# Concept of Git and git-based platforms

# Cloud Services

✓ Documents

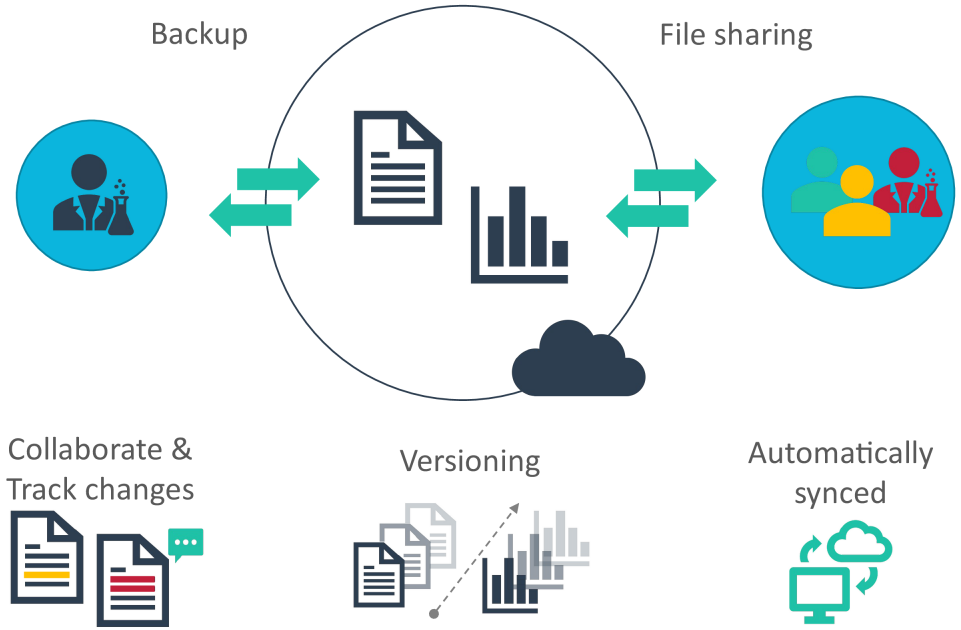
✓ Small data

✓ Presentations

X Code

X Data analytical projects

X Big (“raw”) data



# Git and git platforms

~ Documents

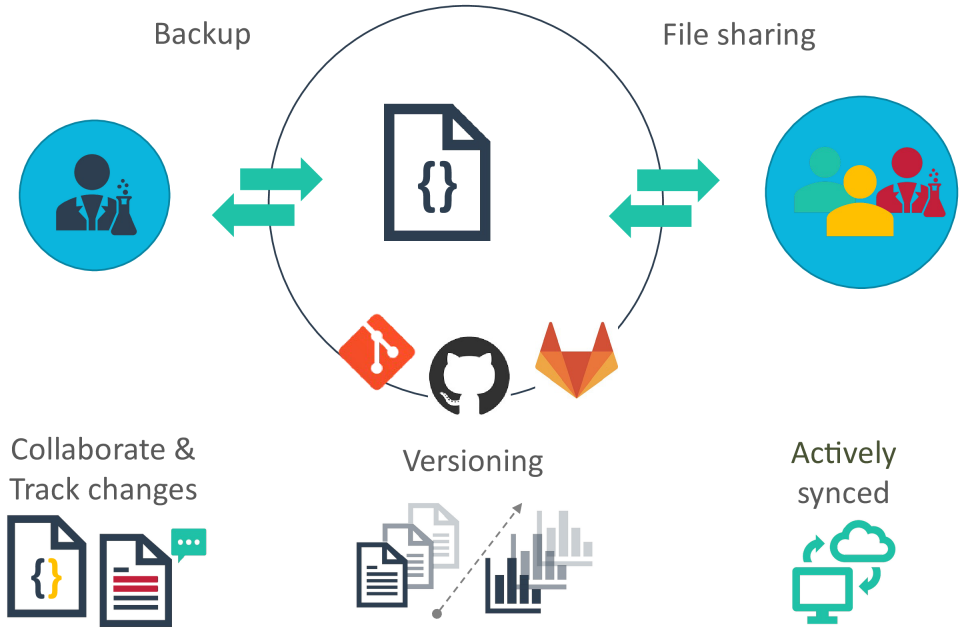
✓ Small data

~ Presentations

✓✓ Code

✓✓ Data analytical projects

~ Big (“raw”) data



# Why git? ≈> Why code?

- Save time
- Avoid doing repetitive tasks “by hand”
- Reuse scripts, analyses, pipelines
- Reproduce results

# A simple example: RNASeq project

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

# A simple example: RNASeq project

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```

Input(s)

# A simple example: RNASeq project

```
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│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
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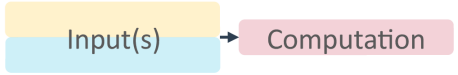
```



# A simple example: RNASeq project

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├── 01_input_data
│   ├── barley_genome_ref.fasta
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│   └── barley_sample03.fastq.gz
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# A simple example: RNASeq project

```
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│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```bash
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

*

Input(s) → Computation → Output

** Disclaimer: this is not a good example for reusable code*

# Take snapshots of your code work...

(... as long as it works)

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

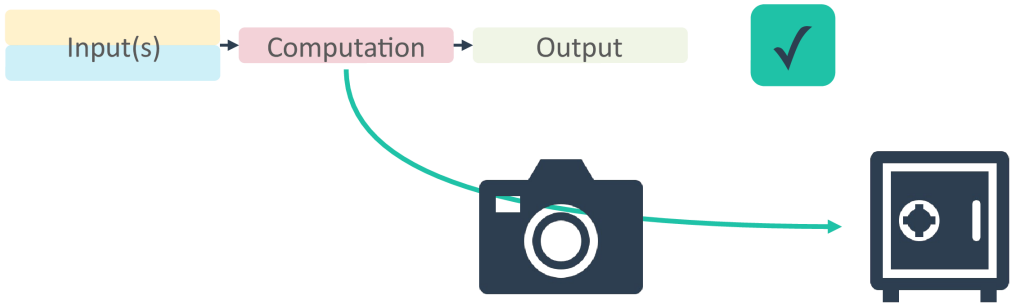
Input(s) → Computation → Output ✓

# Take snapshots of your code work...

(... as long as it works)

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```



# Scenario 1: More data

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   ├── barley_sample03.fastq.gz
│   ├── barley_sample04.fastq.gz
│   ├── barley_sample05.fastq.gz
│   └── barley_sample06.fastq.gz
```

# Scenario 1: More data

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   ├── barley_sample03.fastq.gz
│   ├── barley_sample04.fastq.gz
│   ├── barley_sample05.fastq.gz
│   └── barley_sample06.fastq.gz
```

```bash
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

```bash
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz \
  01_input_data/barley_sample04.fastq.gz \
  01_input_data/barley_sample05.fastq.gz \
  01_input_data/barley_sample06.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

# Scenario 1: More data

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   ├── barley_sample03.fastq.gz
│   ├── barley_sample04.fastq.gz
│   ├── barley_sample05.fastq.gz
│   └── barley_sample06.fastq.gz
├── 02_analysis
│   ├── RNASeq_quant.sh
│   ├── RNASeq_quant_first_samples.sh
│   ├── RNASeq_quant_including_all_samples.sh
│   ├── RNASeq_quant_including_all_samples_updated.sh
│   └── RNASeq_quant_including_all_samples_updated_v2.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz \
  01_input_data/barley_sample04.fastq.gz \
  01_input_data/barley_sample05.fastq.gz \
  01_input_data/barley_sample06.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

# Let git track changes and keep things clean

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   ├── barley_sample03.fastq.gz
│   ├── barley_sample04.fastq.gz
│   ├── barley_sample05.fastq.gz
│   └── barley_sample06.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

Project_barley > 02_analysis > $ RNASeq_quant.sh

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

“version 1”

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz \
  01_input_data/barley_sample04.fastq.gz \
  01_input_data/barley_sample05.fastq.gz \
  01_input_data/barley_sample06.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

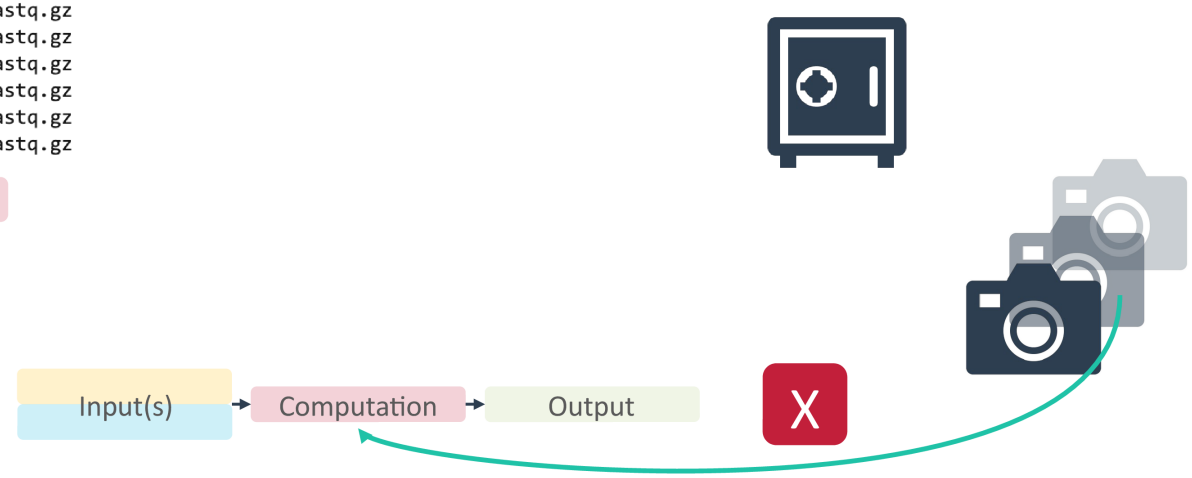
“version 2”

# Scenario 2: Pipeline breaks

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   ├── barley_sample03.fastq.gz
│   ├── barley_sample04.fastq.gz
│   ├── barley_sample05.fastq.gz
│   └── barley_sample06.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

# Revert to snapshot

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   ├── barley_sample03.fastq.gz
│   ├── barley_sample04.fastq.gz
│   ├── barley_sample05.fastq.gz
│   └── barley_sample06.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```




“version xy”

# Scenario 3: New project, same type of data and analysis

```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt

Project_maize
├── 01_input_data
│   ├── maize_genome_ref.fasta
│   ├── maize_sample01.fastq.gz
│   ├── maize_sample02.fastq.gz
│   └── maize_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

# Scenario 3: New project, same type of data and analysis

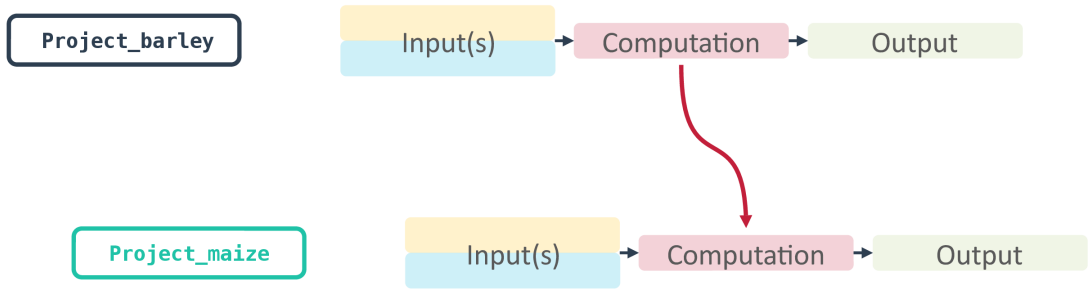
```
Project_barley
├── 01_input_data
│   ├── barley_genome_ref.fasta
│   ├── barley_sample01.fastq.gz
│   ├── barley_sample02.fastq.gz
│   └── barley_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

```
Project_maize
├── 01_input_data
│   ├── maize_genome_ref.fasta
│   ├── maize_sample01.fastq.gz
│   ├── maize_sample02.fastq.gz
│   └── maize_sample03.fastq.gz
├── 02_analysis
│   └── RNASeq_quant.sh
└── 03_results
    └── RNASeq_counts.txt
```

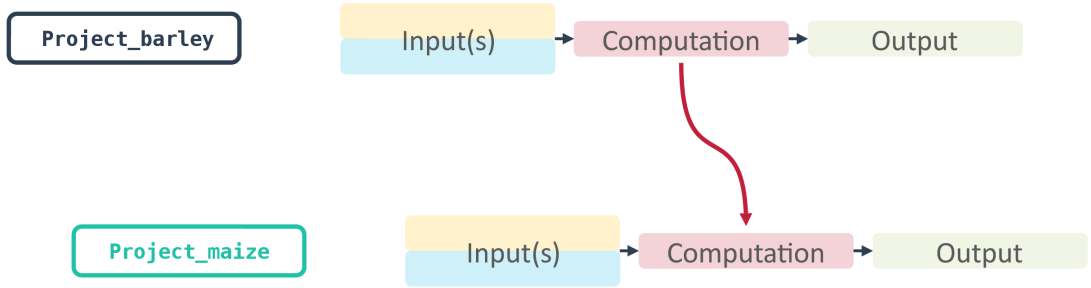
```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

```
# RNASeq quantification

read_trimming -i 01_input_data/maize_sample01.fastq.gz \
  01_input_data/maize_sample02.fastq.gz 01_input_data/maize_sample03.fastq.gz \
  -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/ maize_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

# Re-use code


Project_barley
Input(s)
Computation
Output
Project_maize
Input(s)
Computation
Output

# Re-use code



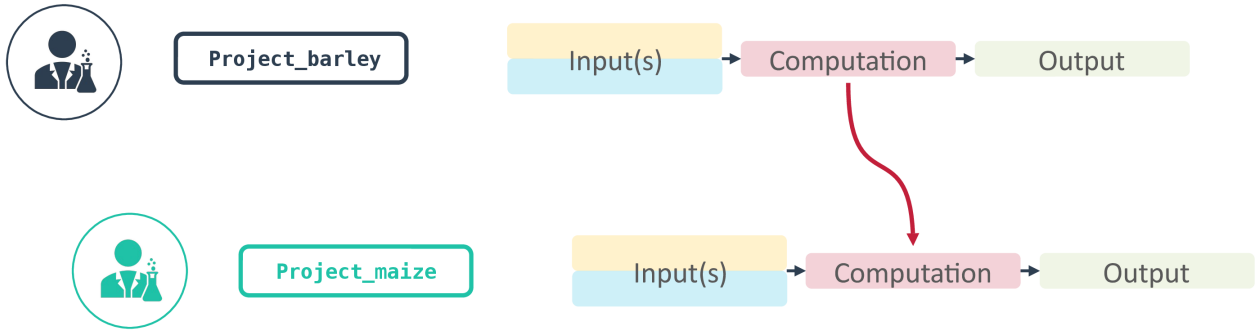

```
# RNASeq quantification

read_trimming -i 01_input_data/barley_sample01.fastq.gz \
  01_input_data/barley_sample02.fastq.gz \
  01_input_data/barley_sample03.fastq.gz \
  -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/barley_genome_ref.fasta \
  -o 03_results/RNASeq_counts.txt
```

“version barley”

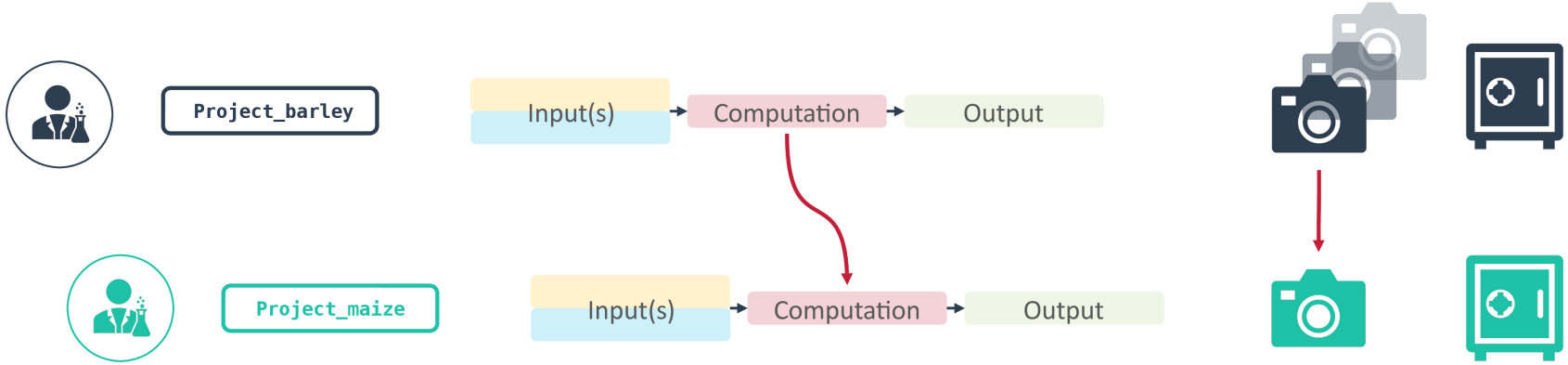
```
# RNASeq quantification

read_trimming -i 01_input_data/maize_sample01.fastq.gz \
  01_input_data/maize_sample02.fastq.gz 01_input_data/maize_sample03.fastq.gz

  -o trimmed_reads/

rna_quant -i trimmed_reads/ -ref 01_input_data/ maize_genome_ref.fasta -o 03_results/RNASeq_counts.txt
```

“version maize”

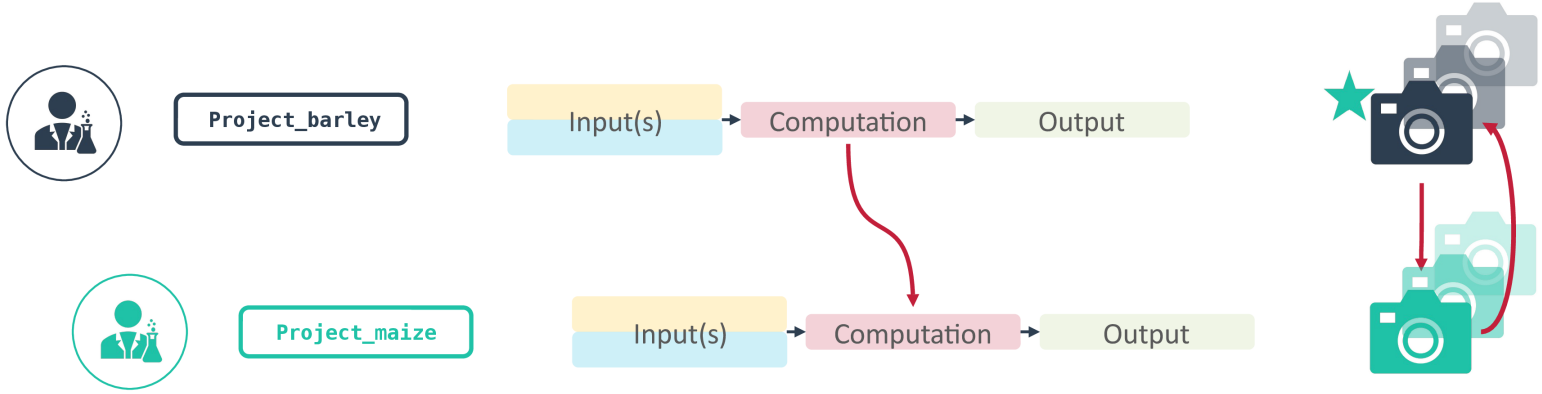
# Re-use code – People have done this



# Re-use code – People have done this



# Re-use code – Link and contribute



# Git: summary

- Version control system
- Git “repository” = a central data package (directory)
- Allows to track changes to any file in the repository
    - **What** was changed
    - **When** was it changed
    - By **whom** was it changed
    - **Why** was it changed?

# GitHub and GitLab

- A well-documented cloud environment
- Active syncing
- Not automatically synced
- Non-automated version control
- You have the control what changes to track and what to sync
- Time machine to go back to older versions

# GitHub and Gitlab team projects

Simplifies concurrent work & merging changes

- Online service to host our projects
- Share code with other developers
- Others can download our projects, work on and contribute to them
- They can upload their changes and merge them with the main project

# Cloud vs. Git

| | Cloud services | Git / GitHub / GitLab |
|---|---|---|
| **Track changes** | ✓ Documents<br>✓ Small data<br>✓ Presentations | ✓ Code<br>✓ Data analytical projects |
| **Collaboration** | | issue tracker, tracked contribution |
| **Versioning** | Automated | Well-documented (commit history) |
| **Syncing** | Automated | Active / controlled by user |
| **Access** | Oftentimes only within organization / institution | Easily collaborate across institutions |
| **Data security** | Private / commercial | GitLab: on-premise and custom solutions |