GVA 2019 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



4 Typical Stages of Variant Analysis



#1 most common question I get asked

- How much sequencing do I need to do?
 - Most applications 30-50 fold coverage, higher for bacteria/small organisms because they smaller and cheaper.
- How do I change reads or lanes into coverage?

Coverage =	(Read Length) x (Sequencing Type) x (Number of Reads)
	Size of Genome
30 =	150 x 2 (if Pair end or 1 if single) x (Number of Reads)
	Size of Genome

Number of reads = ~10% of the genome length
If PE 150bp run.

Steps for GVA



microbial all-in-one: breseq



eukaryotic all-in-one: GATK



Further Resources (online) • Galaxy : https://usegalaxy.org

• Biolteam website (more tutorials, info from other classes):

<u>https://wikis.utexas.edu/display/bioiteam/Bio</u> <u>informatics+Team+Home</u>

- Coursera: Genomic data science : <u>https://www.coursera.org/specializations/gen</u> <u>omic-data-science</u>
- Course instructor. You have my email

What's next

- Today, keep working on tutorials
 Hint hint job submissions!
- Talk to me 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, I really appreciate feedback, it's the only way to make this course better for other people.
- Soon, start analyzing your own data.