it