GVA 2017 Review

Attempts to add perspectives and additional resources.

Reminder of goals and thoughts of how well we met them.

Participant goals:

- Learn how to analyze my data, and have it fully analyzed by the end of the class.
- Learn how to analyze NGS data in general.

Teaching goals:

- Teach the fundamentals of NGS variant analysis.
- Provide context and exposure multiple types of data.
- Use example commands to familiarize you with variety of programs.
- Provide resources to enable you to do analysis you haven't thought of yet.

Stages of NGS analysis

1

Biological Question 2

Design & Conduct Experiment

3

Prepare NGS
Library &
Sequence

4

Sequencing Analysis

4 Typical Stages of Variant Analysis

1

Read Quality Control 2

3

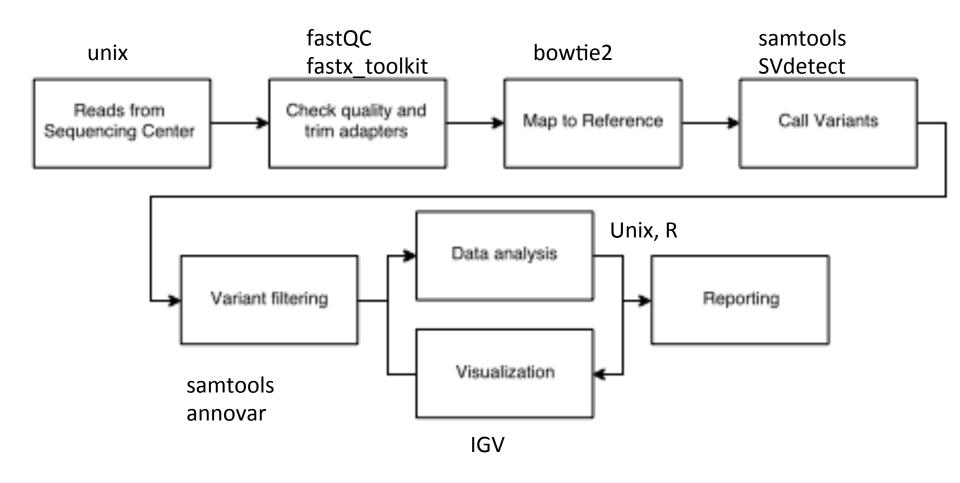
4

Map Reads

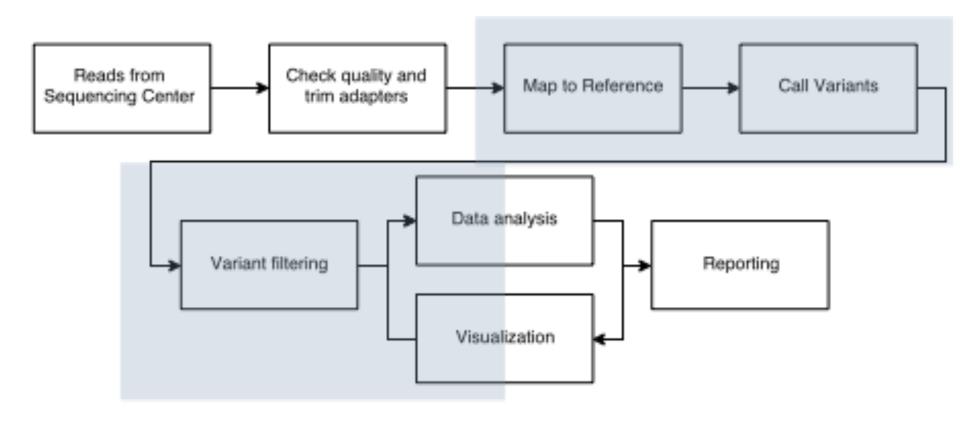
Identify Variants

Visualize Variants

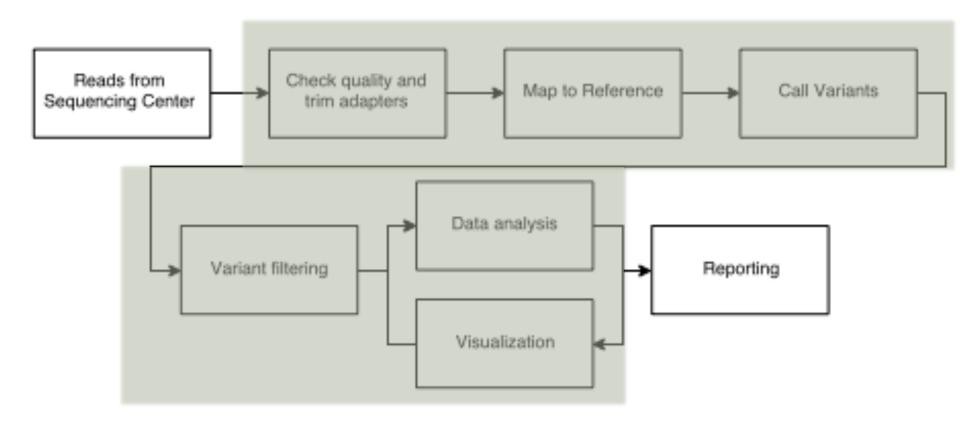
Steps for GVA



microbial all-in-one: breseq



eukaryotic all-in-one: GATK



Further Resources • Galaxy: https://usegalaxy.org

- Biolteam website (more tutorials, info from other classes):
 - https://wikis.utexas.edu/display/bioiteam/ Home
- Coursera: Genomic data science: https://www.coursera.org/specializations/ genomic-data-science

Further Resources (on campus)

- CCBB Short Courses (returning Fall 2017)
- Peer-led working groups (Fall and Spring)
- CCBB Open Coding Hour: Typically
 Wednesdays 4-5, MBB 2.232 (returning Fall)
- ut-open-coding-bio:
 - Slack group for access to local people for questions about all things computation.
 - https://ut-open-coding-bio.slack.com/home
 - Automatic joining from ut email addresses,
 contact me if you lack one.

What's next

- Today, keep working on tutorials
 - Hint hint job submissions!
- Talk to us about what you don't understand about what we have done or why something was important or how it fits together.
- Keep eye out for email from me and from CCBB to review your experience, we LOVE feedback, it's the only way to make this better.
- Soon, start analyzing your own data.