

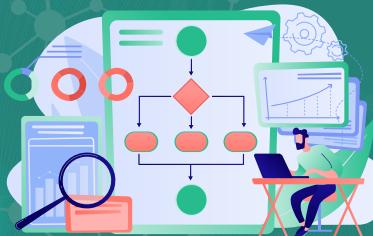
Efficient organization of research data in bioinformatics, genomics, and imaging within a biomedical research environment is vital for optimizing productivity, eliminating redundancy, and preserving data integrity. A systematic and carefully crafted directory structure and naming convention system are paramount to accomplish this. The following directory structure and naming convention guide aim to establish a coherent and well-organized plan explicitly tailored for reNEW Copenhagen's research endeavors.



1. Root Directory:

Create a root directory for your research project. Name it with a relevant and easily identifiable project name, for example,

"reNEW_Copenhagen_Project"



2. Subdirectories:

Within the root directory, create subdirectories for each major research area (bioinformatics, genomics, and imaging). Use a clear, consistent naming convention, such as:

- ▶ 01_Bioinformatics_Data
- ▶ 02_Genomics_Data
- ▶ 03_Imaging_Data



3. Research Themes:

Within each research area, create subdirectories for different research themes or topics. For instance:

01_Bioinformatics_Data:

- 01_Protein_Structure_Analysis
- 02_Gene_Expression_Analysis
- 03_Metagenomics_Analysis

02_Genomics_Data:

- 01_Whole_Genome_Sequencing
- 02_Transcriptomics
- 03_Metagenomics

03_Microscopy_Data:

- 01_Confocal_microscopy
- 02_Brightfield_microscopy
- 03_Light_microscopy



4. Experiments and Timepoints:

Create subdirectories for specific experiments or time points for each research theme or topic. Use a consistent naming convention that includes the date (YYYY-MM-DD) and a short description:

01_Whole_Genome_Sequencing:

- ▶ 2023-04-01_Mouse_Genome_Seq
- ▶ 2023-04-02_Human_Genome_Seq

5. Data Types and Formats:

Create subdirectories for different data types or formats within each experiment or timepoint directory. Examples:

2023-04-01_Mouse_Genome_Seq:

- ▶ 01_Raw_Data
- ▶ 02_Processed_Data
- ▶ 03_Analysis_Results





6. Naming Files:

Use a consistent naming convention for all files, including details like the date, sample identifier, data type, and version (if applicable). Examples:

01_Raw_Data:

- ▶ 2023-04-01_Mouse_Genome_Seq_Sample01_Raw_v1.fastq
- ▶ 2023-04-01_Mouse_Genome_Seq_Sample02_Raw_v1.fastq

7. Metadata and Documentation:

Include a metadata file and a README file in each experiment or timepoint directory, with detailed information about the experiment, data types, formats, and processing steps. Name these files:

- ▶ Metadata_2023-04-01_Mouse_Genome_Seq.csv
- ▶ README_2023-04-01_Mouse_Genome_Seq.txt



8. Backup and Version Control:

Ensure regular data backups and use a version control system (e.g., Git) to track script changes, analysis pipelines, and other relevant files.



By adhering to the principles outlined in this directory structure and naming convention guide, you can establish a systematic, user-friendly framework for managing and storing research data at reNEW Copenhagen, streamlining access to crucial information and facilitating entry and facilitating entry and facilitating seamless collaboration across diverse research teams.

