

LESSON PREPARATION FORM

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| Lecturer: Helena Rasche | |  | Date: |
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| Group: ATGM/BML | Number of students: 10 | | Classroom: |
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| 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.*

In this class students are in their Third Year, in a Bioinformatics Minor within the BML department.

This a class in the “Computational Biology” course.   
The course covers: command line computer skills, de-novo assembly from reads, quality control, annotation, and variant calling.

Students will attend this lesson with previous theoretical experience doing assemblies from Year 2 classes, so this portion is a review for them.

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.

*1*

**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+Concetual)



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| **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 Apply an algorithm and begin to Analyze 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 Understand+Procedural 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 Remember+Procedural 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 Apply+Procedural knowledge from the previous step to do the assembly and then Analyse+Factual 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 Remember+Procedural 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 Apply+Procedural knowledge from the previous step to do the assembly and then Analyse+Factual results of their process. Additionally they need to Evaluate+Procedural 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 Evaluate+Factual 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 Evaluate+Conceptual their results and check for inconsitencies. |
| **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. |