

Scientific Programming

Practical 1 (QCB)

Introduction

Luca Bianco - Academic Year 2020-21
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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

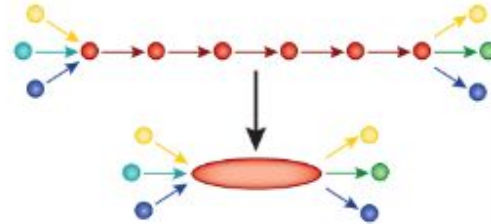
1. Fragment DNA and sequence



2. Find overlaps between reads

...AGCCTAGACCTACA**GGATGCGCGACACGT**
GGATGCGCGACACGTCGCATATCCGGT

3. Assemble overlaps into contigs



4. Assemble contigs into scaffolds



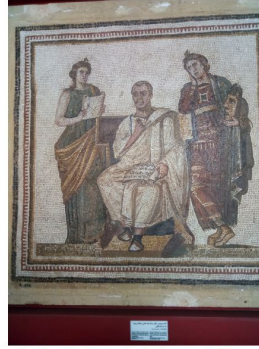
In a nutshell... (Tunis' version...)



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

Input data:

Illumina: ~60x – 100x PE information + (mate pairs for Apple)

Pacific Biosciences ~ 30x + 30x (35x only for Apple)

Bionano optical maps: ~ 600x (for both)

Hi-C: pear only

Genetic maps: integrated genetic map from 21 mapping populations (Apple only)

Output result (example for Apple):

Chromosome scale assembly

Contigs: 2150 for a total of **625Mb**

N50 Contigs (hybrid dbg2olc): ~ **620Kbps**

280 Scaffolds, for an N50 **5,6Mb**

17 chromosomes + 1g0 unanchored sequences

[Daccord et al, Nature Genetics, 49, 2017; Linsmith et al., GigaScience, 2020]





Bix @FEM - Examples

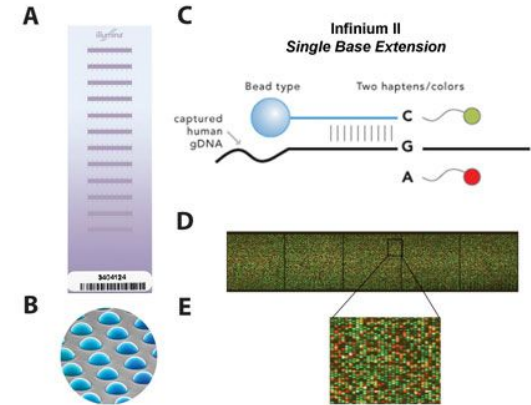
SNP-Chips development for GWAS

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!





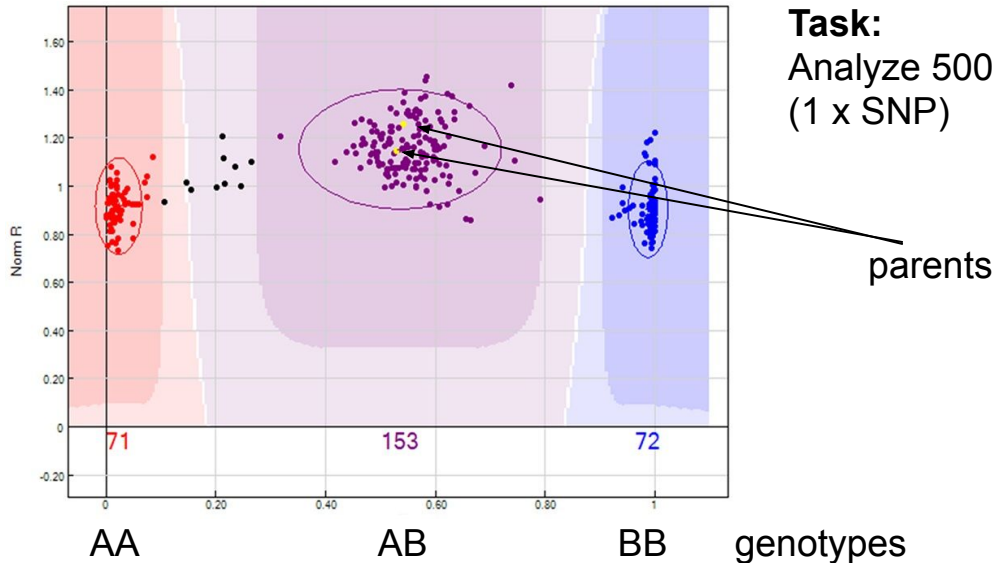
Bix @FEM - Examples

SNP-Chips development for GWAS

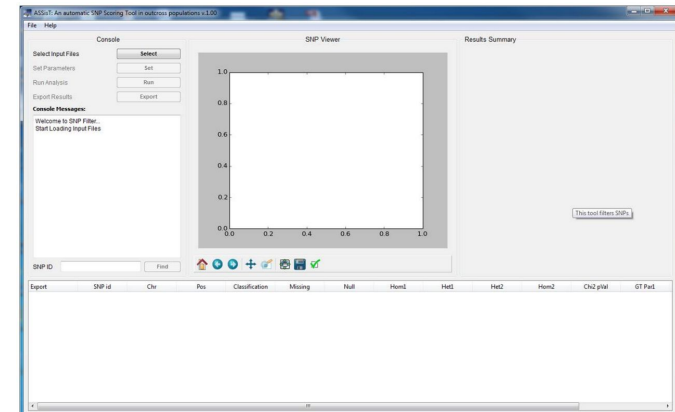
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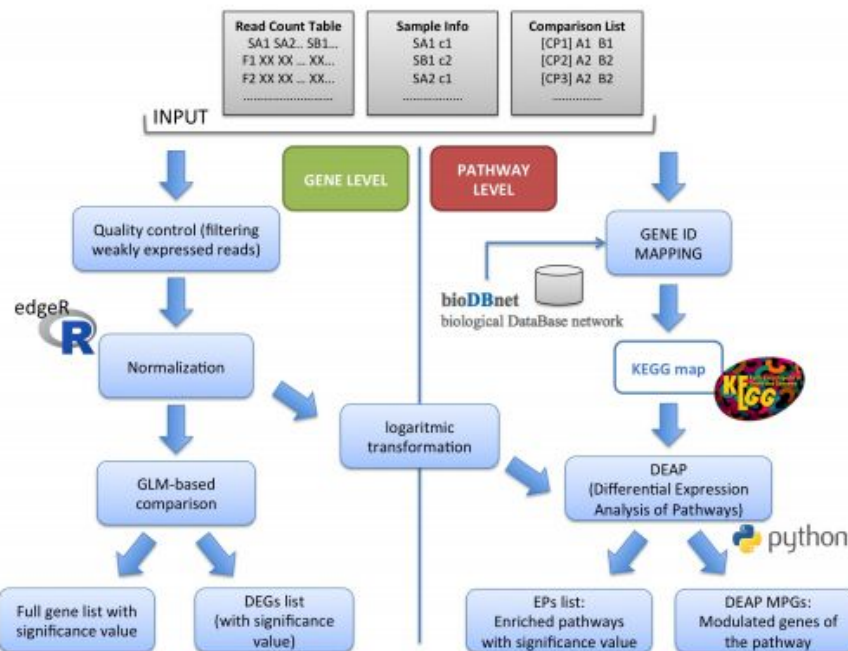
ASSiST



[Di Guardo et al., Bioinformatics, 2015]

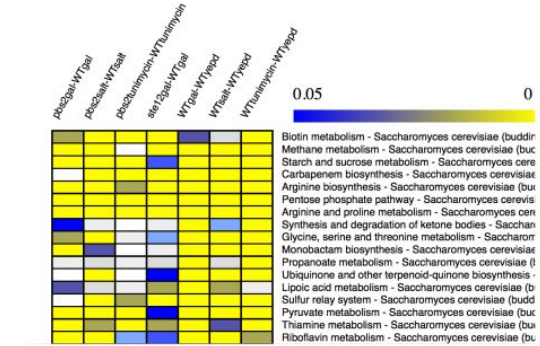
Bix @FEM - Examples

RNAseq data analysis with Pathway Inspector



Bix @FEM - Examples

RNAseq data analysis with Pathway Inspector



Intersection pbs2salt-WTsalt WTtunimycin-WTyept pbs2gal-WTgal WTgal-WTyept

Gene	Comparison	P-value	Fold Change	FDR
YOR04W	pbs2salt-WTsalt	0.028480382028946	0.2420313772254	0.0481361748189205
	WTtunimycin-WTyept	2.38460349315057e-07	0.524172138345184	4.474873128653e-07
	pbs2gal-WTgal	0.00087890548504028	-0.30105531814261	0.0207830810500887
	WTgal-WTyept	2.86788386434103e-15	0.83218803220708	7.1912488256014e-15
YIL140W	pbs2salt-WTsalt	3.85247540741733e-08	0.833589168058476	1.85448837803052e-07
	WTtunimycin-WTyept	1.58617870171733e-24	1.001609102893	5.82391038177541e-24
	pbs2gal-WTgal	1.87826251172733e-09	0.30764051192865	1.49862020124624e-08
	WTgal-WTyept	0.0034912842367044	0.276548277440217	0.0548210627660931
YLR130C	pbs2salt-WTsalt	0.301481010188815	0.31882150138888	0.0308287774872549
	WTtunimycin-WTyept	3.0140342077802e-06	-1.58765788614284	3.8332178378679e-05
	pbs2gal-WTgal	2.7670331688813e-09	0.488214138134541	2.3895374291845e-08
	WTgal-WTyept	8.8037203388888e-18	-0.83121887730747	1.8224549730366e-17
YOR011W	pbs2salt-WTsalt	1.00574728111917e-16	0.72183031688741	8.2817487473501e-16
	WTtunimycin-WTyept	0.010862387803186	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

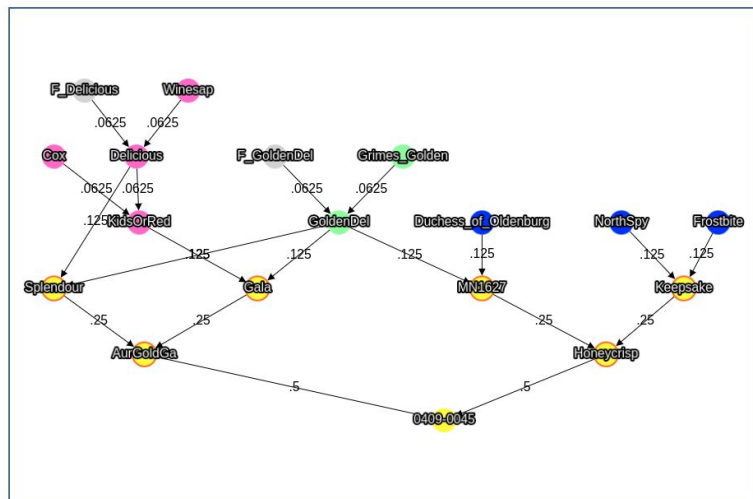
Family of sample: 0409-0045

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

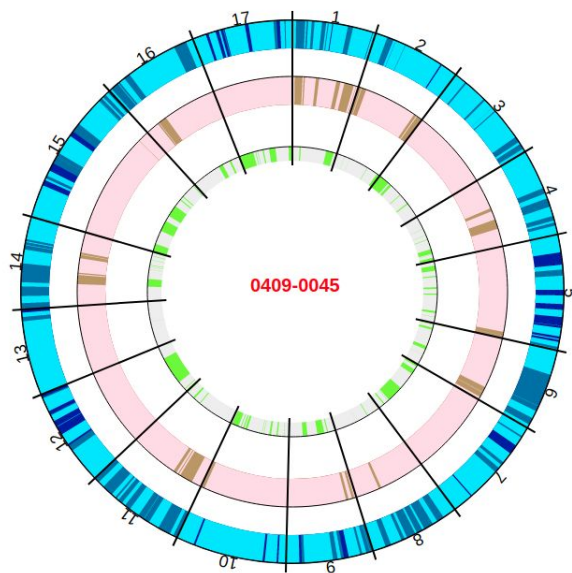
Analyze

Relatedness

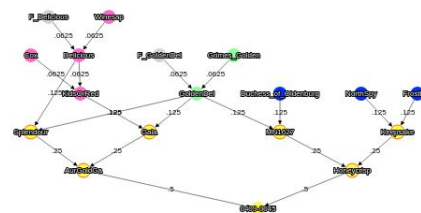
Temporary access: <http://77.72.197.129:8081>

Bix @FEM - Examples

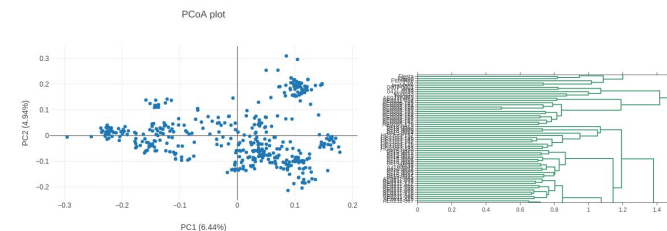
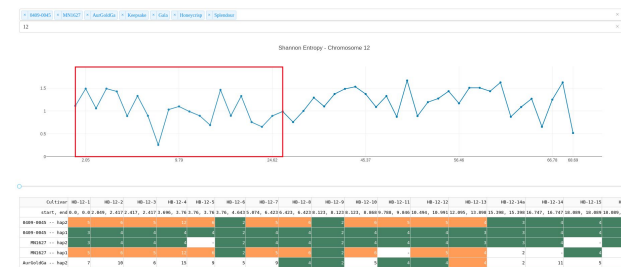
Pedigree-based haplotype visualization



Pedigree of 0409-0045

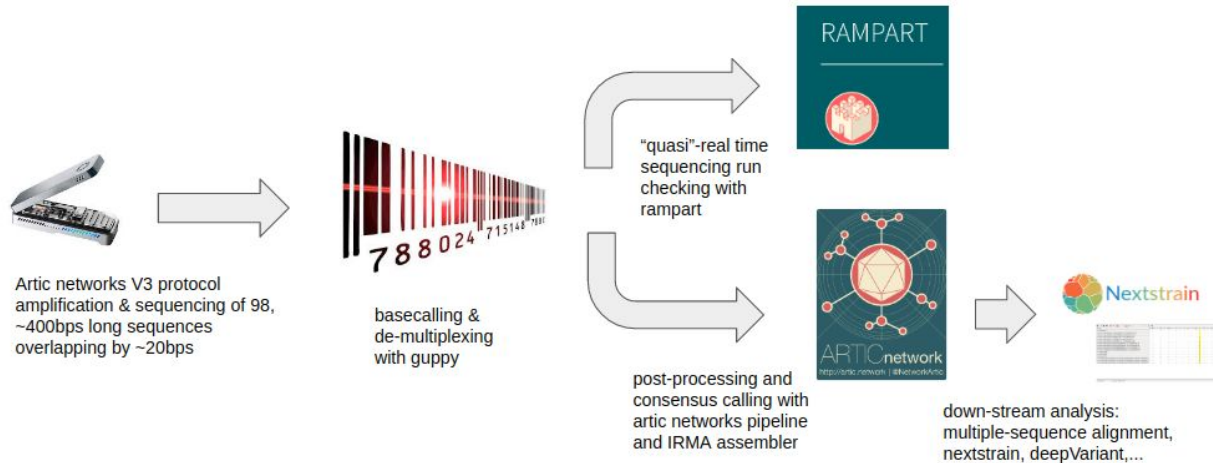


Cultivars	Relatedness	Color	
MN1627	0.39	1CE6FF	✓
AurGoldGa	0.55	FF4A46	✓
Keepsake	0.42	008FA6	✓
Gala	0.48	FFDBE5	✓
Honeycrisp	0.52	0000A6	✓
Splendour	0.48	B79762	✓



Bix @FEM - Examples

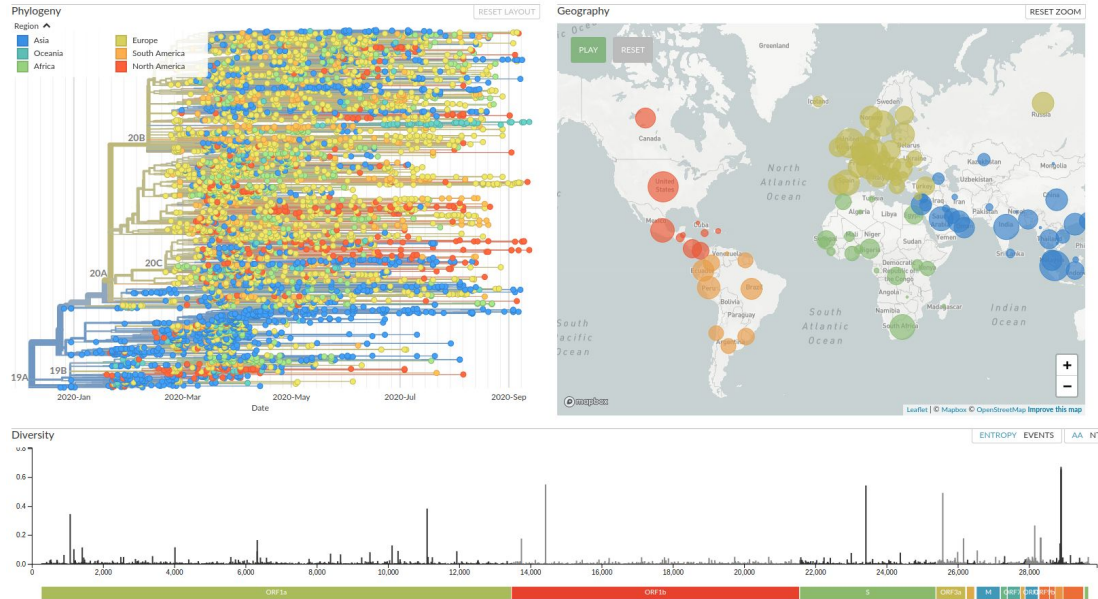
Sequencing and assembling of Sars-Cov-2 samples from the Province of Trento (sponsored by Fondazione VRT)



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.



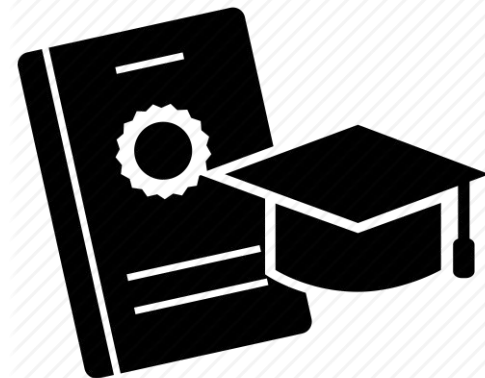
Opportunities @FEM

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



Scientific Programming Practical

Back to business now!



Scientific Programming Practical

In this practical you will

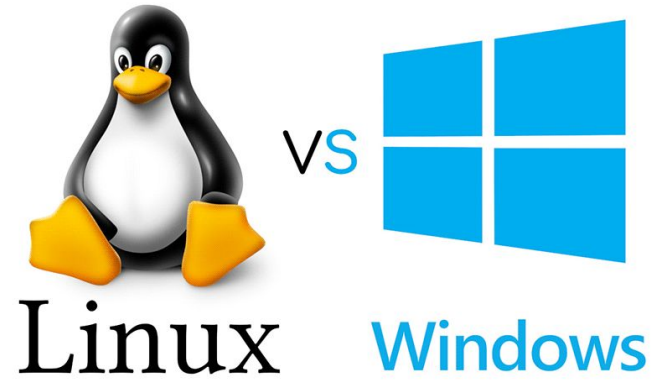
1. Install Python 3.x (and pip)
2. Install Visual Studio Code
3. Get familiar with the Python console
4. Start using Visual Studio Code and advanced features (like debugging)
5. End the session with some exercises



Linux or Windows?

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

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

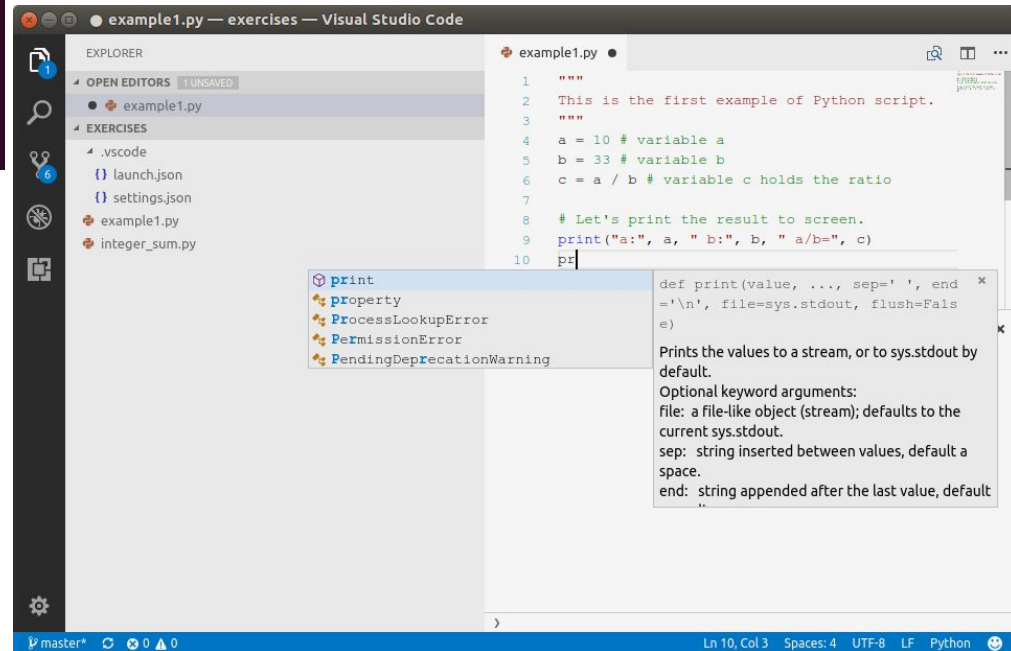


Scientific Programming Practical

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

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```

The debugger

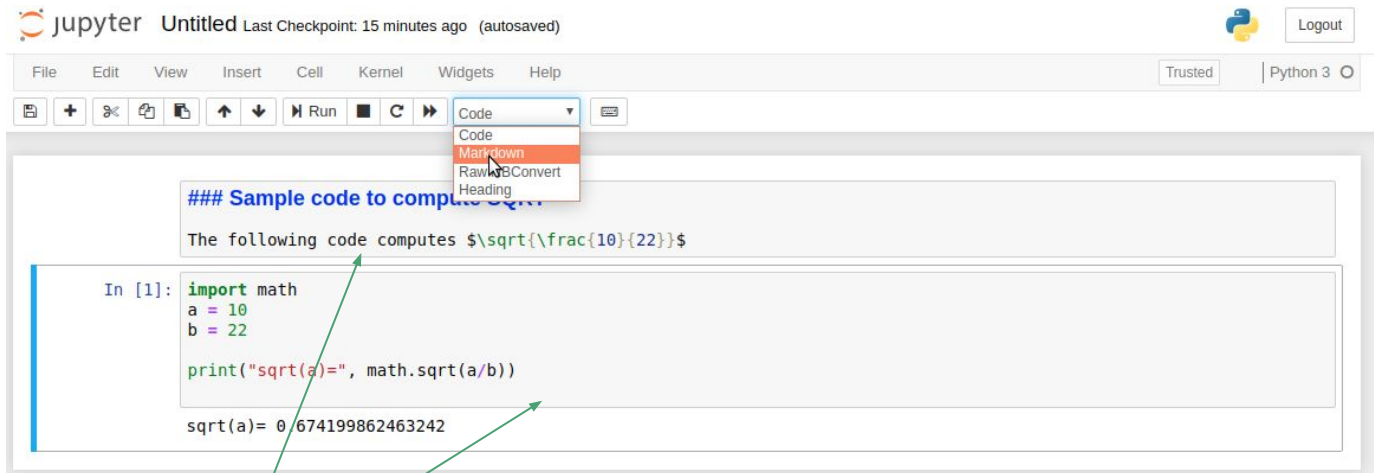


Notebooks and Jupyter

“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.



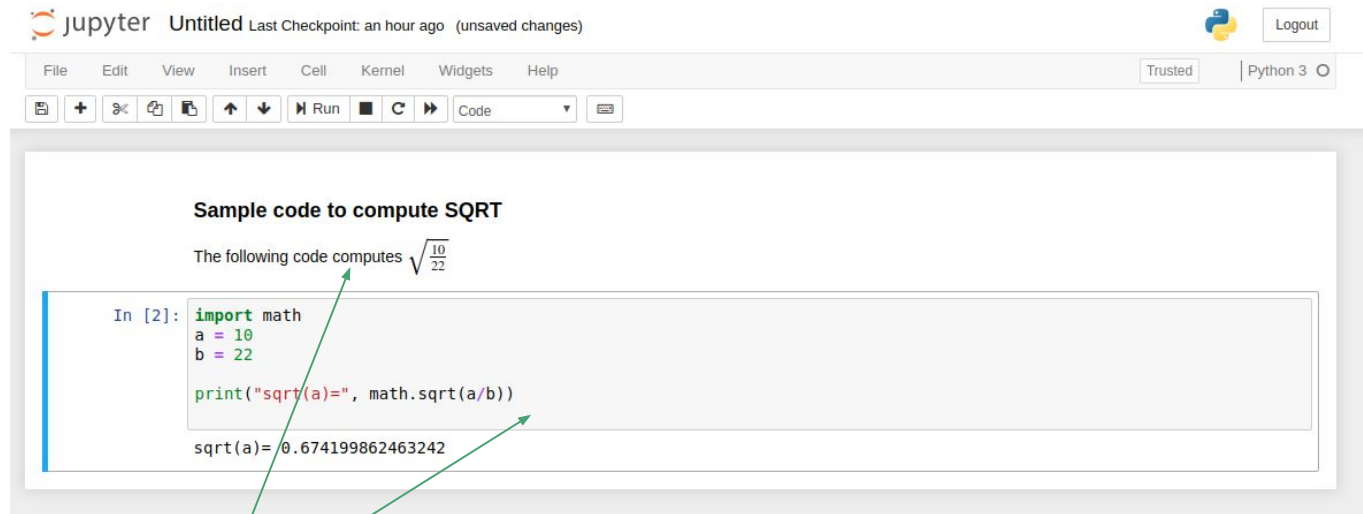
Cells

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

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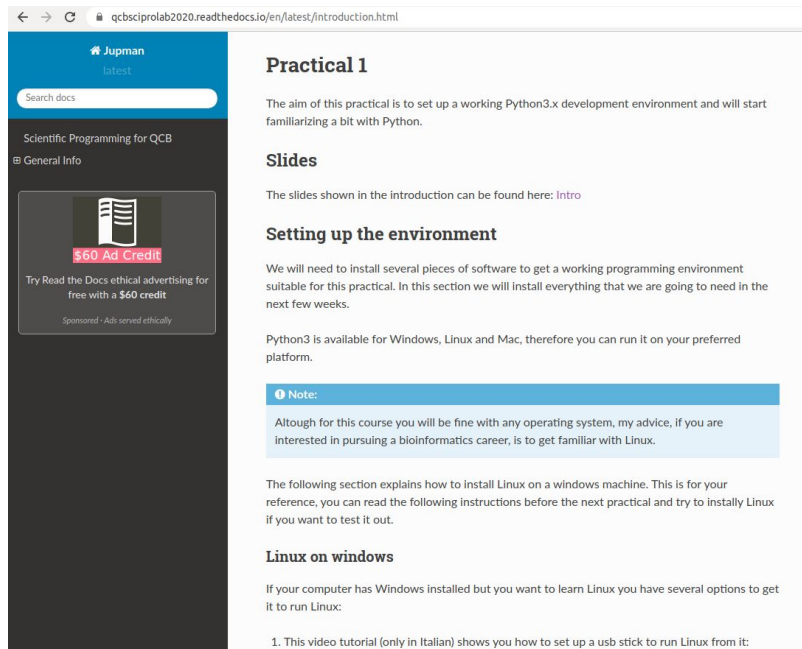


luca.bianco@fmach.it

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.
- Python3** is available for Windows, Linux and Mac, therefore you can run it on your preferred platform.
- 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.
- 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.
- Linux on windows**: If your computer has Windows installed but you want to learn Linux you have several options to get it to run Linux:
 1. This video tutorial (only in Italian) shows you how to set up a usb stick to run Linux from it:



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