Otago Bioinformatics Spring School

https://otagocarpentries.github.io/bioinformatics-spring-school-2020/

@murraycadzow

Event Overview

Free, In-person, 5 day event

Apply to attend

Mixture of speakers and workshops each day

Day 1 covered introductory topics

Days 2-5 themed days by genomic technology

Supported by Genomics Aotearoa and NeSI

Expressions of Interest

“I have previously attended the following workshops…”

“What are your motivations for attending Bioinformatics Spring School 2020?”

Carpentries, GA, and Otago Workshops

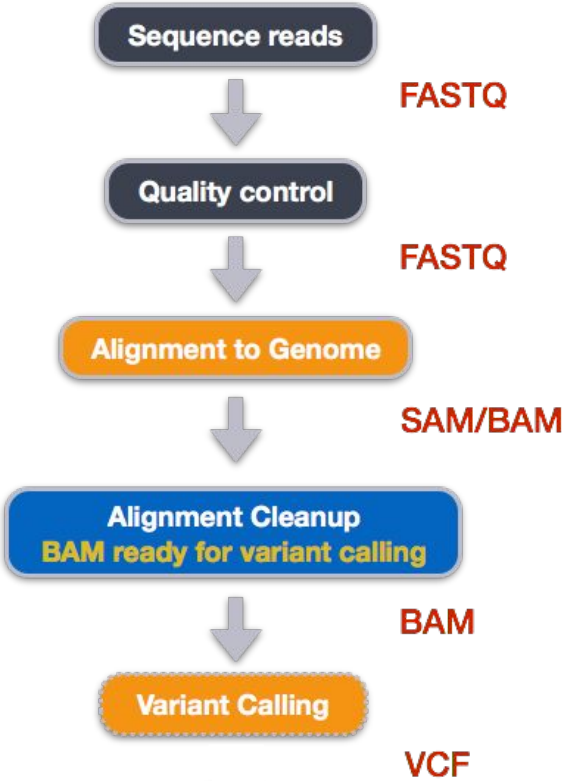
- Genomic Data Carpentry
- RNAseq
- Genotype-by-sequencing
- Environmental DNA

Genomic Data Carpentry

Introduction to BASH

Introduction to Cloud (or NeSI)

Introduction to DNA variant calling

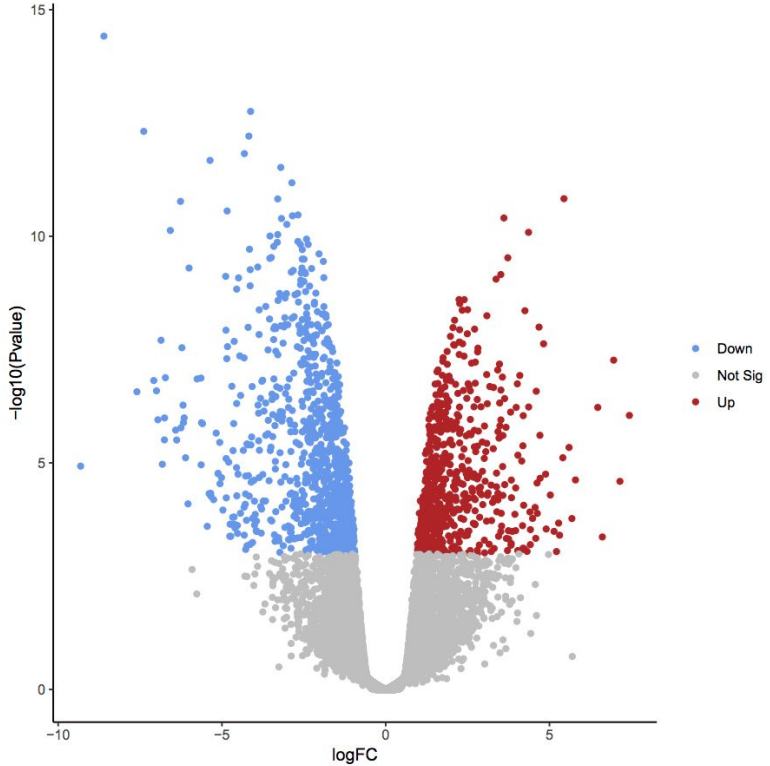


RNAseq

Introduction to BASH

Introduction to R

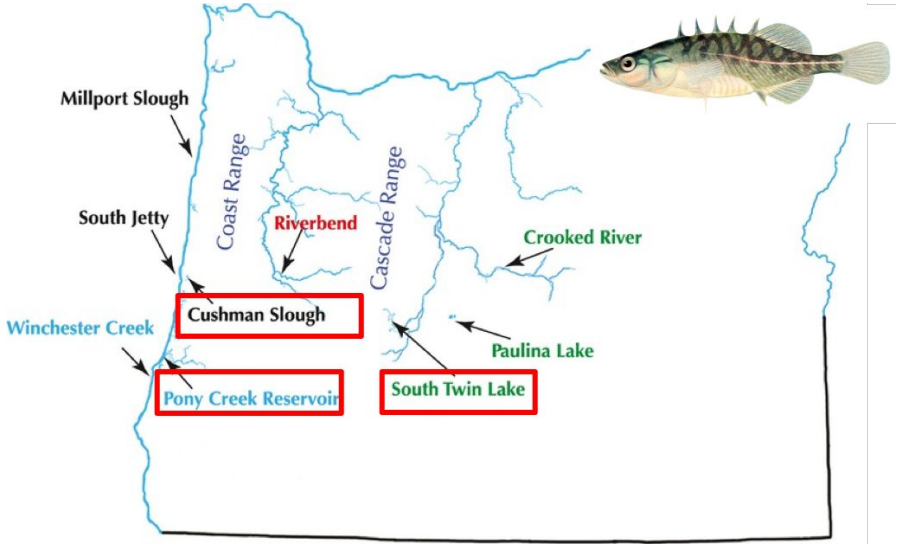
Introduction to RNAseq analysis



Genotype-by-sequencing

Introduction to BASH

Genotype-by-sequencing analysis

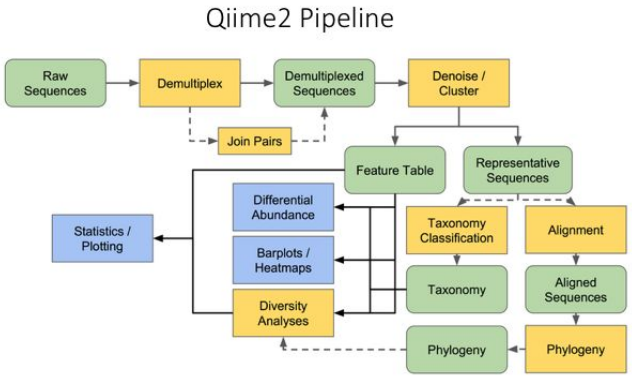


Environmental DNA

Introduction to BASH

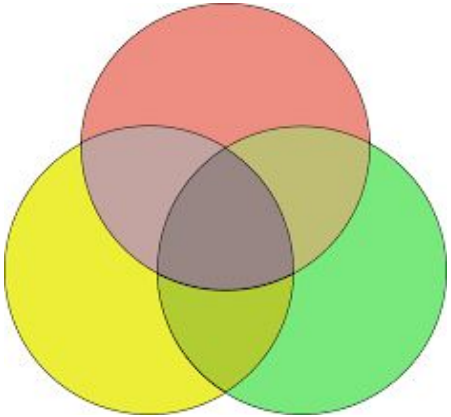
Introduction to R

Environmental DNA analysis



Workshop Overlaps

- Access to NeSI
- BASH
- R
- Data QC



Data formats

- Fastq
- SAM/BAM
- VCF

Add ins

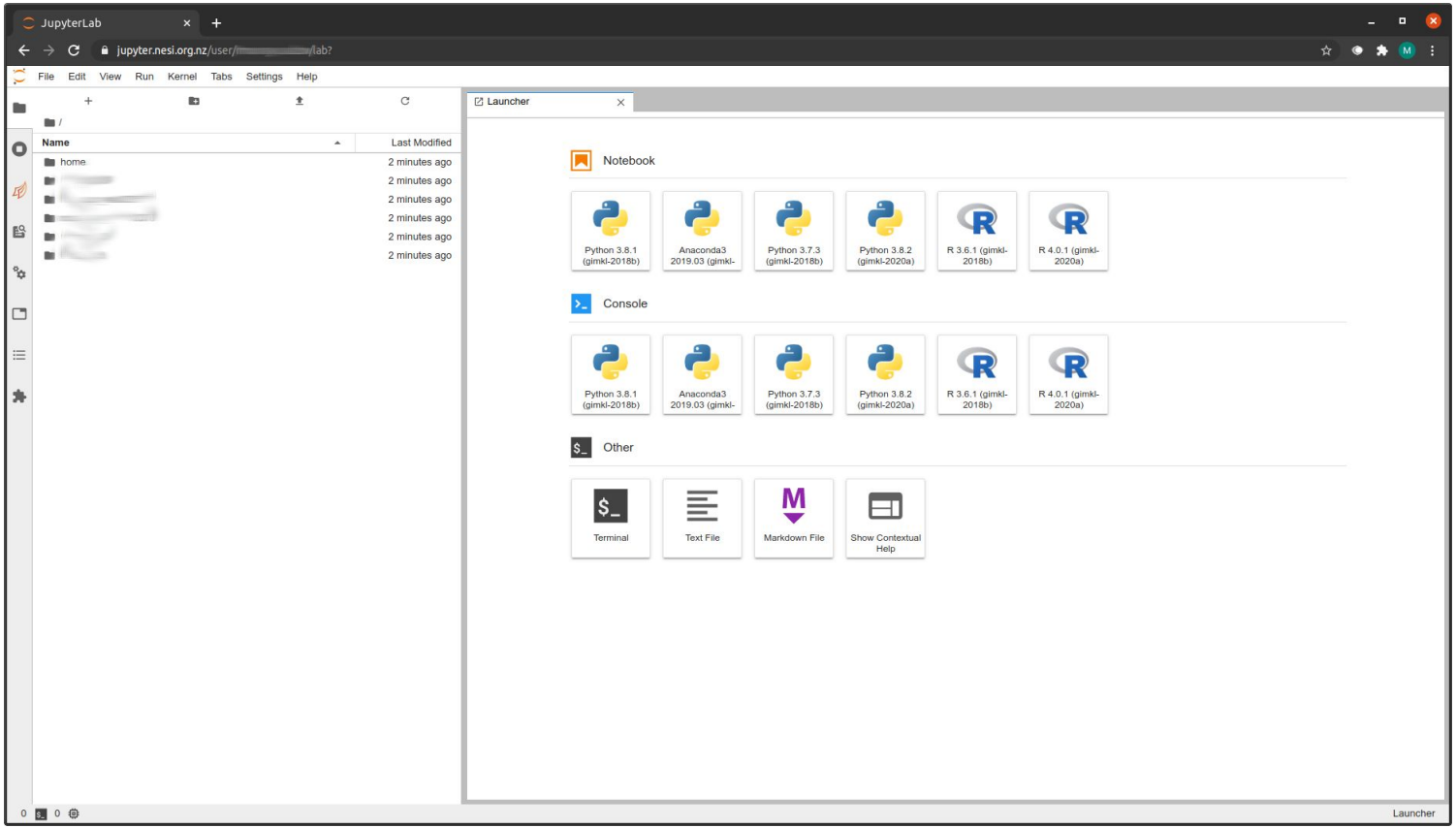
Introduction to version control

Jupyter on NeSI

BASH scripts

Schedule

	Genomic Variant Calling	**Genotype-by-sequencing**	**RNAseq analysis**	**eDNA**
Keynote	Speaker(s)	Speaker(s)	Speaker(s)	Speaker(s)
Intro to NeSI and Jupyter	Genomic Data Carpentry	Variant calling	RNAseq alignment	eDNA metabarcoding
Intro to BASH	Intro to version control (GIT)	Intro to SLURM	Differential expression analysis	Taxonomy Assignment
Intro to R	Intro to BASH scripts	Population genetic analysis		Statistical analyses of eDNA


JupyterLab
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Launcher
Notebook
Python 3.8.1 (gimkl-2018b)
Anaconda3 2019.03 (gimkl-
Python 3.7.3 (gimkl-2018b)
Python 3.8.2 (gimkl-2020a)
R 3.6.1 (gimkl-2018b)
R 4.0.1 (gimkl-2020a)
Console
Python 3.8.1 (gimkl-2018b)
Anaconda3 2019.03 (gimkl-
Python 3.7.3 (gimkl-2018b)
Python 3.8.2 (gimkl-2020a)
R 3.6.1 (gimkl-2018b)
R 4.0.1 (gimkl-2020a)
Other
Terminal
Text File
Markdown File
Show Contextual Help
0 0
Launcher

How do it go?

Very highly demanded

Feedback was good, people found it useful

Improvements

- Reduce cognitive load
  - Diagrams for scaffolding content
  - Consistency of notes and command format
  - Pre-setup home dirs
- Spend more time fundamentals
- Renforcement of differences/similarities between each day
- Include practice for people uploading/downloading data
- “Sprint sessions” on NeSI about jupyter/bash beforehand
- The topics were fairly stand-alone

What went well

- Zero install issues for attendees!!!
- Plenty of opportunity for people to practice core skills (BASH/R)
- Good learning environment
- Number of people to room size
- NeSI staff on hand were super useful
- Things went wrong (provided learning opportunities)
- Mix of follow-along and free-form

How did it differ from other workshops?

Having speakers contextualised the learning

Extra time to form networks

Apply to attend meant people had more “buy-in”

Post-event

- Highlighted a strong desire from the community for this training.
- Further development to make both the lessons AND data available.
- Think about offloading Intro content into a pre-workshop
- More training on use of Github Pages

Already planning to run 2021

Questions?