

LESSON PREPARATION FORM

Lecturer: Helena Rasche

Date:

Group: ATGM/BML

Number of students: 10

Classroom:

Subject/lesson: Computational Biology, Lesson 3: Genome Assembly

Starting situation:

What do the students already know about the subject and what can they already do? How do they feel about it? Have they already gained work experience? Describe the composition of the group. When and where does the lesson take place? And similar.

Students will attend this lesson with previous theoretical experience doing assemblies, this portion is a review for them. They have gone through the motions of assembly but not done it by hand, nor understood the intricacies of parameter selection. Students at this stage in their career are planning to go on to a company or research institute where they will need to apply these skills to analyse genomic sequences and help coordinate and design sequencing projects. When those sequencing experiments occasionally fail for various reasons, they will need to understand why they failed and how to resolve those issues, be it parameter exploration or resequencing. This lesson should serve students well as a very practical lesson delving into comparative analysis which provides key information for them.

Objective/lesson objective:

Describe the objective(s) of the lesson according to the 3C model, taking account of the taxonomy level according to Bloom.

LO1: Compute multiple whole genome assemblies in such a way to develop big data processing skills (Apply+Procedural)

LO2: Learn to evaluate quality metrics so that they can separate good and bad assemblies (Analyse+Conceptual, Evaluate+Procedural)

LO3: Visualise assemblies so that they understand presentation of various failure modes (Apply+Procedural, Evaluate+Conceptual)

Educational resources:

Which learning materials do you use during your lesson? (book, smartboard, whiteboard, paper, etc.)

Presentations (powerpoint), documentation (webpages), assembly activity (web-based group activity with paper assembly fallback during in-person lessons), compute cluster which students access remotely to run computations and get hands-on experience.

Assessment procedure:

Provide a description of the final assessment of the unit of study and at which of Bloom's taxonomy levels the assessment will be carried out.

At the end of the lesson they will go home with an assignment including an unknown genome sequence which they will need to assemble and check for quality. (Apply+Procedural) This task will require re-assembling the genome with several different parameters to optimise the assembly and get the best genome out (Evaluate+Procedural). They will then need to write a short statement on why they choose those parameters and what has led them to believe that that is the optimal genome assembly (Evaluate+Conceptual)

Schedule (how long?)	Content (what?)	Teaching and learning activities/work forms (how?)		Justify: how will this be used to reach the objective?
		Teacher	Student	
"Cold Open" 20 minutes	We'll begin with the assembly exercise, students given either paper or digital pieces of paper that they need to re-assemble into their original sentence. Some will have mistakes or low coverage portions so they can make some guesses	Activity introduction, Observation	Students will apply existing knowledge from e.g. legpuzzel solving to assemble the sentences	This goes towards LO1 , learning about the procedure of whole genome assembly by giving them a fun introductory activity where they can transition from excitement of being in the class to a critical thinking state and begin to <u>Apply</u> an algorithm and begin to <u>Analyze</u> the algorithm they're making intuitively.
Lecture ~20 min	Now we'll take the applied knowledge and turn theoretical, focusing on how algorithms work in practice	Presentation	Listen / note taking / knowledge integration	Here we focus on the <u>Understand+Procedural</u> components of LO1 , allowing students to know how assembly algorithms work at a theoretical level so they can begin understanding what parameters they can adjust, and what effect they might have.
Assembly: Demo ~10 minutes	Here students will see a demo of assembly and listen to the teacher's explanation of parameters	Demonstration	Listen / note taking / memorisation	Students now obtain the precise knowledge they'll need to <u>Remember+Procedural</u> steps required to accomplish assembly (LO1)
Assembly: Hands-on ~20 minutes	Students move into breakout rooms where they do the assembly for multiple genomes, and report on their results. (most/fewest contigs (grep), biggest/smallest (wc))	Observation	Hands-on activity where students work in duos to accomplish the activity and report back results	Students <u>Apply+Procedural</u> knowledge from the previous step to do the assembly and then <u>Analyse+Factual</u> results of their process. (Complete LO1)
~15 min	Break			
Quality Contrtol: Demo ~20 minutes	Instructor demonstrates quality control and discusses several metrics that are used. Demonstrates QUAST. Demonstrates Bandage.	Demonstration	Listen / note taking / memorisation	Students now obtain the precise knowledge they'll need to <u>Remember+Procedural</u> steps required to accomplish assembly (LO2 & LO3)
Quality Control: Hands on ~30 minutes	Students move into breakout rooms where they do the quality metrics across their genomes, and investigate bandage where necessary.	Observation	Hands-on activity where students work in duos to accomplish the activity and report back results	Students <u>Apply+Procedural</u> knowledge from the previous step to do the assembly and then <u>Analyse+Factual</u> results of their process. Additionally they need to <u>Evaluate+Procedural</u> to conclude the best/worst assemblies. (Complete LO2 & LO3.)
Group Discussion 10 minutes	Students return from breakout rooms and discuss their results. Which were best, which were worse, did anyone have differing observations	Lead discussion	Students report on their results, and discuss when there are conflicting answers	Here they <u>Evaluate+Factual</u> results of their assemblies against other groups. Potentially the ordering can be different due to factors teachers control, giving room for discussion. They need to <u>Evaluate+Conceptual</u> their results and check for inconsistencies.
Conclusion: ~5 Min	Recap k-mers, assembly, tools used (conda, spades, quast, bandage), discuss homework assignment (assemble and change parameters to optimise! Read the documentation!)	Presentation	Listening	Students will now need to use what they learned from LO1 , LO2 , & LO3 to evaluate an unknown genome's assembly and optimise the results, as well as explainin why they choose those parameters based on available information. They will need to read documentation to accomplish this.