Canadian Centre for Computational Genomics

C3G Analysis Workshop: RNA-Seq

Day2: Recap & Review

22-23 January 2019

Outline:

Good Morning!

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- What we covered yesterday
- What we will cover today
- Questions or Comments?

Recap:

What we covered yesterday

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- What is Compute Canada?
- What is GenPipes?
- What files do you need to run GenPipes? what info do they contain?
- What are the main steps in RNASeq?
- What are some of the resources that can help you when you get stuck with your analysis?

What is Compute Canada?

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- Compute Canada (CC) is a Canada-wide organization that provides researchers with compute infrastructure free of charge.
- Most known CC servers: Guillimin (Beluga), Cedar, Graham, Mammouth

- For more info, take a look at their website:
  - https://www.computecanada.ca/about/
  - https://docs.computecanada.ca/wiki/Compute_Canada_Documentation

What is GenPipes?

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- GenPipes is a Framework / Workflow Management System that simplifies multistep processing. GenPipes includes 12 pipelines for genomics analysis.

- GenPipes tutorials: http://www.computationalgenomics.ca/tutorials/
- GenPipes Code: https://bitbucket.org/mugqic/genpipes/src

- Why do we need a "Workflow Management System" anyway?
  - Less micro managing of analysis; less wasted time
  - Portable system across servers
  - It just makes life easier…

What files do you need to run GenPipes? what info do they contain?

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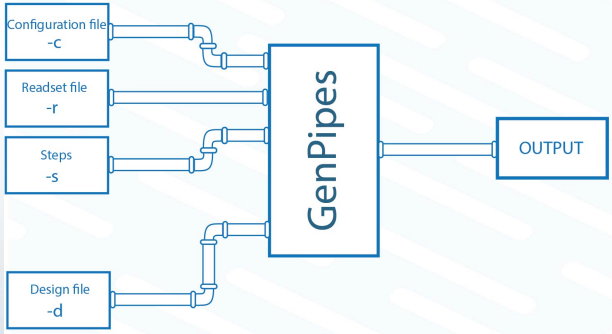
GenPipes requires setting up 3 files:

- Configuration "ini" file: contains parameters used by tools in the pipeline. Provided with GenPipes.
- Readset file: contains details about your samples. You need to create it.
- Design file: contains details about sample comparisons. You need to create it. NOT needed by all pipelines.



What are the main steps in RNASeq?

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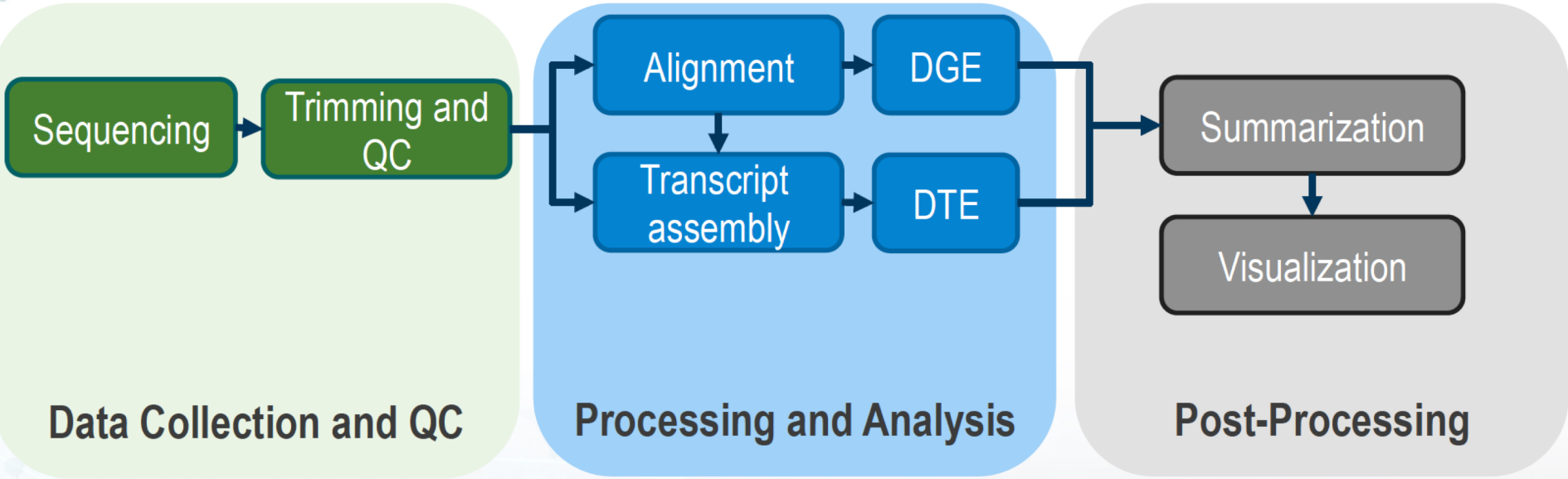

What we aim to cover today?

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- We looked at how to launch the full GenPipes RNAseq pipeline yesterday.
- Today, we will be looking under the hood. We will look in more details at mapping, differential analysis and data visualization.
- We will also take a look at Job monitoring, GenPipes errors and relaunch.

GenomeQuébec

GenomeCanada

Ontario Genomics

McGill

C3G
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Computational
Genomics

SickKids

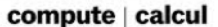
McGill initiative in
Computational Medicine

Thank you!

HPC4Health

bioinformatics.ca

IHEC
International Human Epigenome Consortium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Terry Fox
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