



CEPLAS

Cluster of Excellence on Plant Sciences

# CEPLAS RNA-Seq Workshop 2022

August 22-24, 2022

Alisandra Denton & Dominik Brilhaus



# Housekeeping





# Who we are



Alisandra Denton



Dominik Brilhaus



# Housekeeping (Corona and drinks)

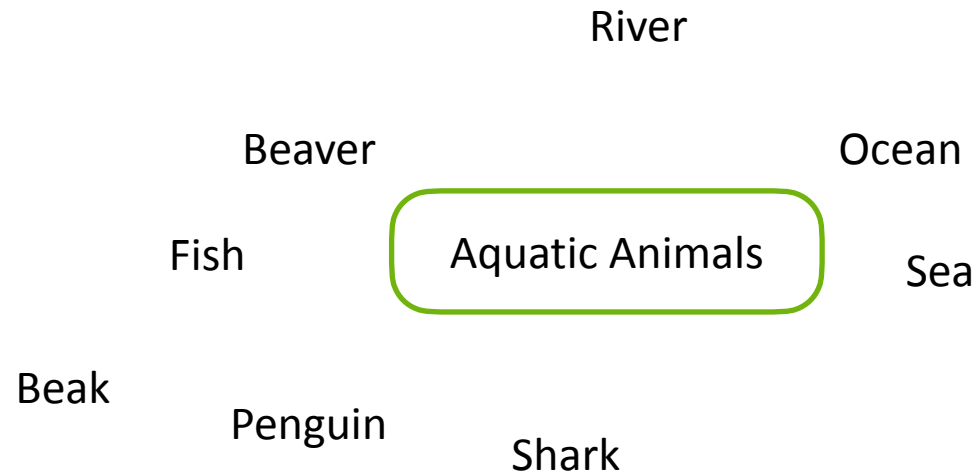
- Please wear a mask in the course room (voluntary)
- Please avoid to drink and eat in the course room (officially forbidden)
- Feel free to take drink / eat / mask-off / bio breaks anytime





# Before we start – Association Map

- Get up
- Tell us who you are and where you are from
- Write any association with “RNA-Seq” (one term) on the board
- Try to place it close to suitable terms.





<https://pad.hhu.de/Qlsi4q9fQ9-YPmzv6Ryeog?both>



# Pizza on Wednesday evening?





# What to expect

- “RNA-Seq” is a broad field
  - Many different implementations, outputs, flavors, etc.
  - For many purposes and biological questions
  - Many (computational) tools and workflows
- We walk through one way of analyzing RNA-Seq data
- We recommend common tools and tasks
- ...and encourage you to explore others







# From your responses

Basic steps to analysis

How to approach to the data

Common sources for errors

Introduction to RNA-Seq analysis and what to do when presented with RNA-Seq data

Theory and practical advices in dualRNAseq

What kind of information can I get from RNA-Seq data?

Data normalisation/transformation

What can/should I do when comparing data of different quality/origin?



# Not covered in this course (but worth thinking about)

- Full-fledged training on
  - code, programming
  - git and version control
  - virtual environments or containerization
  - research data management
- Training on specialized experimental designs, data types and analyses





# After this course you should...

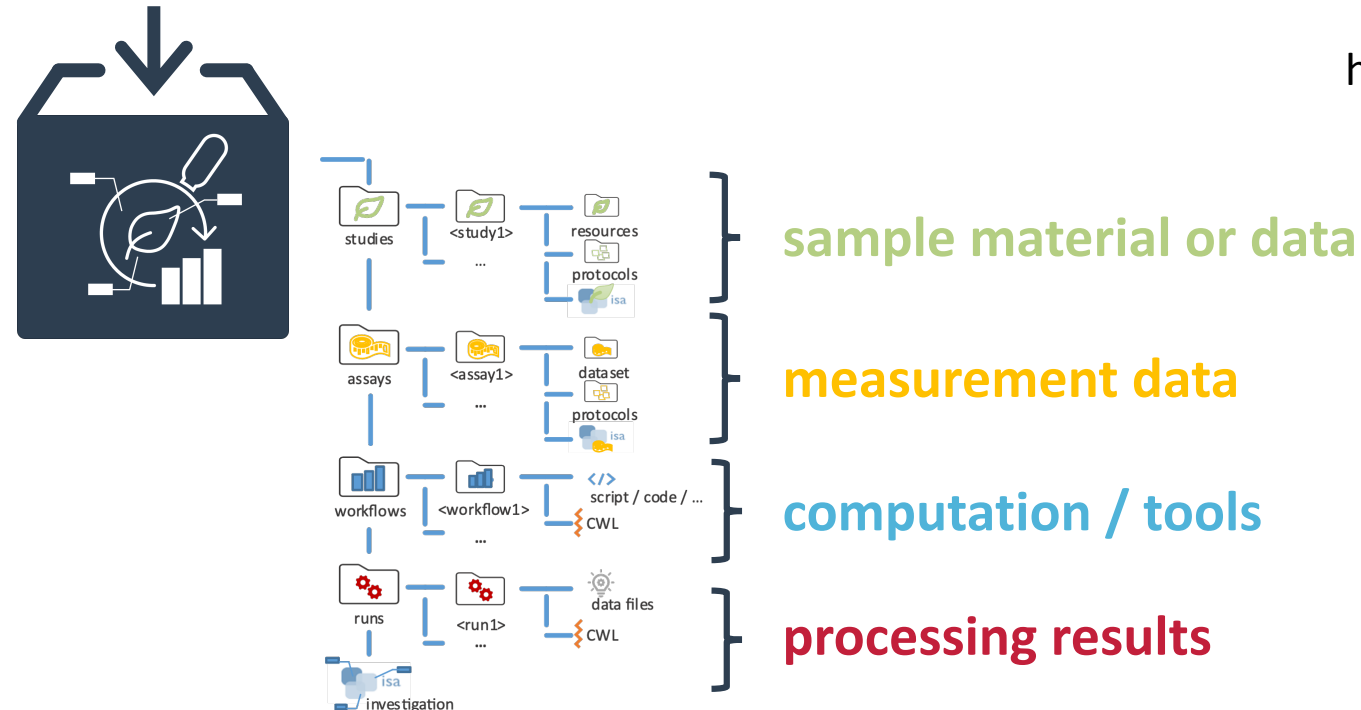
- Feel comfortable to design and perform an RNA-Seq experiment
- Have an idea what RNA-Seq data looks like ...
  - ...what biological information may be found in the data
  - ...and where to get started analyzing the data.
- Feel comfortable to explore other tools and workflows
- Not fear the command line or other code environments :)





# ARC: Annotated Research Context

A real-world ARC is a folder structure



DataPLANT  
<https://nfdi4plants.org/>

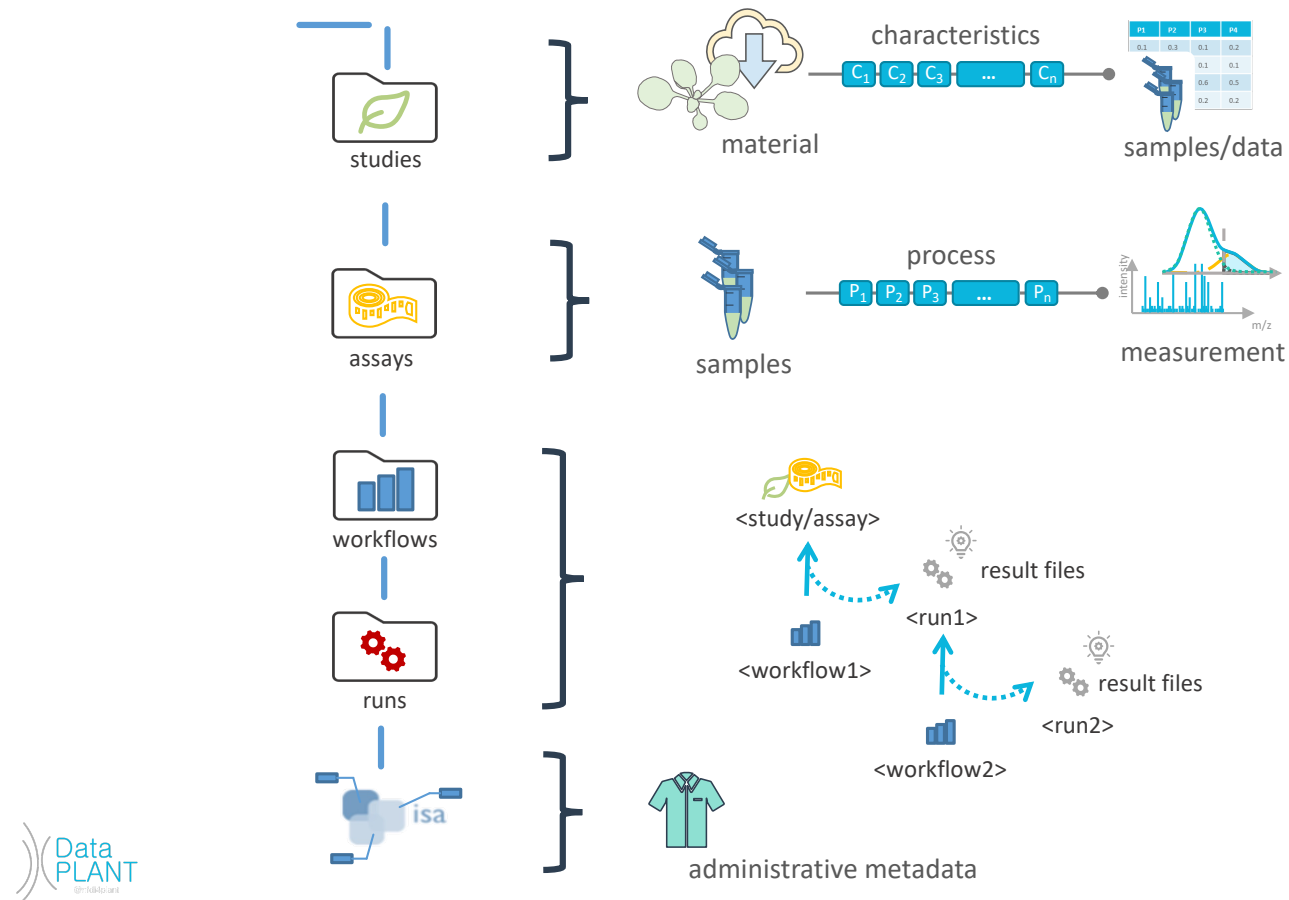
User-friendly scaffold for research data and analyses, including a change tracking system to ensure provenance





# ARC: Annotated Research Context

A real-world ARC is a folder structure



DataPLANT  
<https://nfdi4plants.org/>





# The ARC to this workshop

Server maintenance will occur on Monday, 15th August at 14:00 CEST. Expected downtime is 4 hour. GitLab will not be available in that time period.

Dominik Brilhaus > RNaseq-Workshop

**RNaseq-Workshop** Project ID: 129

🔔 50 Commits 🔗 1 Branch 🏷️ 0 Tags 💾 8.8 GB Project Storage

main rnaseq-workshop / +

Find file Web IDE ⬇️ Clone

**part 2 isoseq** 6c3499e8   
Dominik Brilhaus authored 1 week ago

README Auto DevOps enabled Add LICENSE Add CHANGELOG Add CONTRIBUTING

Add Kubernetes cluster Configure Integrations

<https://git.nfdi4plants.org/brilator/rnaseq-workshop>



# The ARC to this workshop



Name	Last commit	Last update
.arc	arc init	2 weeks ago
_handouts	reorder things	2 weeks ago
_reader	add to arc	12 hours ago
_software	restructure	16 hours ago
assays	move around isoseq processed data	2 weeks ago
runs	part of isoseq on linux	1 week ago
studies	part of isoseq on linux	1 week ago
workflows	move around isoseq processed data	2 weeks ago
.gitattributes	part of isoseq on linux	1 week ago
.gitignore	part of isoseq on linux	1 week ago
ARCification.md	restructure	16 hours ago
README.md	switch to relative paths: isoseq section 1	2 weeks ago
isa.investigation.xlsx	add isooseq study	2 weeks ago

Day 1







# Agenda

09:00	10:00	Welcome and intro
Coffee		
10:20	12:00	Intro to code
Lunch		
13:00	15:00	First looks at RNA-Seq data
Coffee		
15:20	17:00	From Reads to Quantified Transcripts