

# Genomes Workflow - LBCM

## 01 - Introduction

General guidelines

Wednesday 9<sup>th</sup> July, 2025

# 1 Overview

## 1.1 Module Objectives

This module covers:

Learning goals

- Repository organization.
- Available scripts.
- General pipeline structure.
- Modules organization.

# 2 Background

## 2.1 General Context

Key concepts:

Why this matters

- The integration between biological knowledge and IT or bioinformatics tools can be harsh.
- The presence and interference of multiple key concepts of each area creates a big wall on newcomers.
- Explain key features and provide support in a organized way can help to circumvent this initial barrier.

# 3 Tools & Software

## 3.1 Required Software

Installation notes

- **Primary tool:** Tool name and version
- **Dependencies:** Required libraries/packages
- **Optional:** Additional helpful tools

## 3.2 Installation Guide

```
1 # Installation commands
2 conda install -c bioconda tool_name
3 # or
4 sudo apt-get install package_name
```

Listing 1: Software installation

# 4 Workflow & Methods

## 4.1 Step-by-Step Protocol

Key parameters

1. **Data preparation:** Input requirements and formatting
2. **Quality control:** Initial data assessment

3. **Main analysis:** Core computational steps
4. **Result interpretation:** Output analysis and validation

**Example 4.1.** Practical example with real genomic data.

## 5 Practical Examples

### 5.1 Example 1: Basic Analysis

Input/output files

- **Input:** Sample data description
- **Command:** Based on approach from **example2024**
- **Output:** Expected results and file formats

```
1 # Example command with typical genomic data
2 tool_name -i input_file.fasta -o output_file.txt --parameter
  value
```

Listing 2: Basic command example

### 5.2 Example 2: Advanced Usage

Complex parameters

```
1 # Multi-step analysis pipeline
2 step1_tool input.fasta | step2_tool --param1 value1 >
  intermediate.txt
3 step3_tool intermediate.txt --param2 value2 -o final_result.txt
```

Listing 3: Advanced analysis pipeline

## 6 Results & Interpretation

### 6.1 Output Files

Common output formats and their interpretation:

File formats

- **Format 1:** Description and typical contents
- **Format 2:** When and how to use this output
- **Quality metrics:** How to assess result quality

**Remark 6.1.** Important note about result interpretation following **author2024**.

## 7 Scripts & Code

### 7.1 Helper Scripts

```
1 #!/usr/bin/env python3
2 """
3 Helper script for genomic data processing
4 Usage: python script.py input.fasta output.txt
5 """
6
7 def process_sequences(input_file, output_file):
8     """Process genomic sequences"""
```

```
9     with open(input_file, 'r') as f:
10         sequences = f.read()
11
12     # Processing logic here
13     processed = sequences.upper()
14
15     with open(output_file, 'w') as f:
16         f.write(processed)
17
18 if __name__ == "__main__":
19     import sys
20     process_sequences(sys.argv[1], sys.argv[2])
```

Listing 4: Data processing script

## 7.2 Quality Control

```
1 #!/bin/bash
2 # Quality control pipeline for genomic data
3
4 # Check file format
5 file_format_check.py $INPUT_FILE
6
7 # Basic statistics
8 sequence_stats.py $INPUT_FILE > stats.txt
9
10 # Quality assessment
11 quality_assessment_tool $INPUT_FILE --output qc_report.html
```

Listing 5: QC pipeline

## 8 Troubleshooting & Best Practices

### 8.1 Common Issues

Error solutions

- **Memory errors:** Reduce dataset size or increase available RAM
- **Format issues:** Check input file formatting and encoding
- **Parameter tuning:** Guidelines for optimization

### 8.2 Best Practices

- **Data backup:** Always keep original data copies
- **Version control:** Track analysis versions and parameters
- **Documentation:** Record all analysis steps and decisions
- **Reproducibility:** Use consistent environments and seeds

## 9 References

- Key papers: **example2024**; **author2024**; **smith2024**
- Software documentation: [Tool official docs]
- Related modules: [Other workflow modules]

## 10 Exercises & Next Steps

- [TODO]: Practice with provided sample data
- [TODO]: Try different parameter settings
- Apply to your own genomic dataset
- [TODO]: Explore advanced features

## 11 Research Notes

Additional observations and module-specific notes...

**Key insight:** Connection between this tool and genome annotation pipeline

**[IDEA]: Extension:** Integration with other bioinformatics tools in the workflow