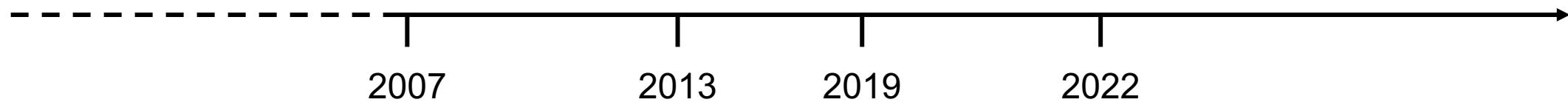




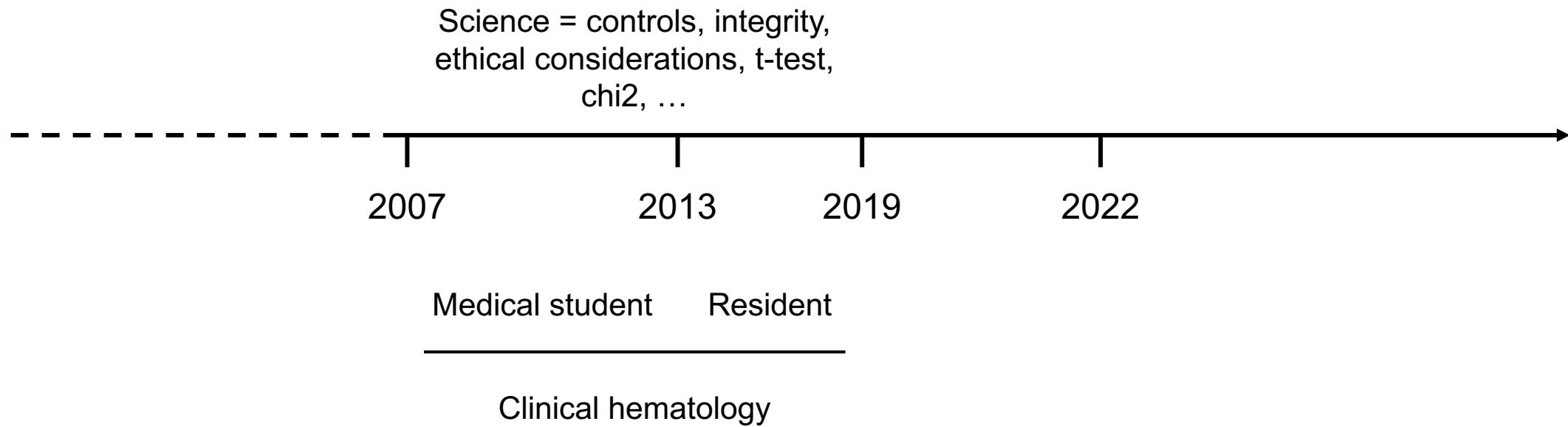
# Everyone can learn how to Guix

Dr Nicolas VALLET, MD, PhD  
Assistant Professor  
Hematology and Cell Therapy Department,  
University Hospital Center Tours  
Inserm U1069 N2COx

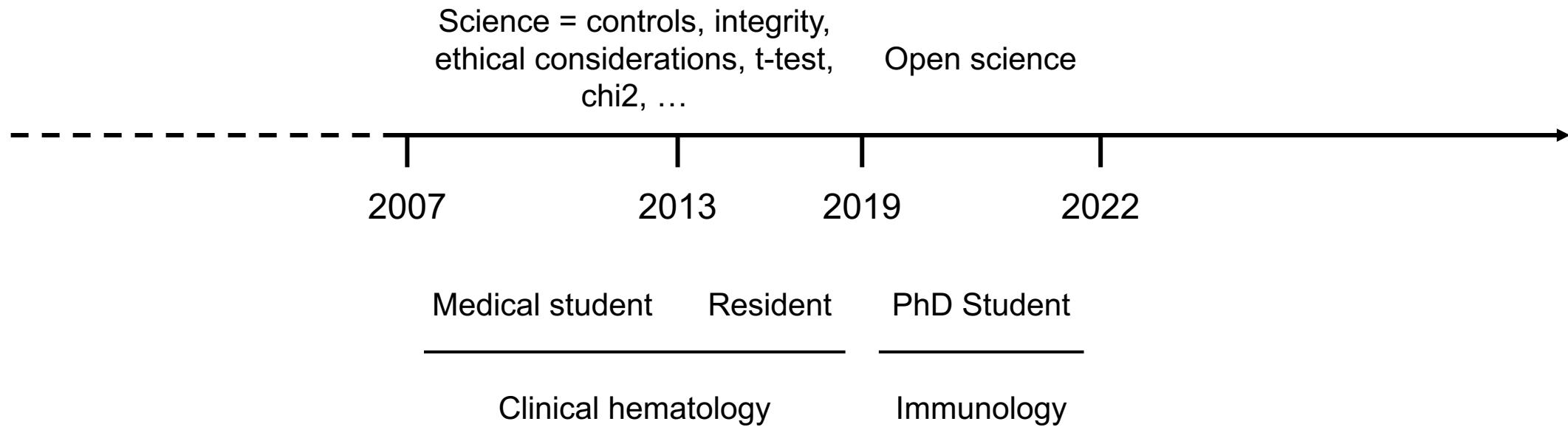
## **My background**



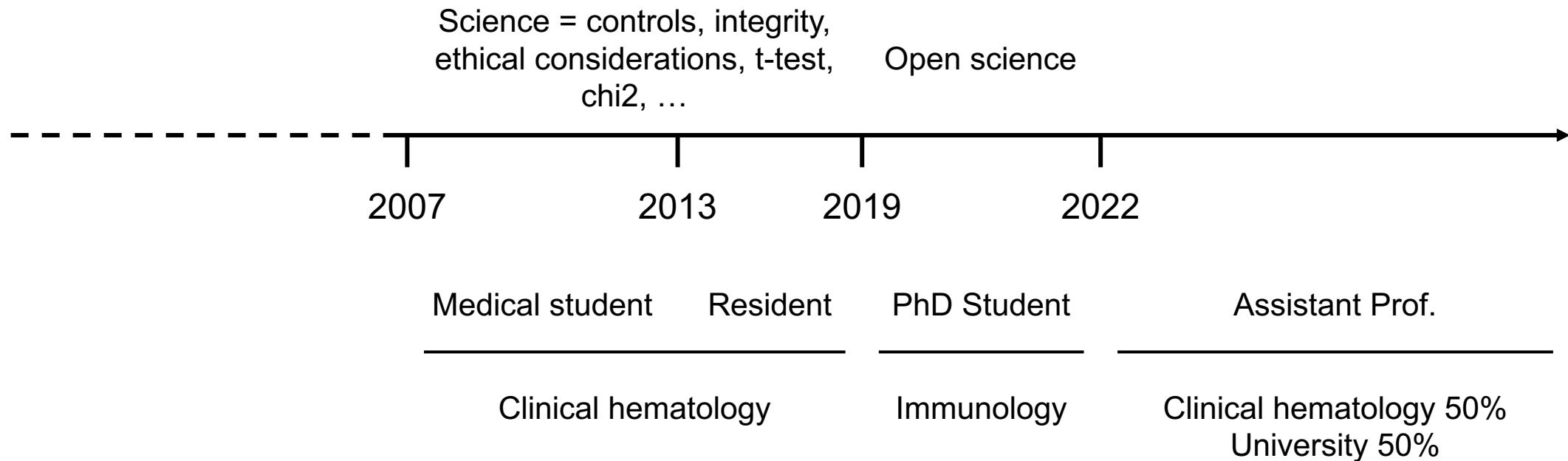
## My background



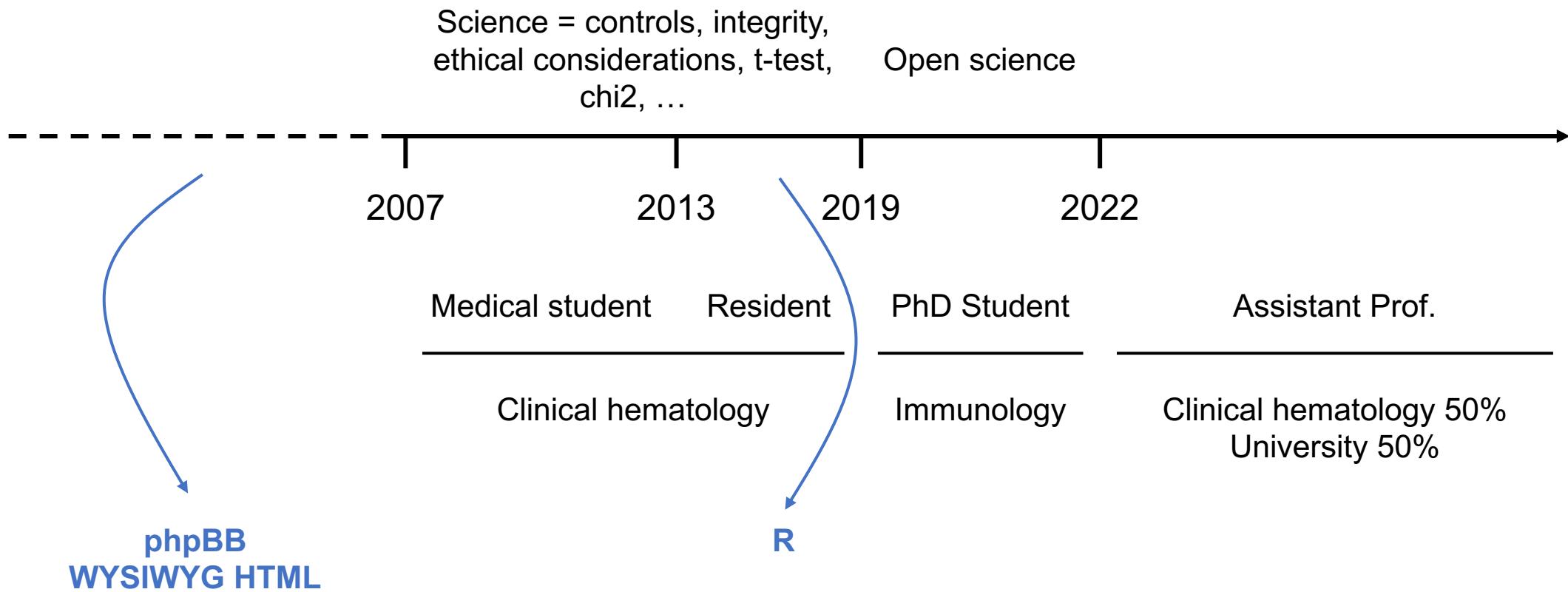
## My background



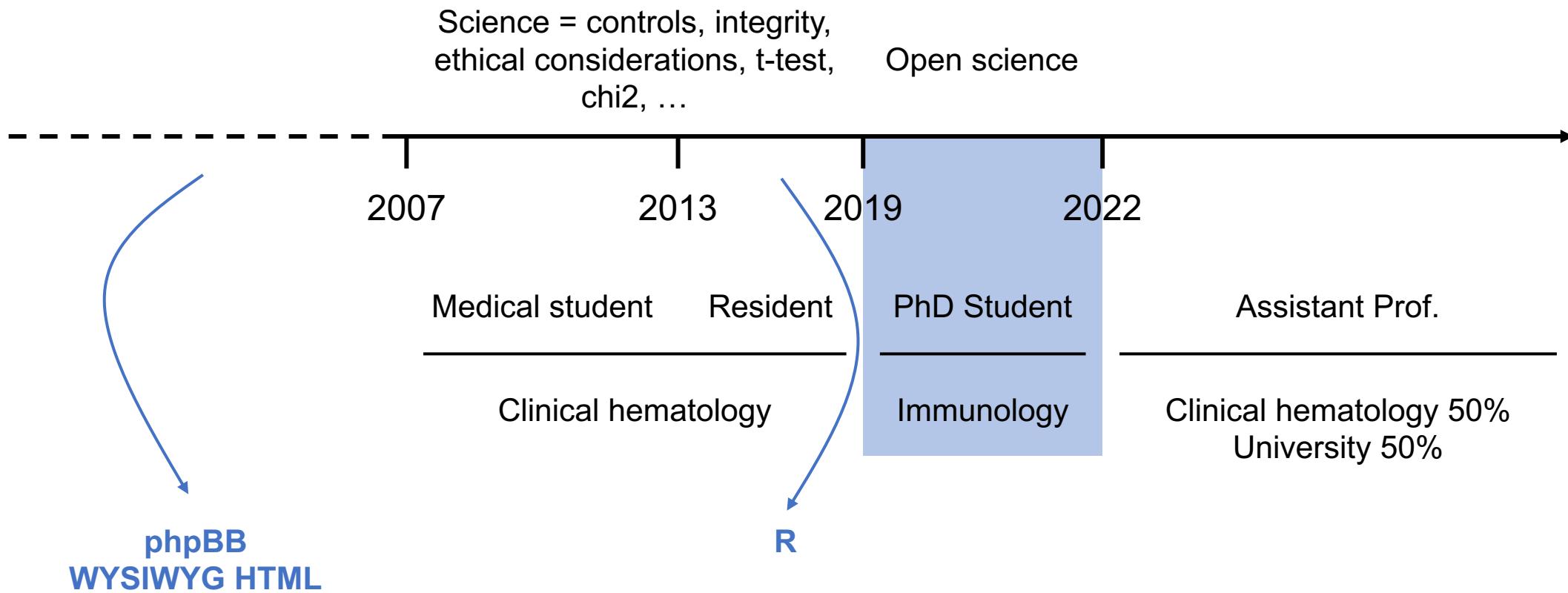
## My background



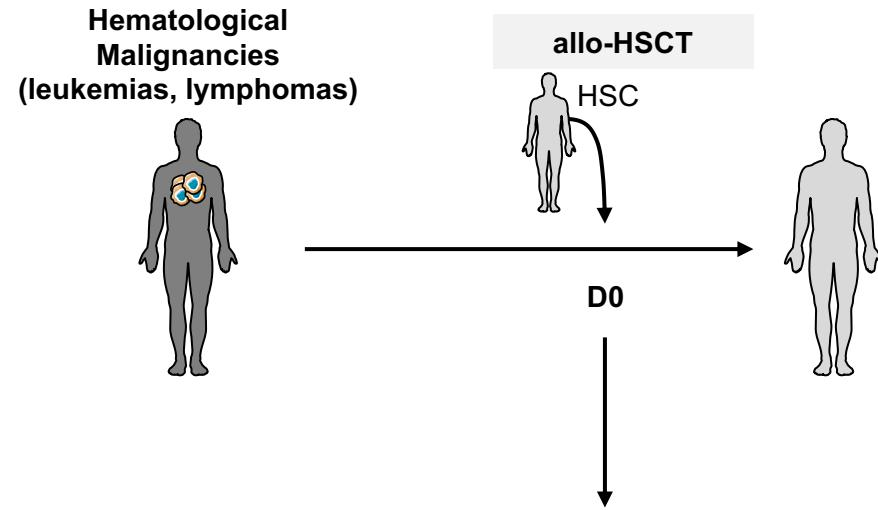
## My background



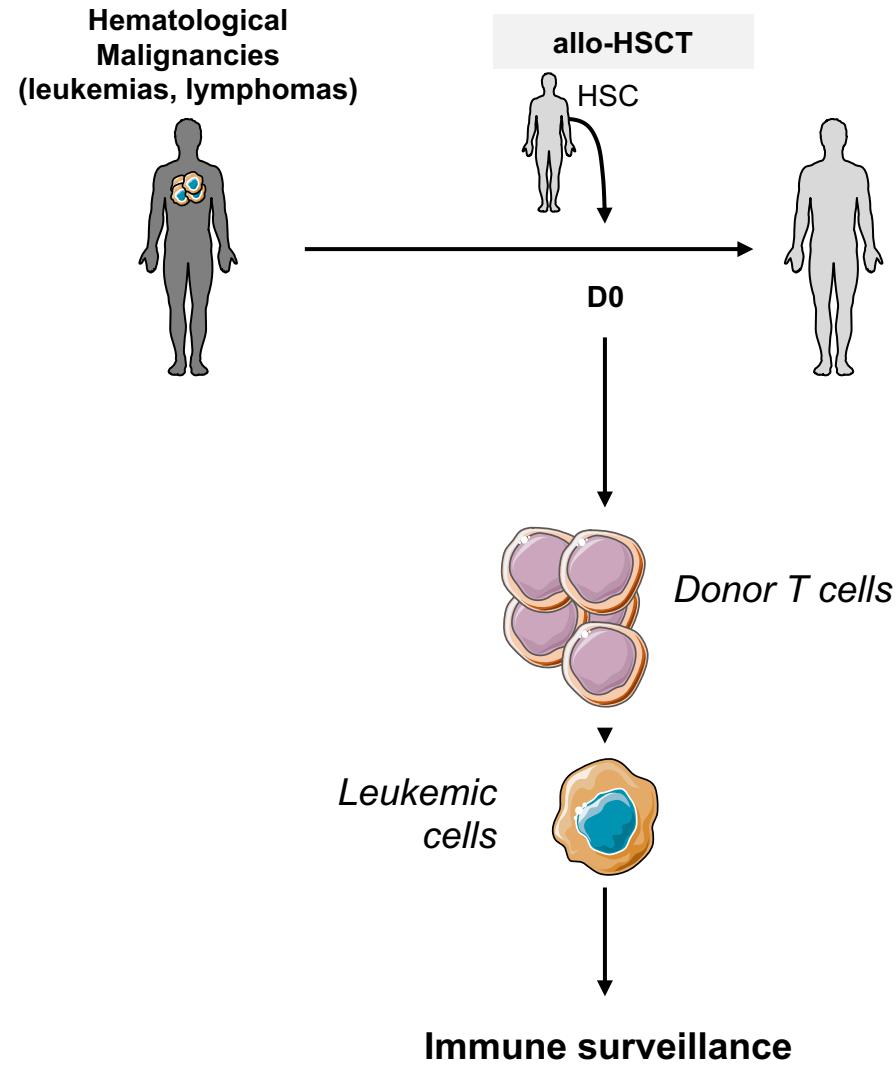
## My background



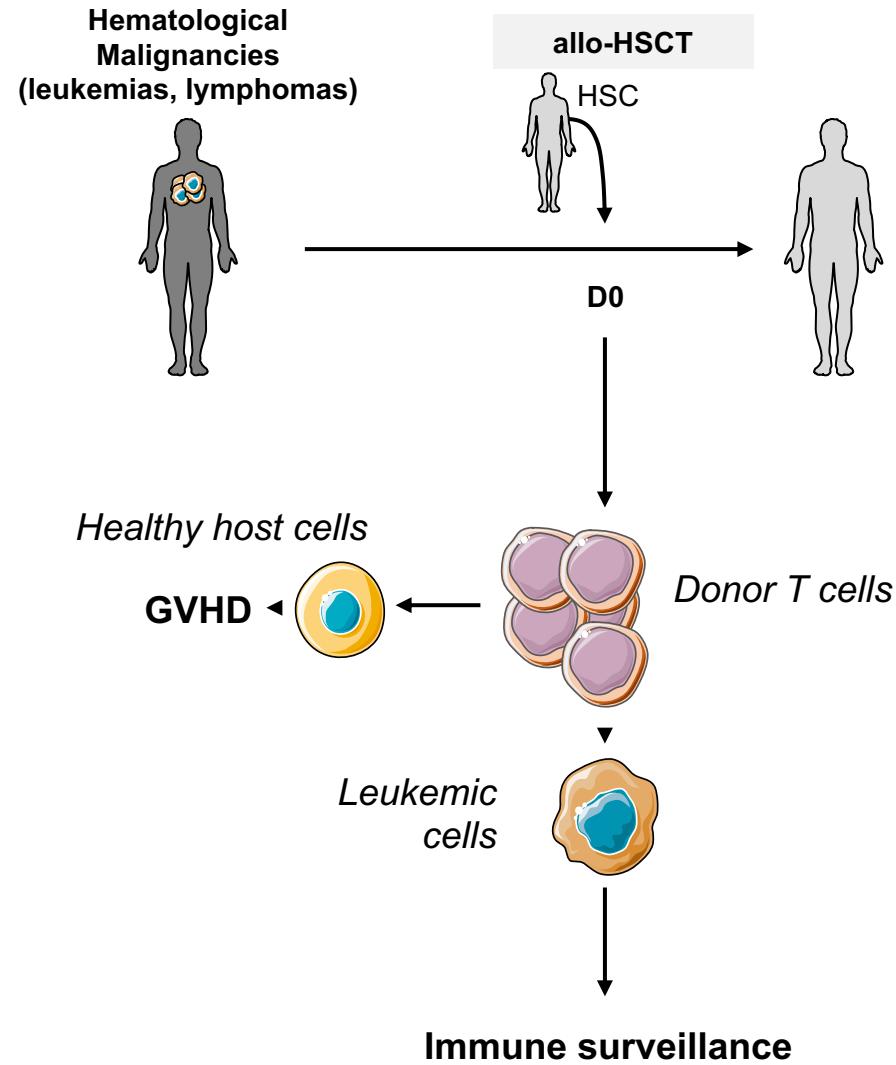
# Context



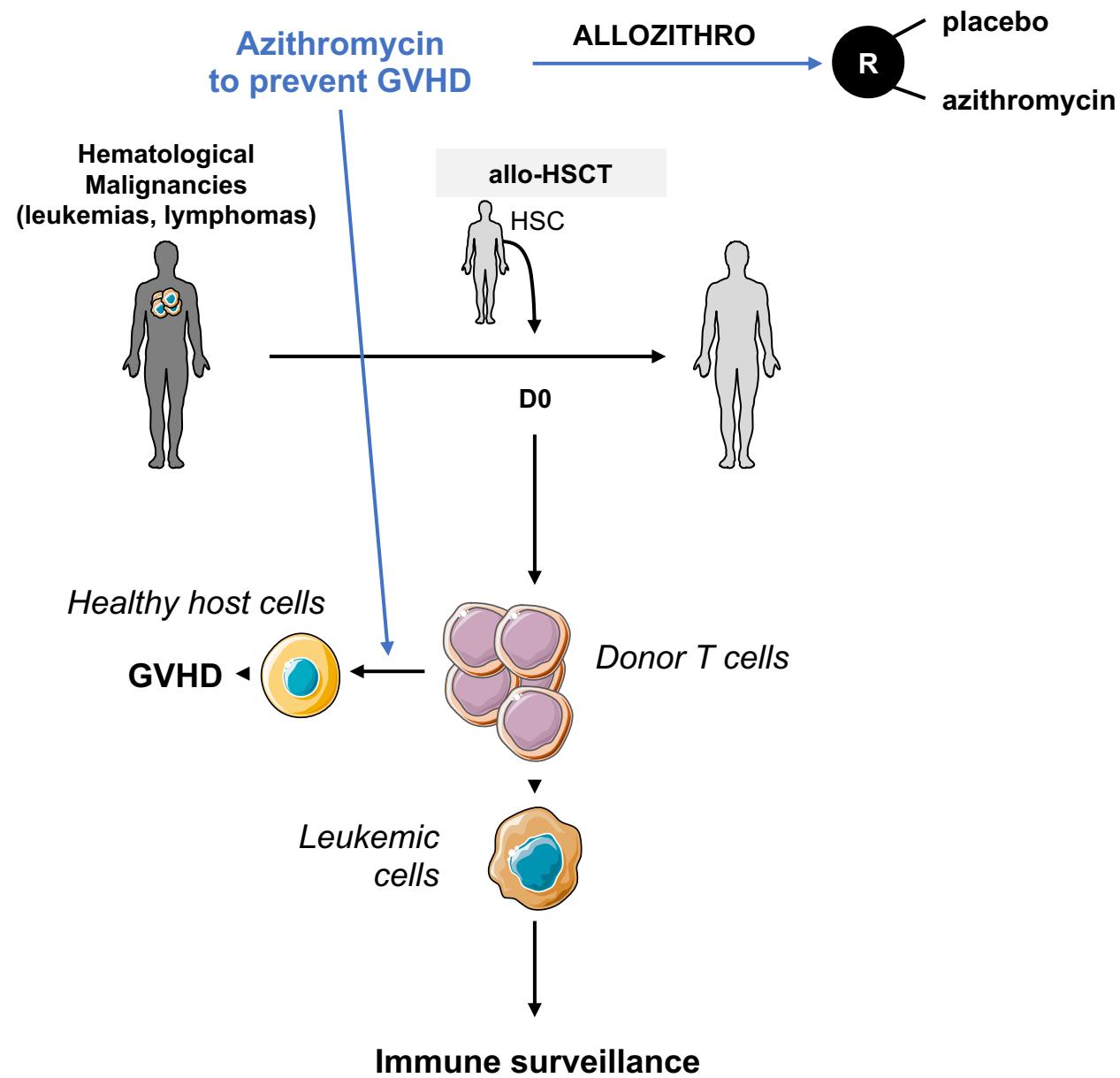
# Context



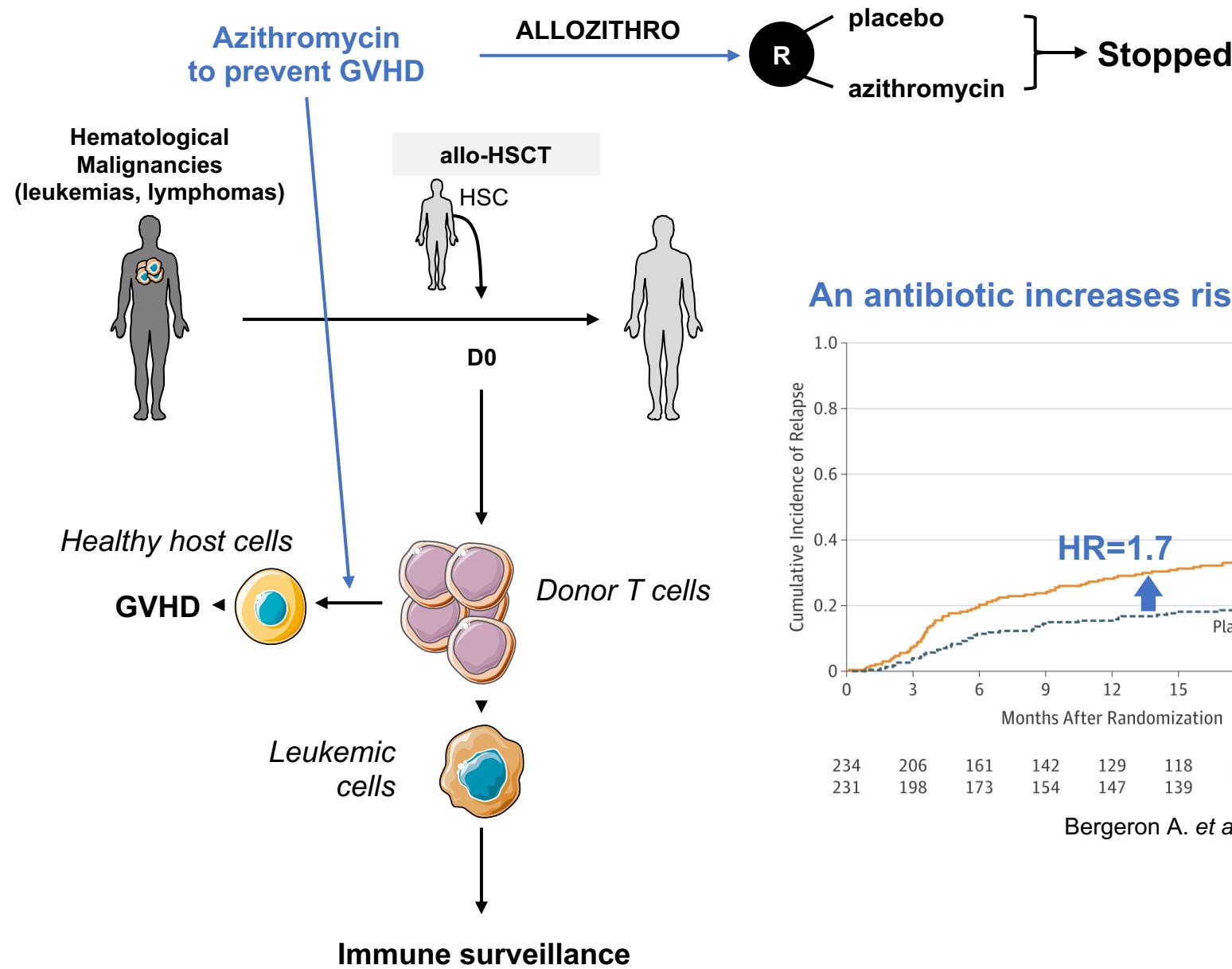
## Context



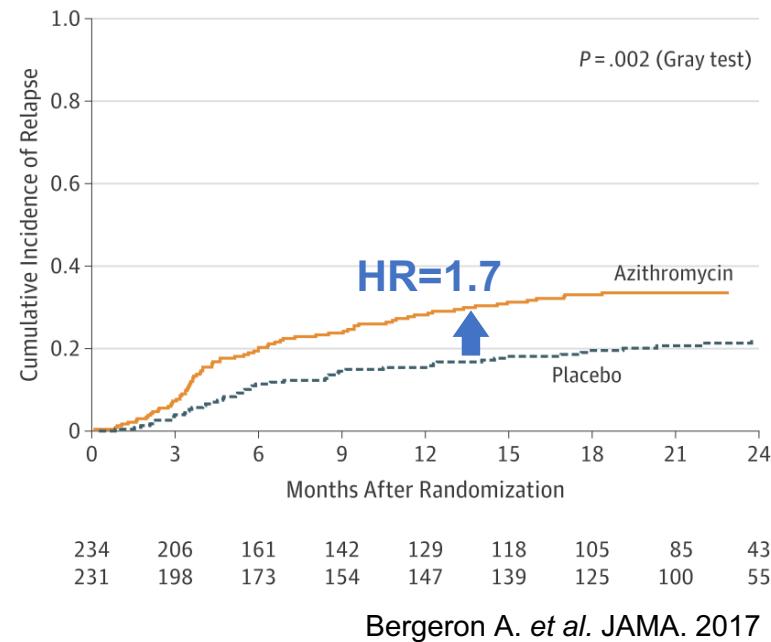
## Context



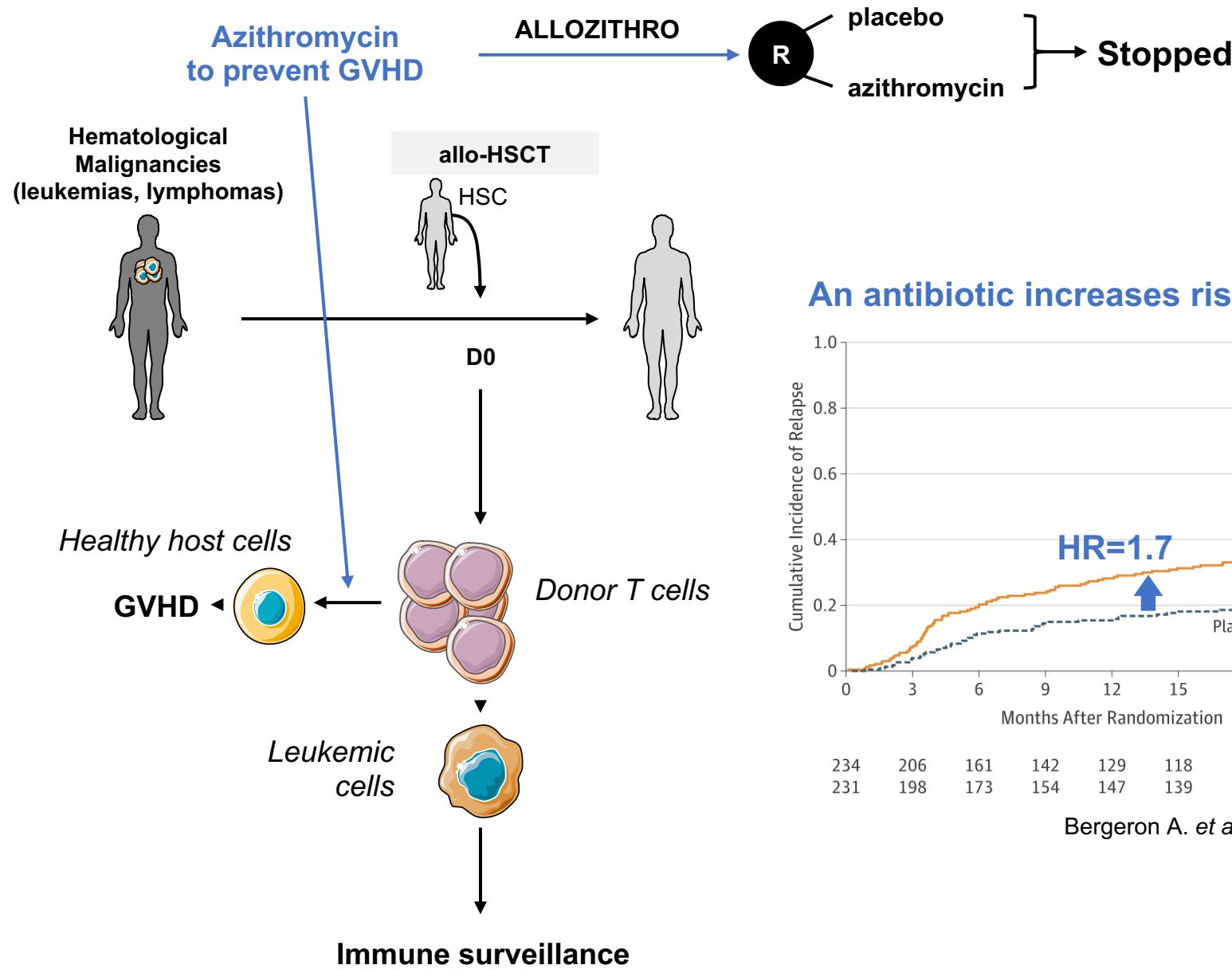
## Context



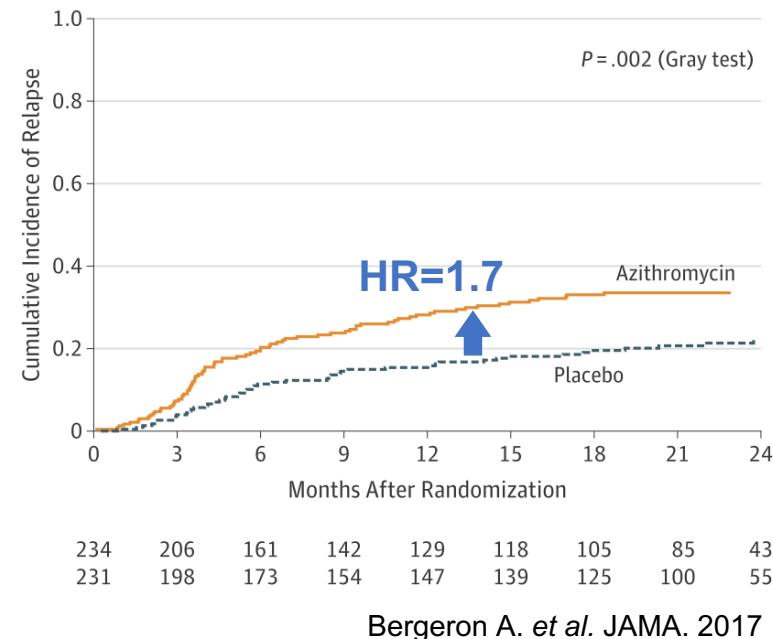
An antibiotic increases risk of relapse



## Context



An antibiotic increases risk of relapse

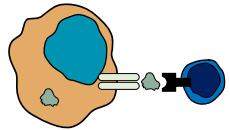


How could an antibiotic dampen antitumor immune responses ?

# Hypotheses

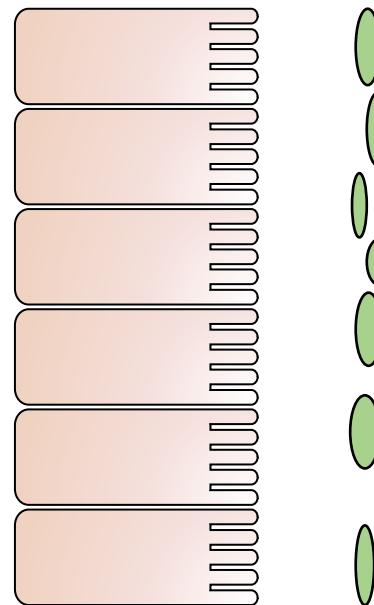
**Antibiotic  
Azithromycin**

Relapse ←



**Dampened anti tumor  
Immune responses**

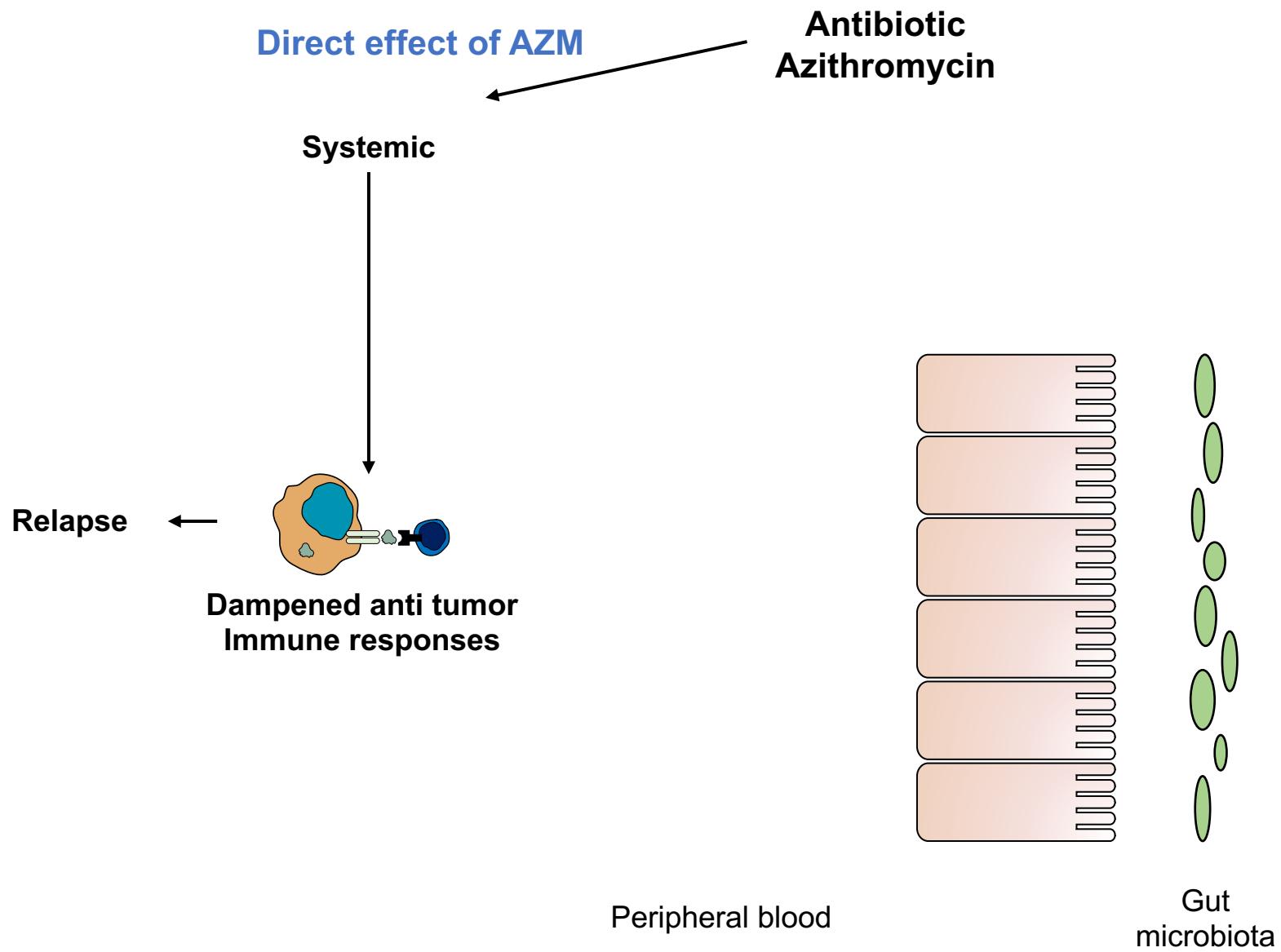
Peripheral blood



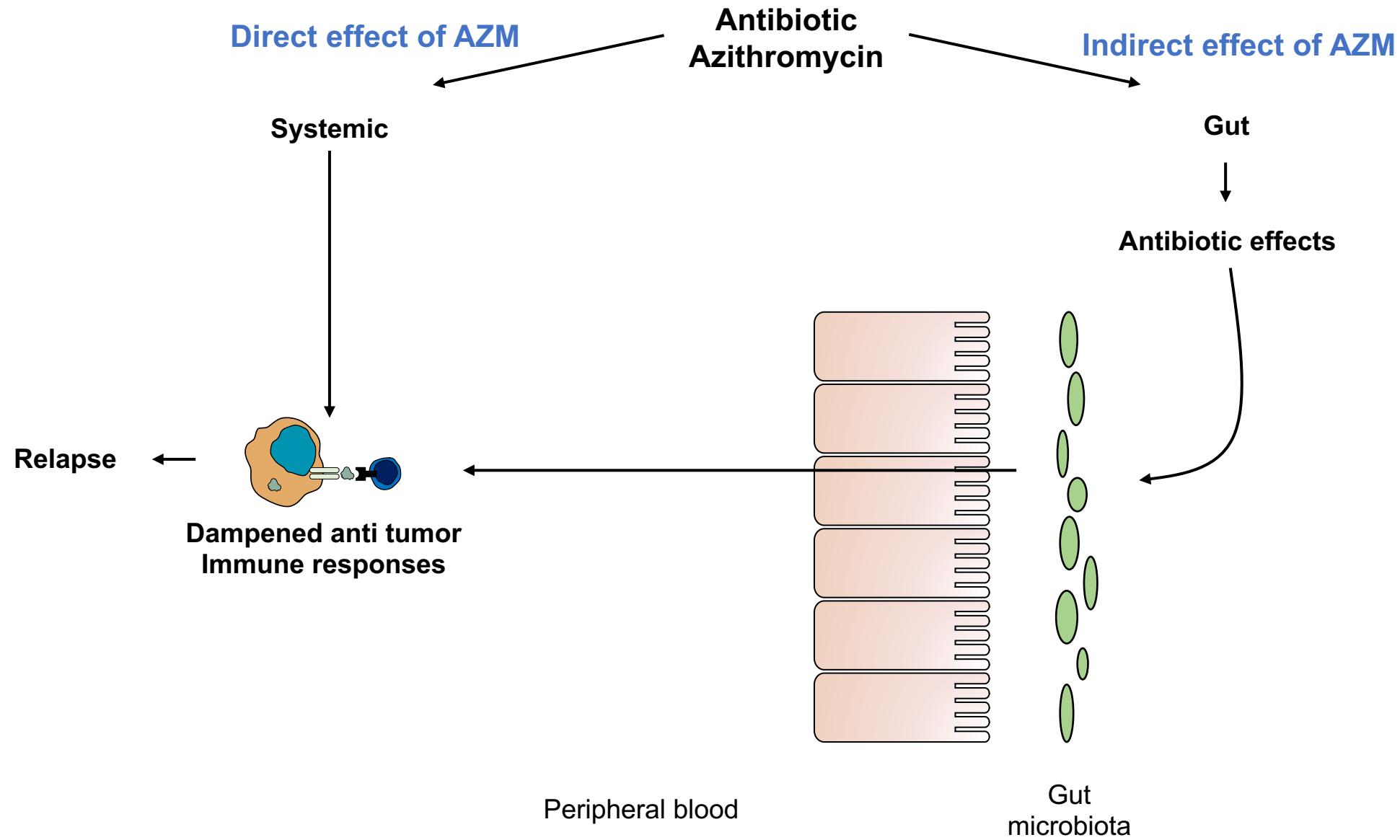
Gut  
microbiota



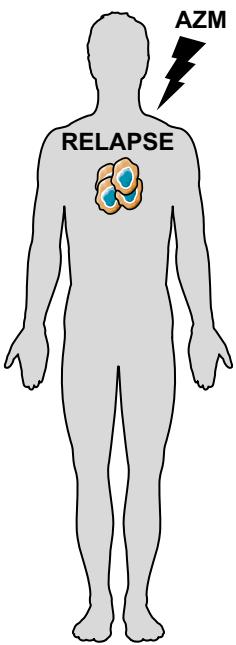
# Hypotheses



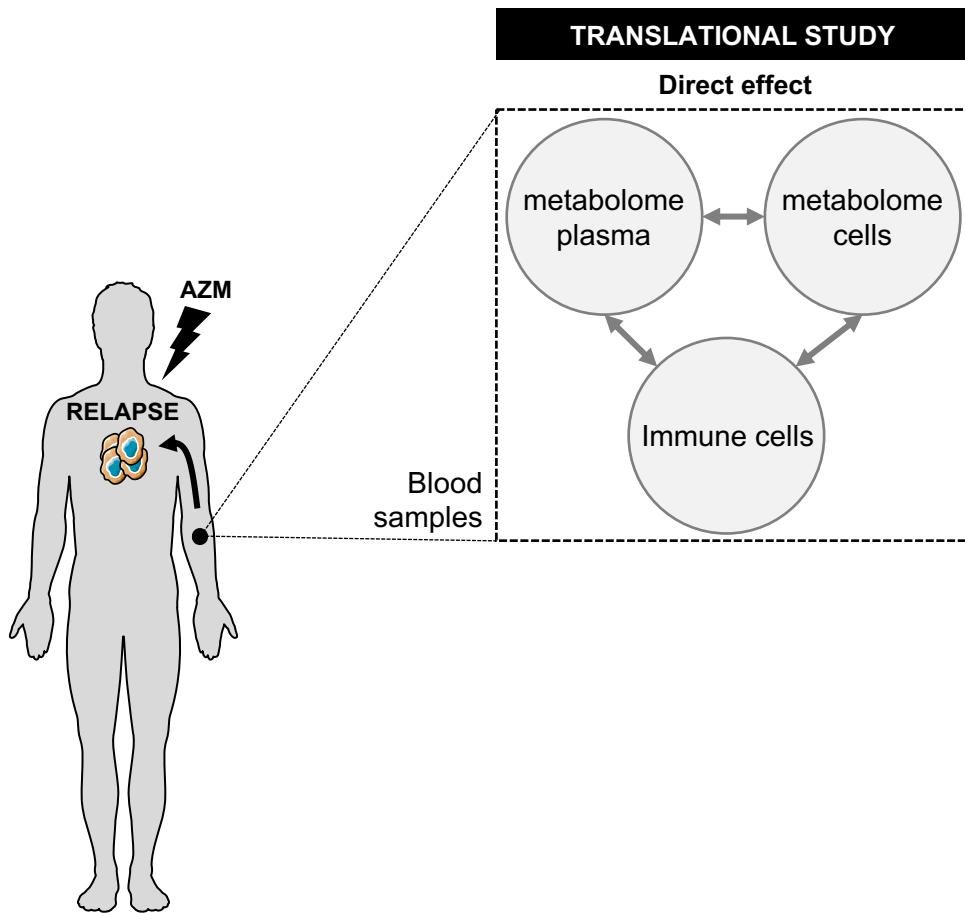
# Hypotheses



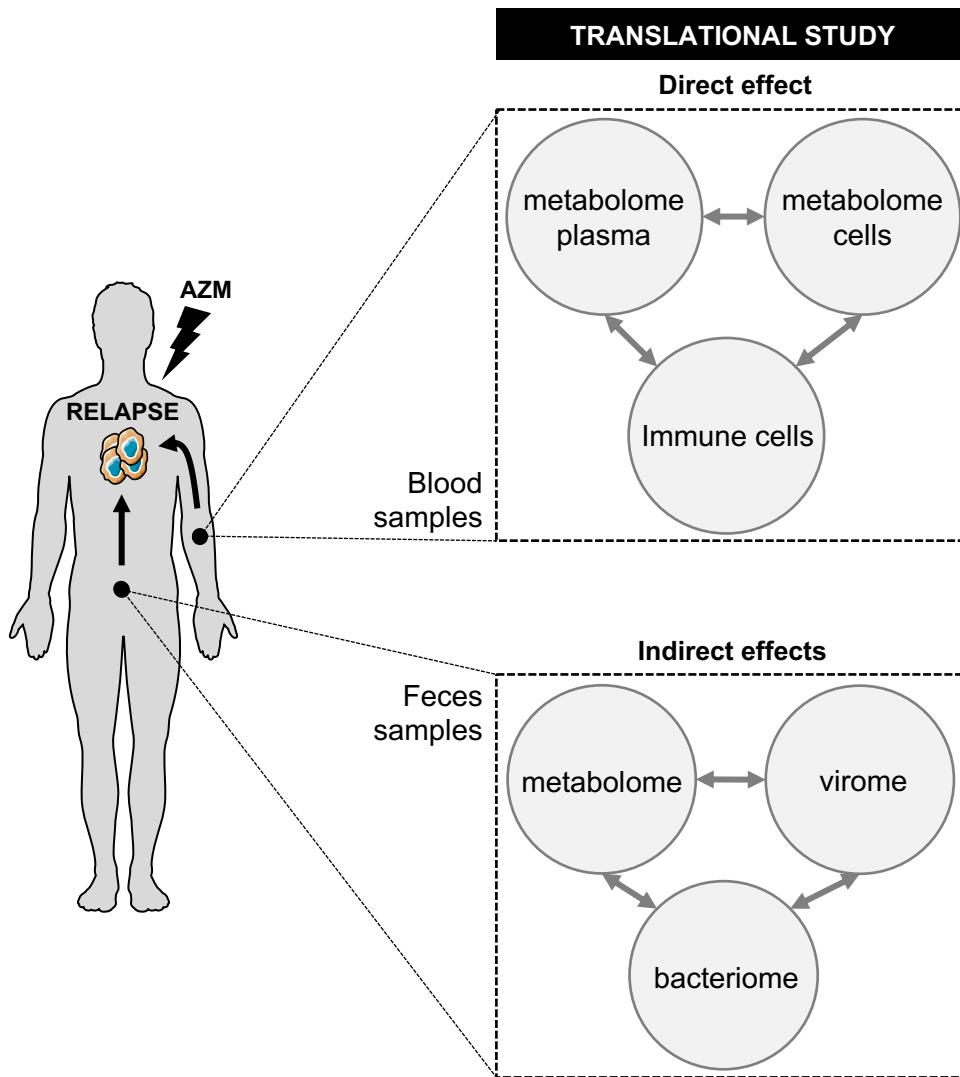
# Methods



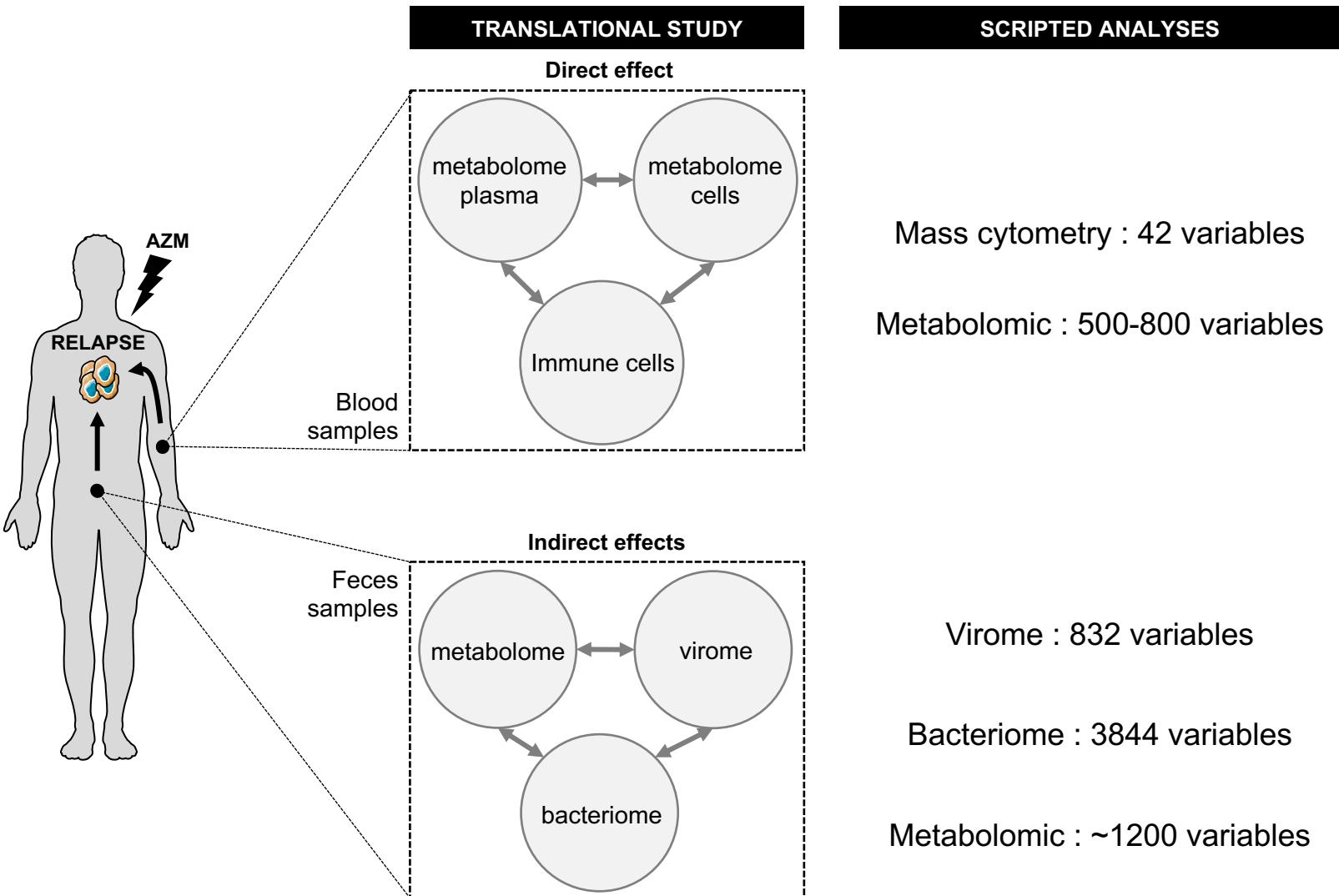
# Methods



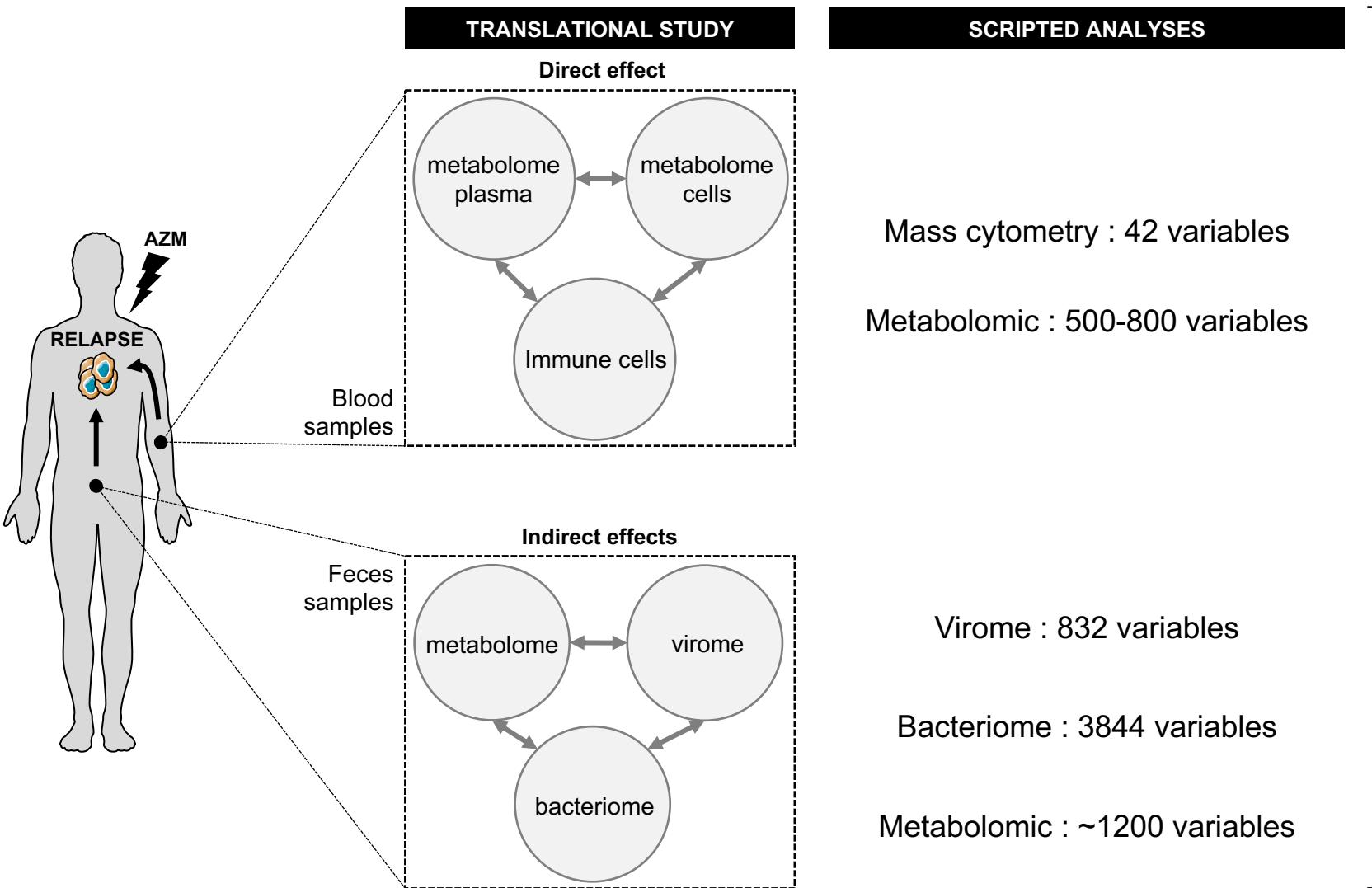
# Methods



# Methods



# Methods



How could we ensure reproducibiliy of our work?

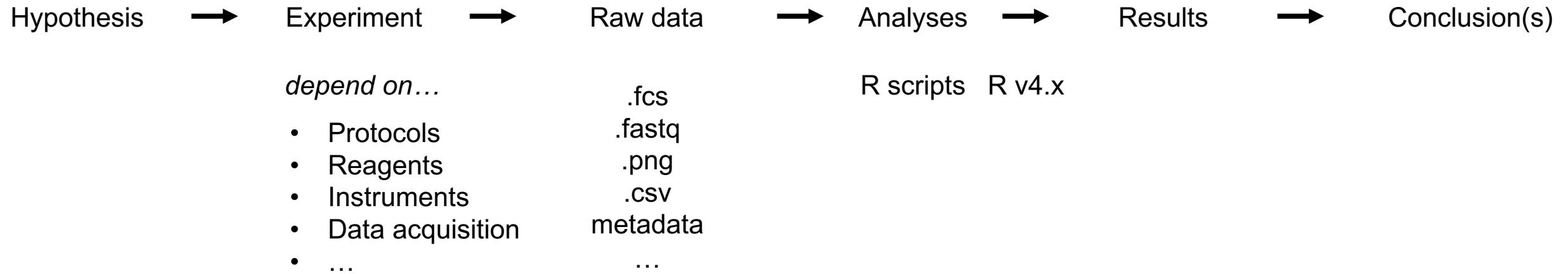
## Reproducibility planning from the beginning of the project

Hypothesis → Experiment

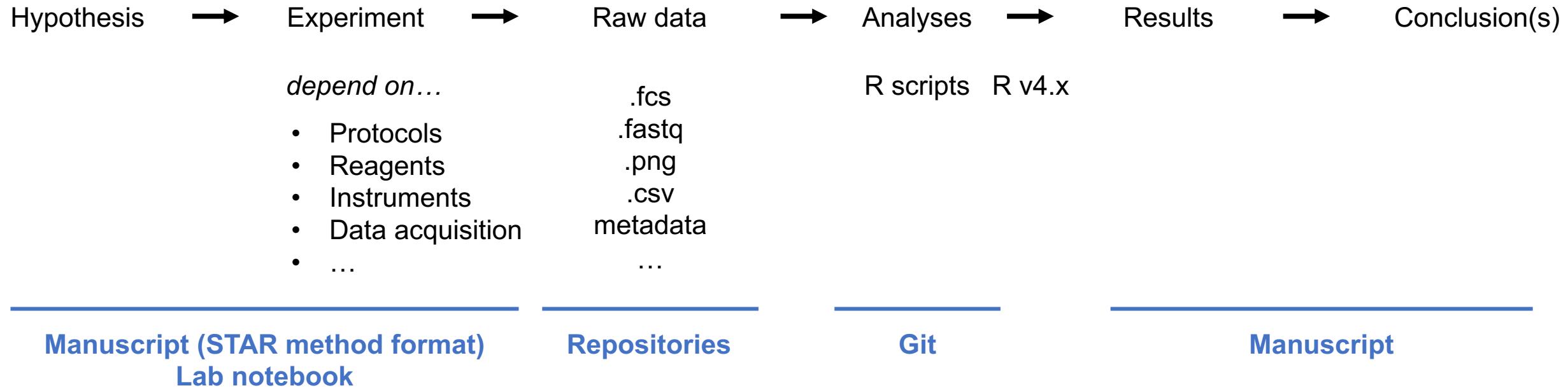
*depend on...*

- Protocols
- Reagents
- Instruments
- Data acquisition
- ...

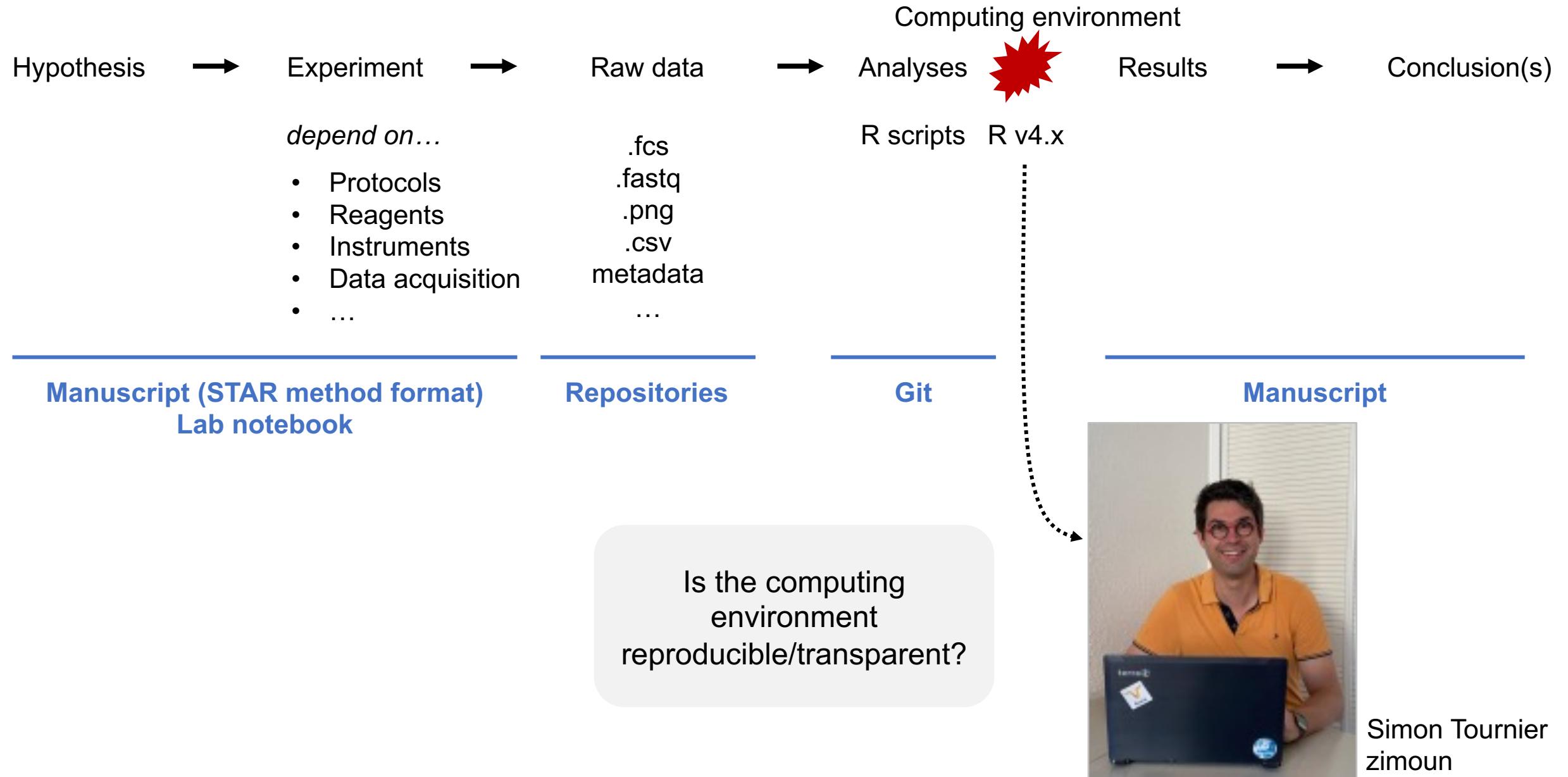
# Reproducibility planning from the beginning of the project



# Reproducibility planning from the beginning of the project



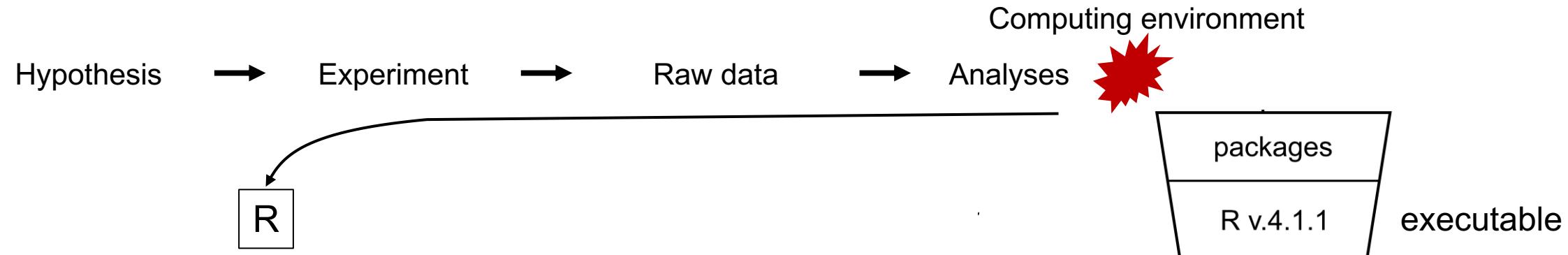
# Reproducibility planning from the beginning of the project



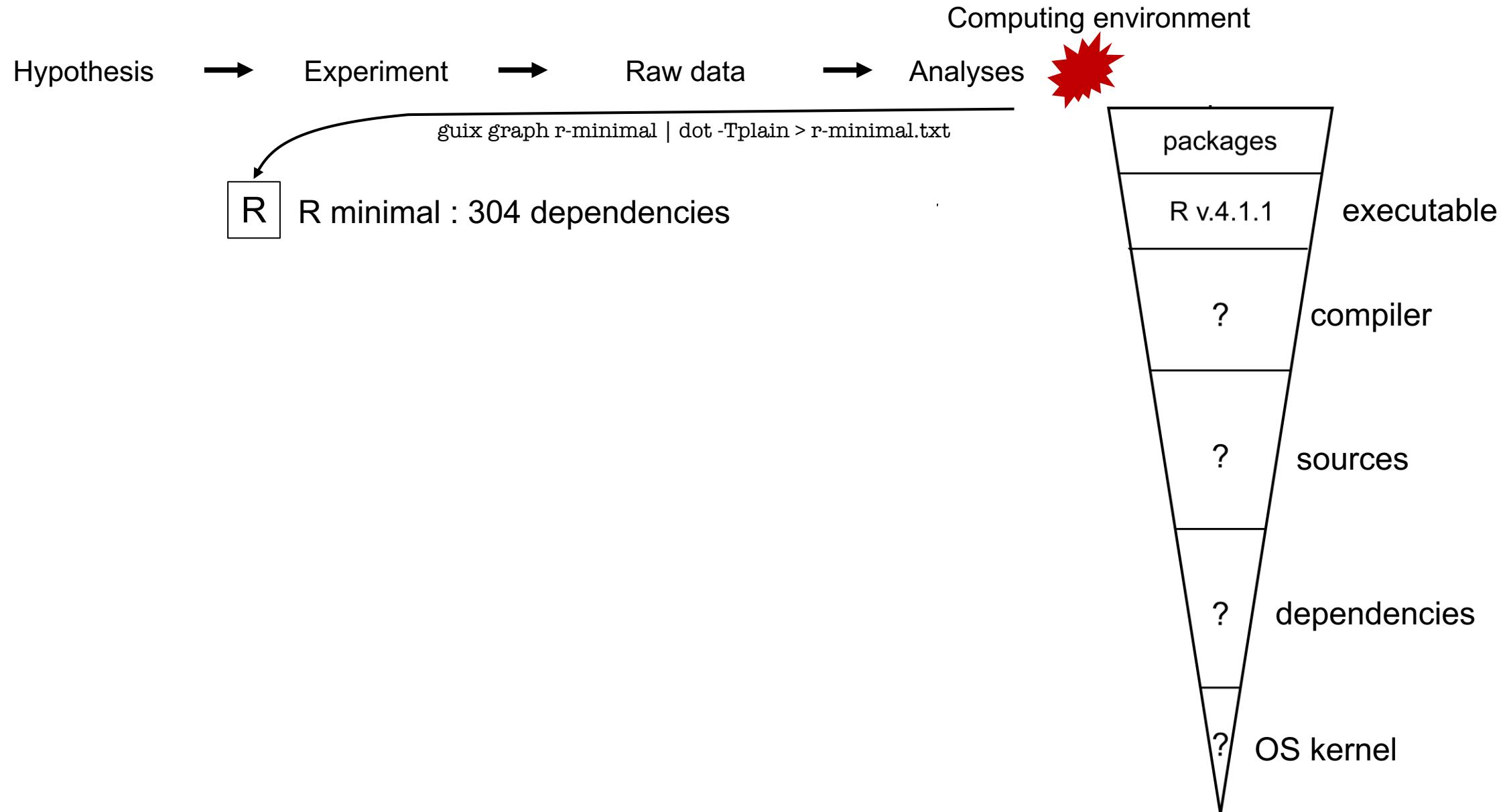
## Dependencies hell



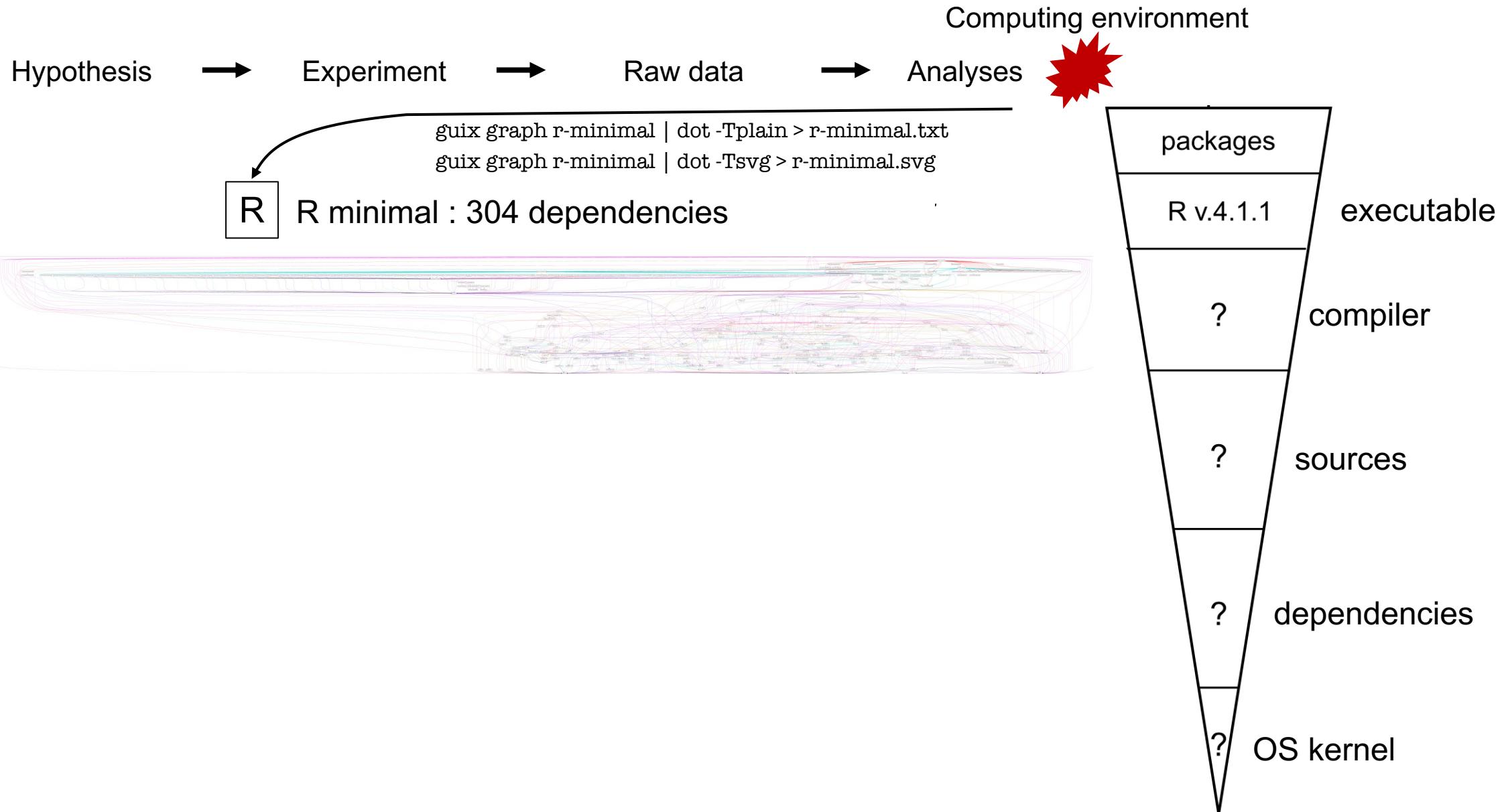
## Dependencies hell



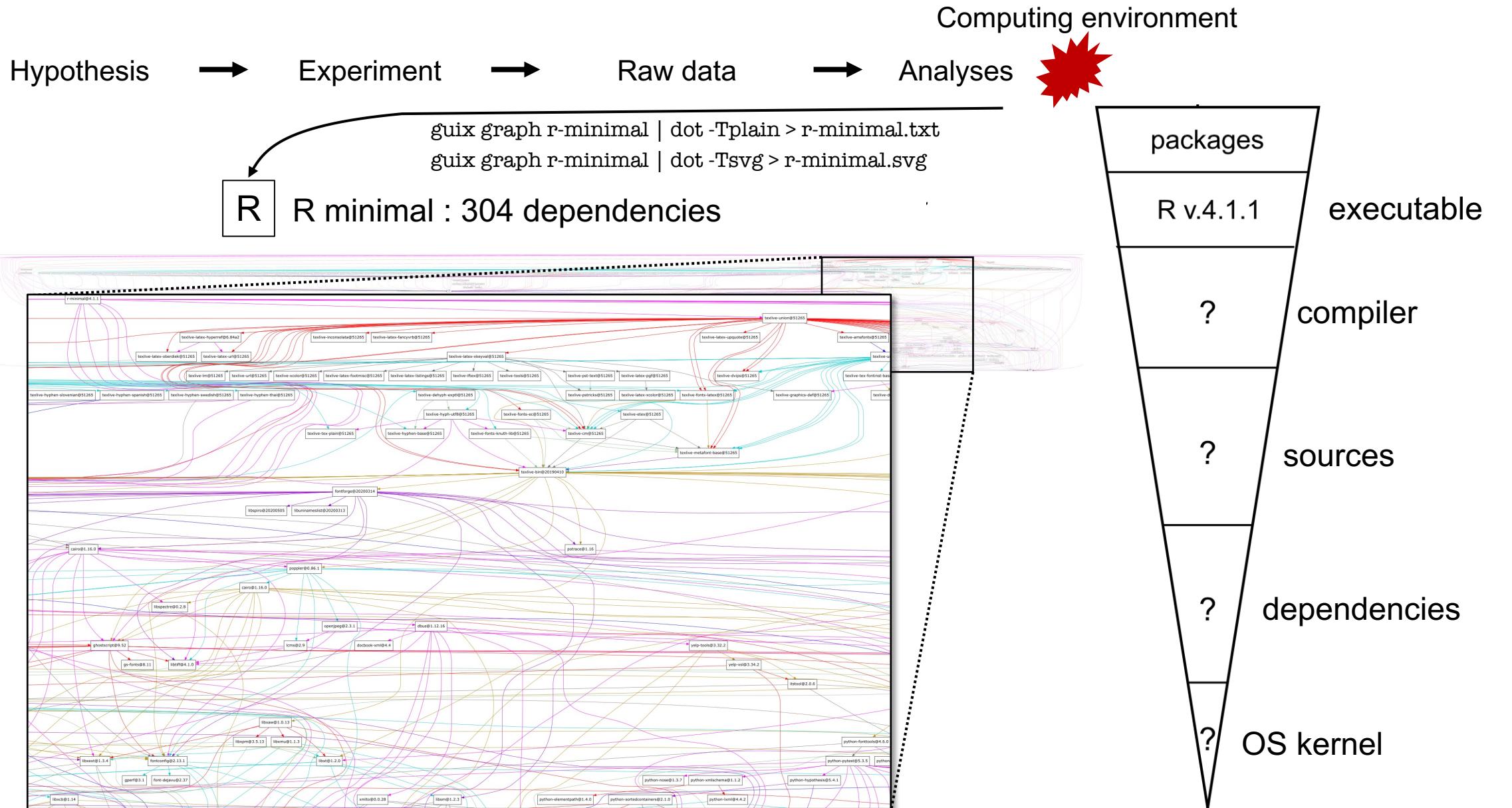
# Dependencies hell



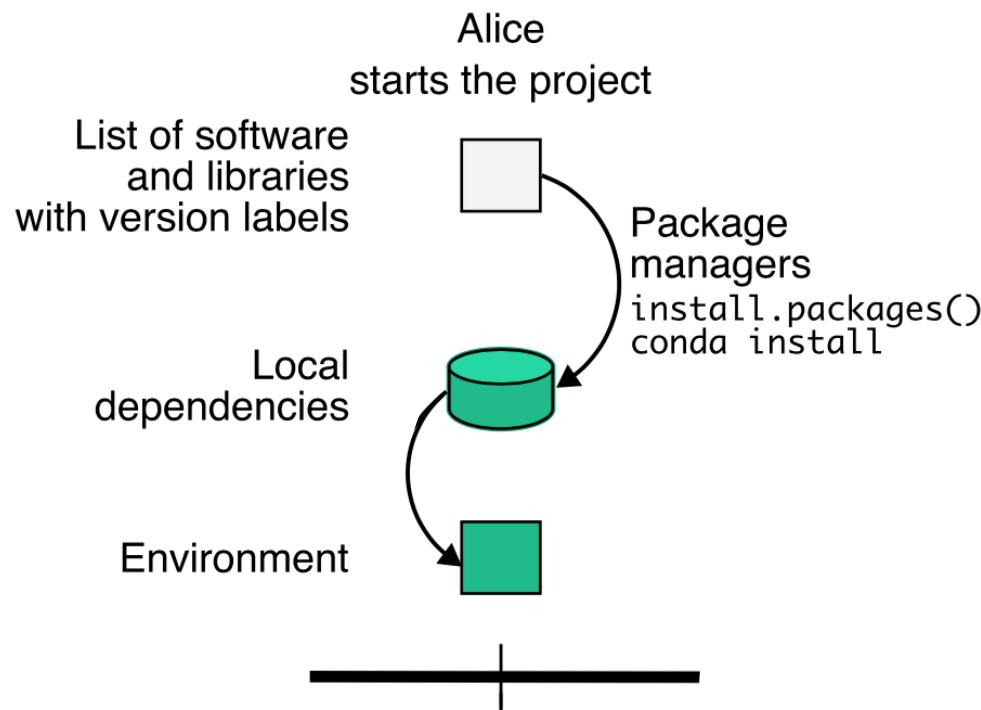
# Dependencies hell



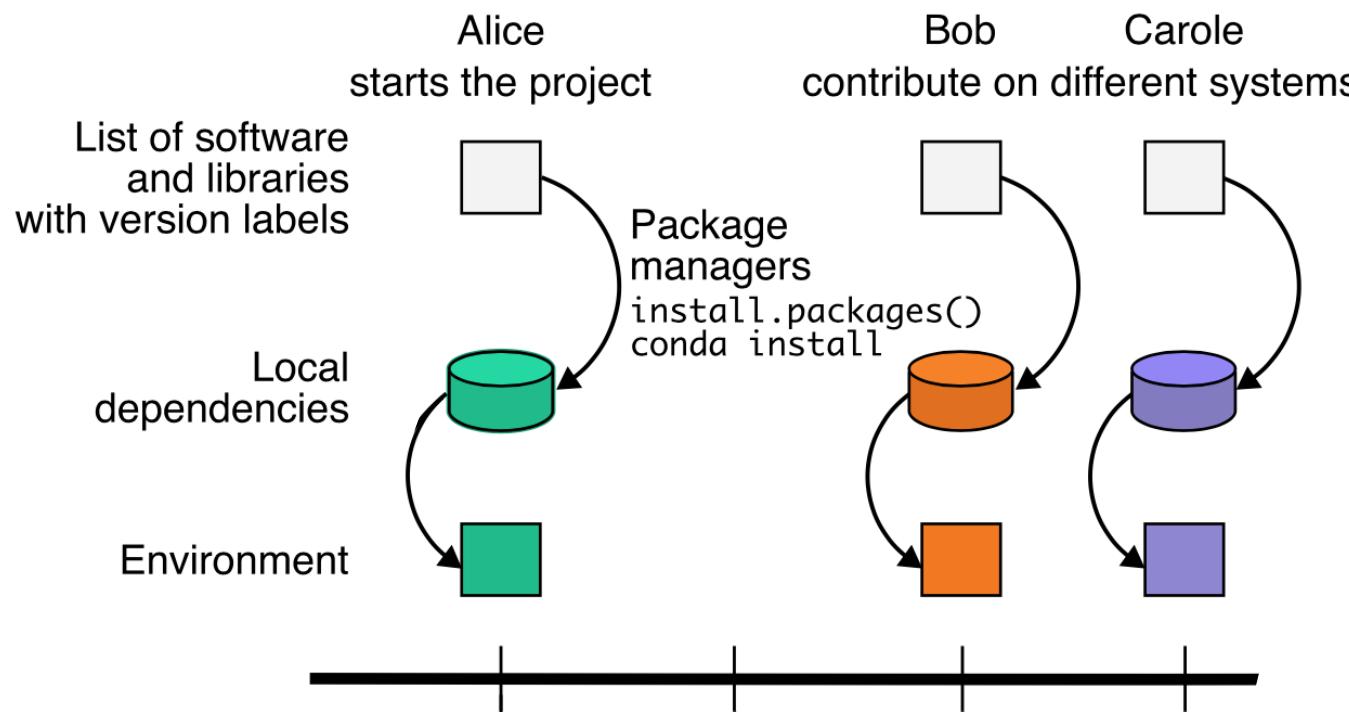
# Dependencies hell



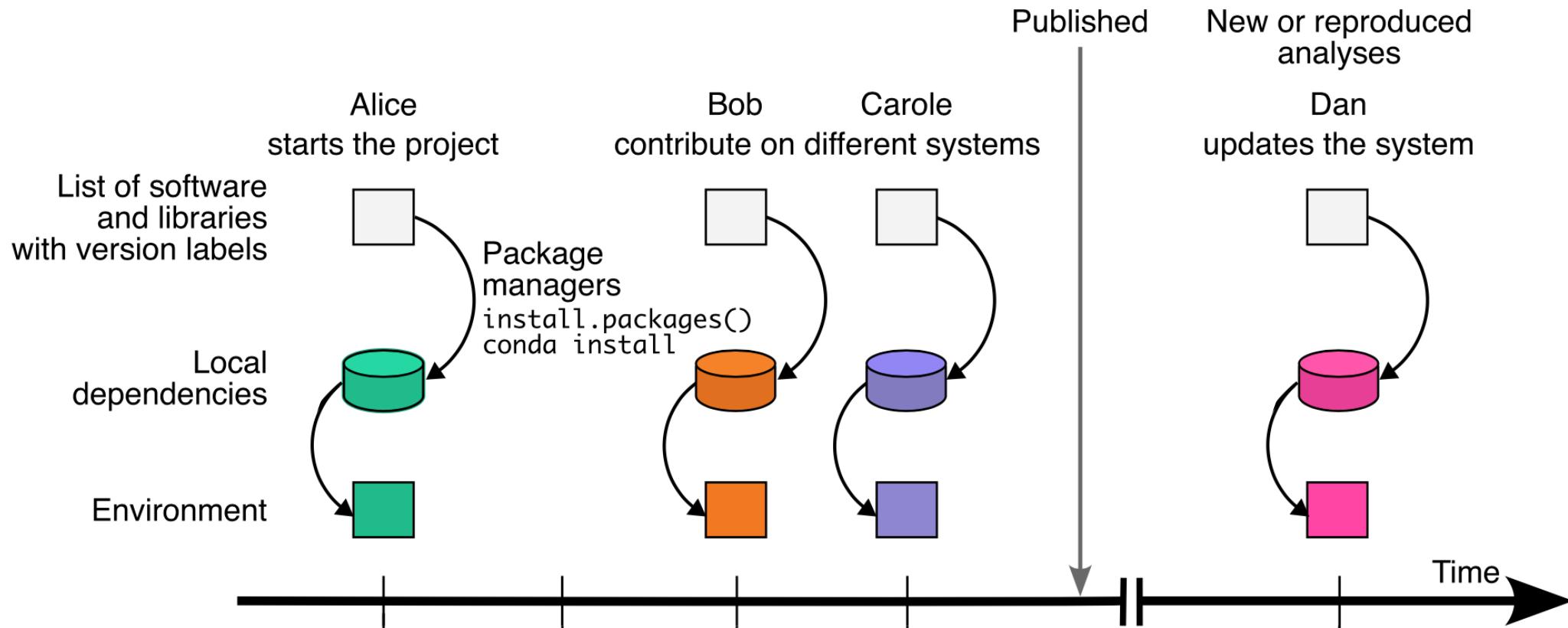
# Different computing environments



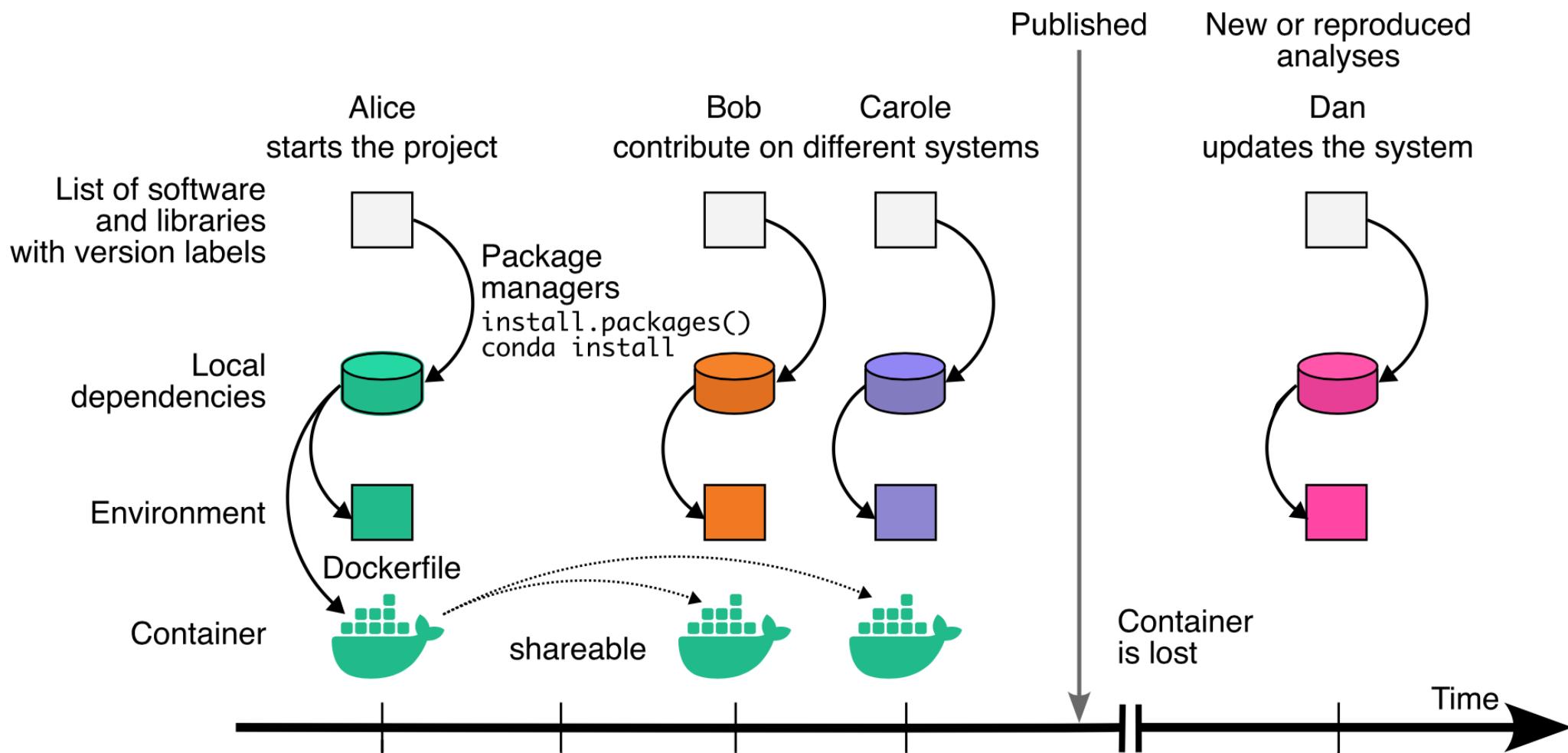
# Different computing environments



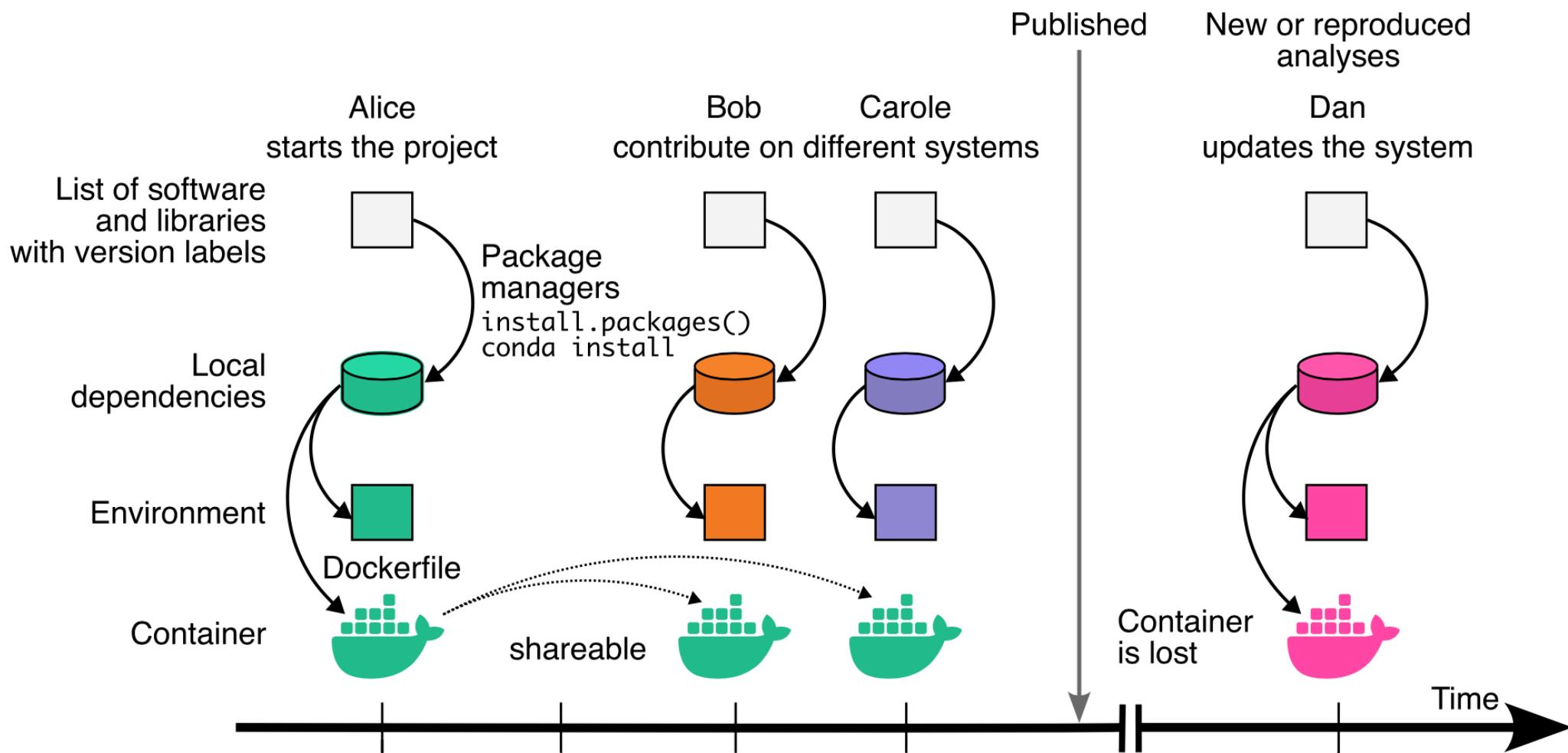
# Different computing environments



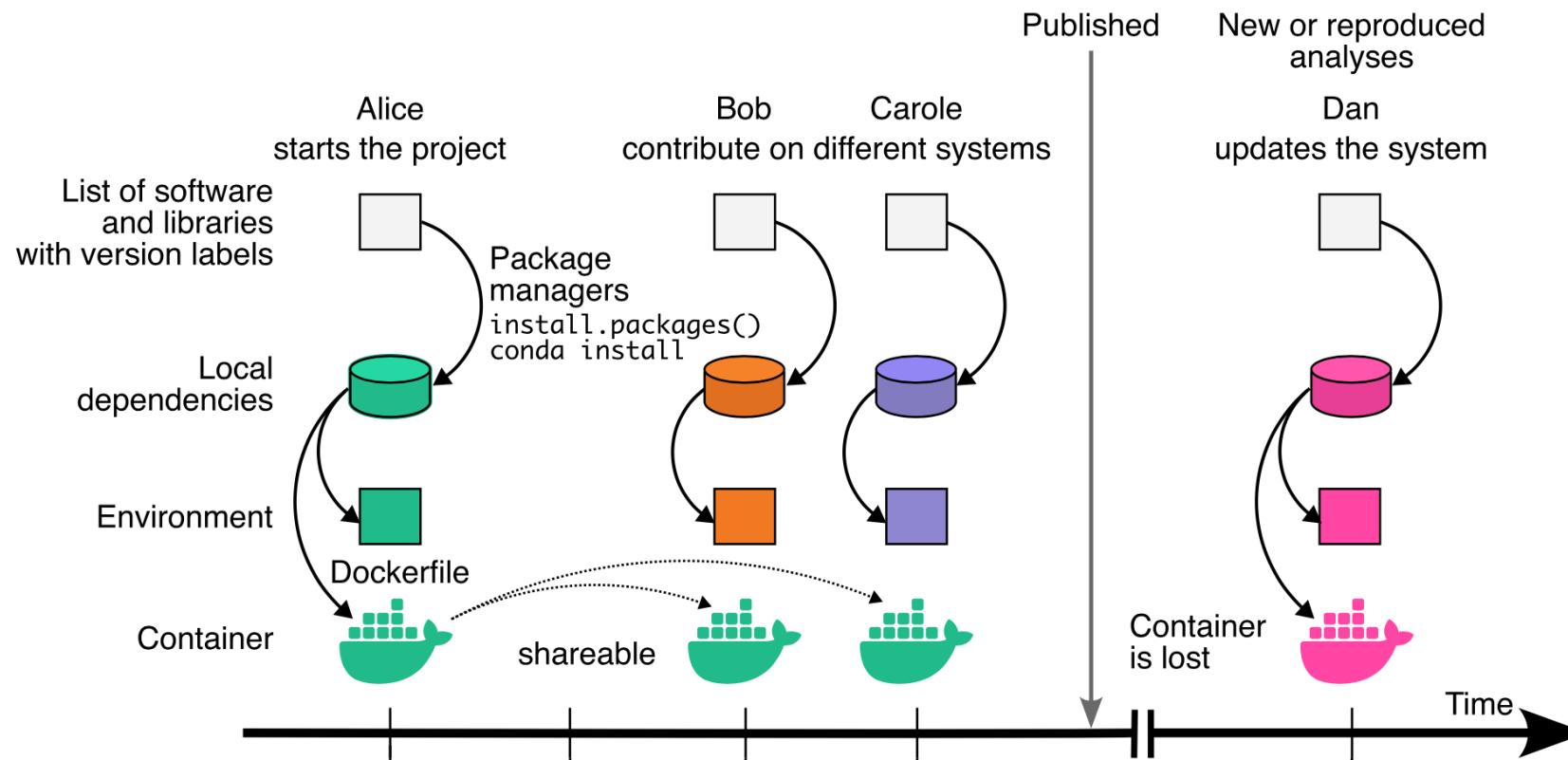
# Containers are not enough



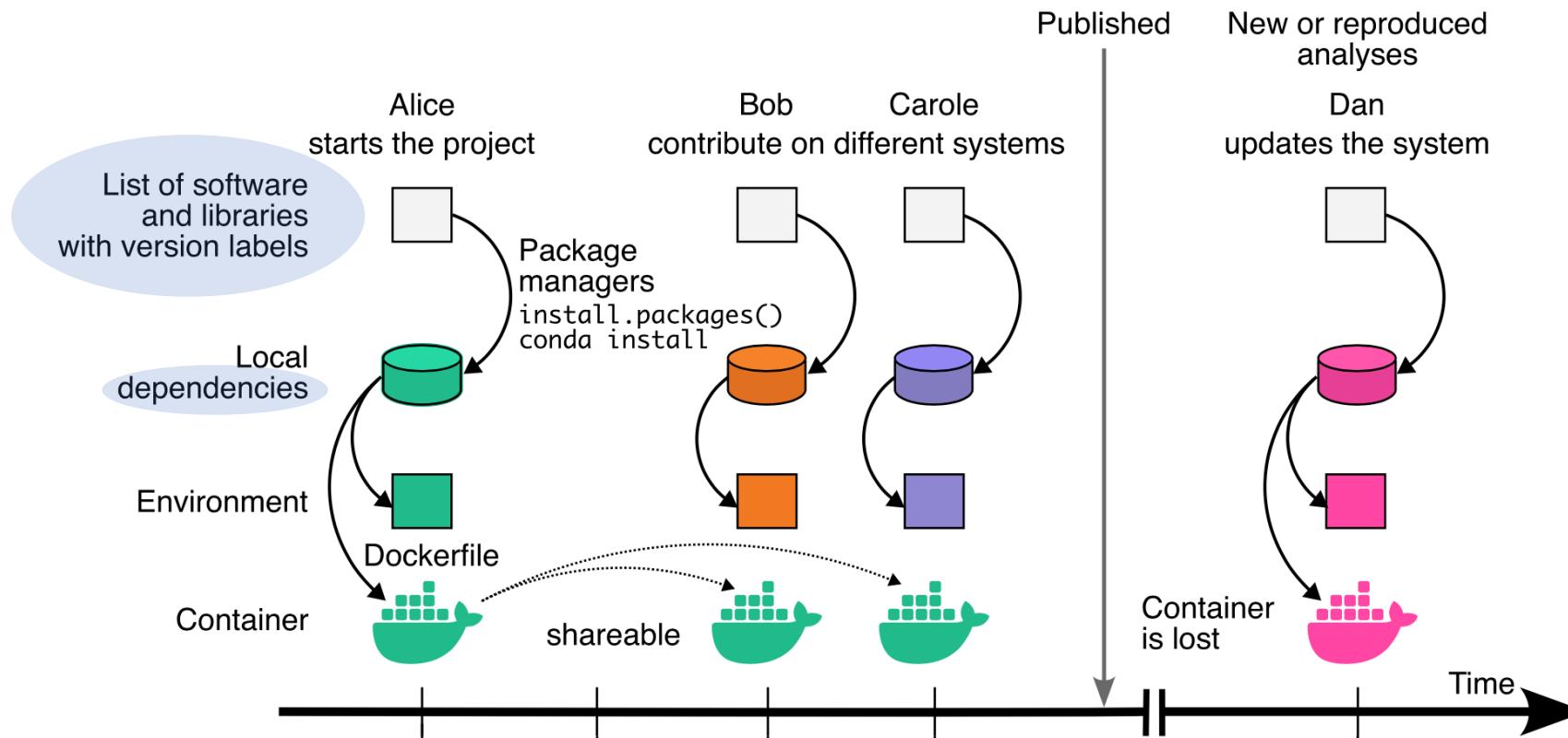
# Containers are not enough



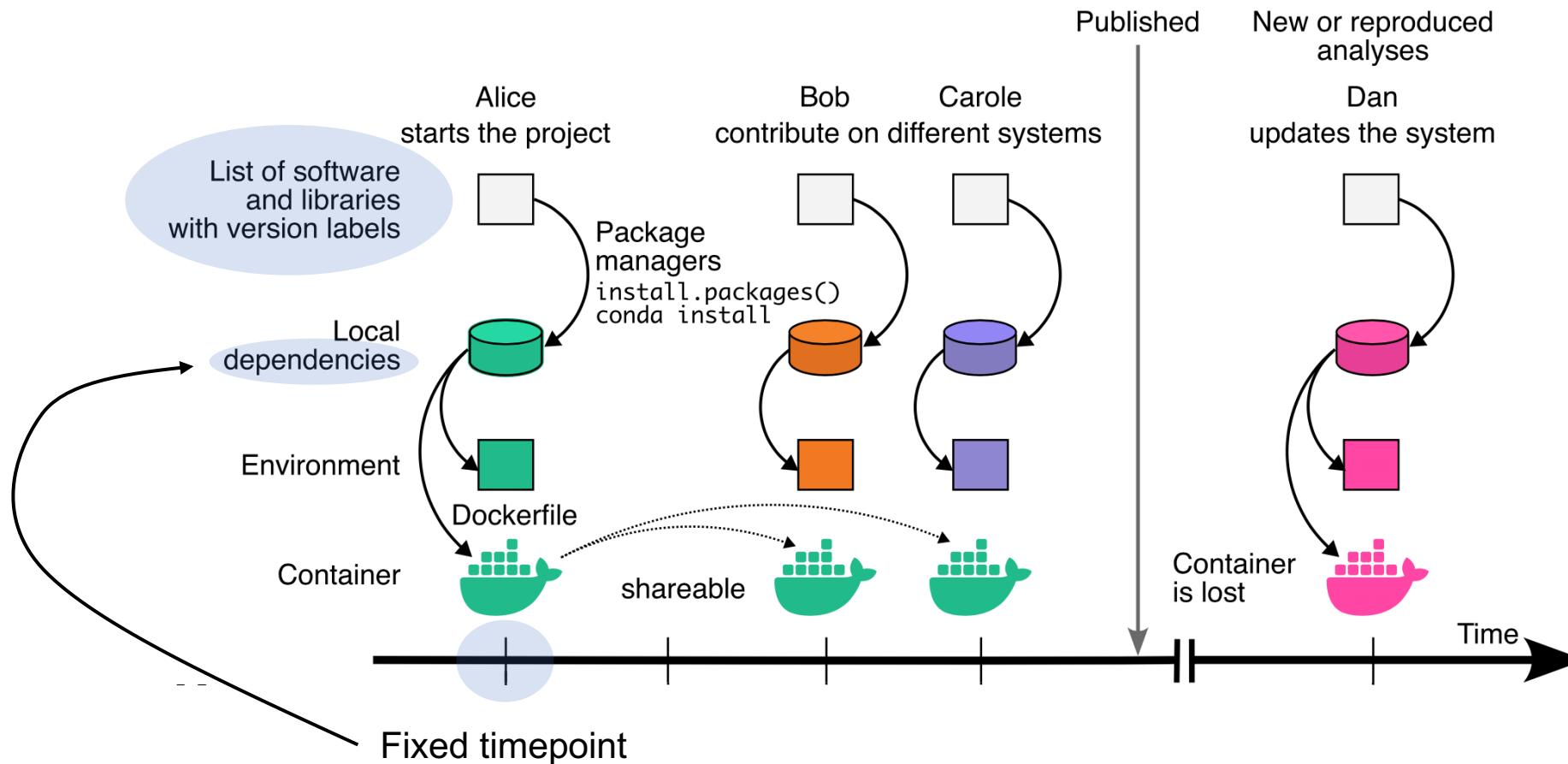
# Minimum required data to reproduce an environment



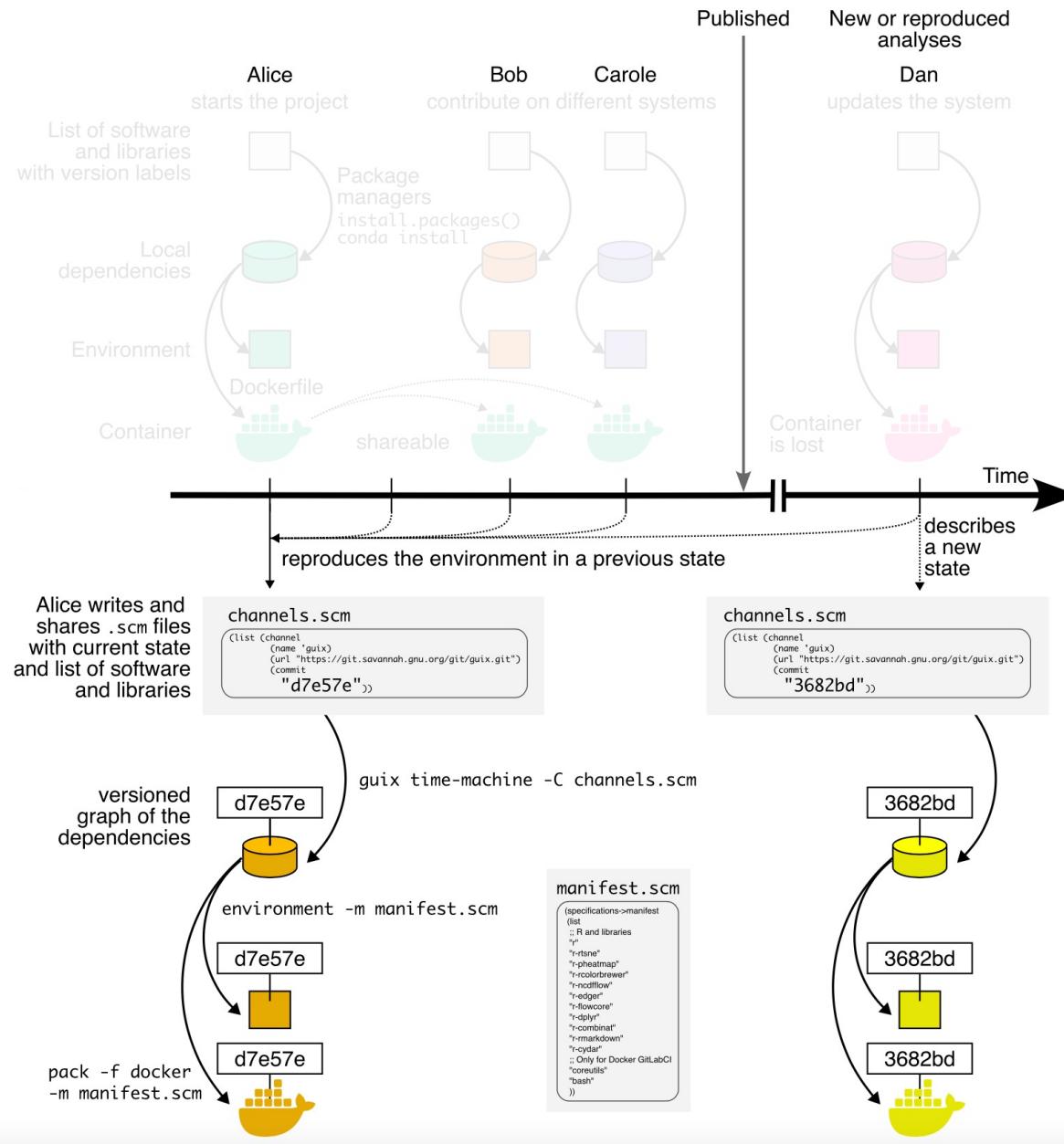
# Minimum required data to reproduce an environment



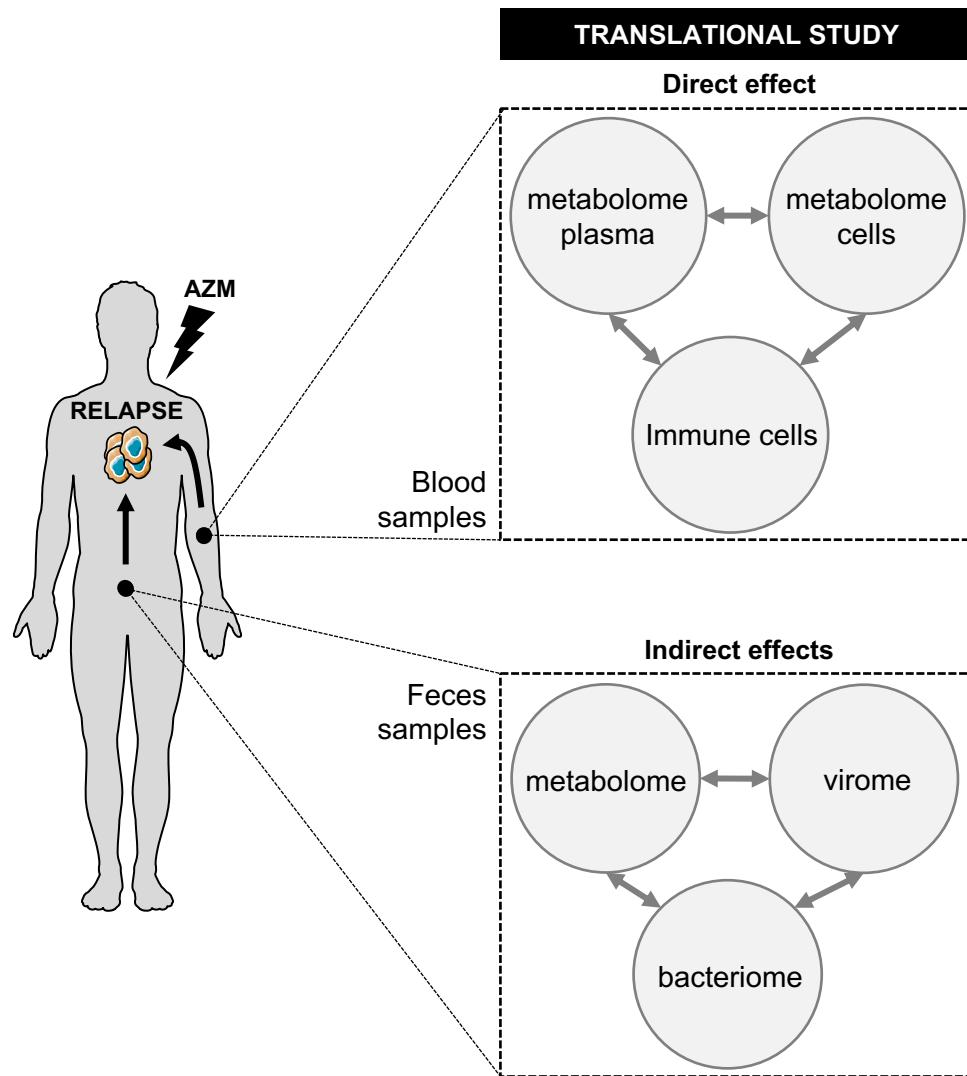
# Minimum required data to reproduce an environment



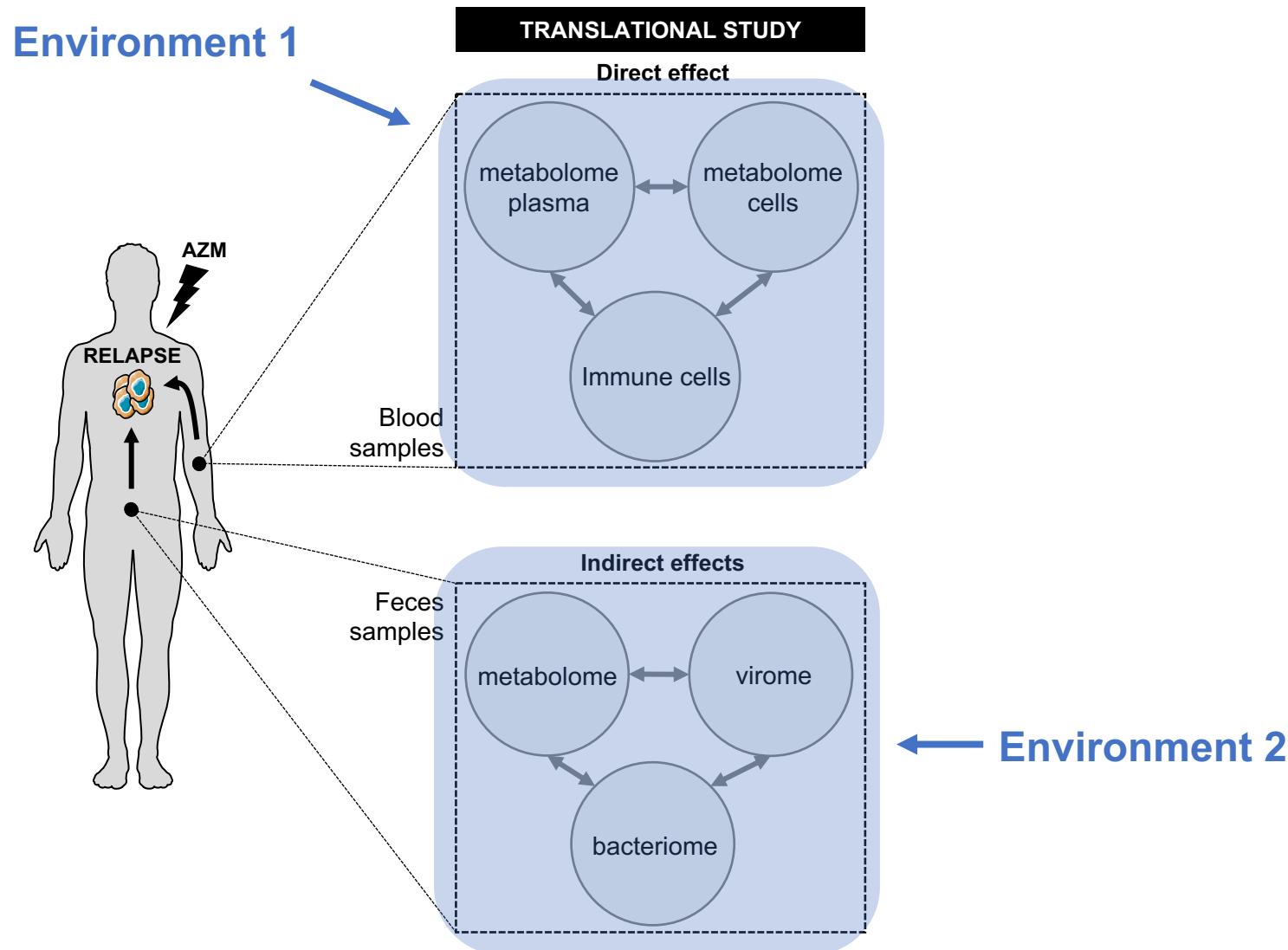
# Using Guix to save, share and reproduce the environment



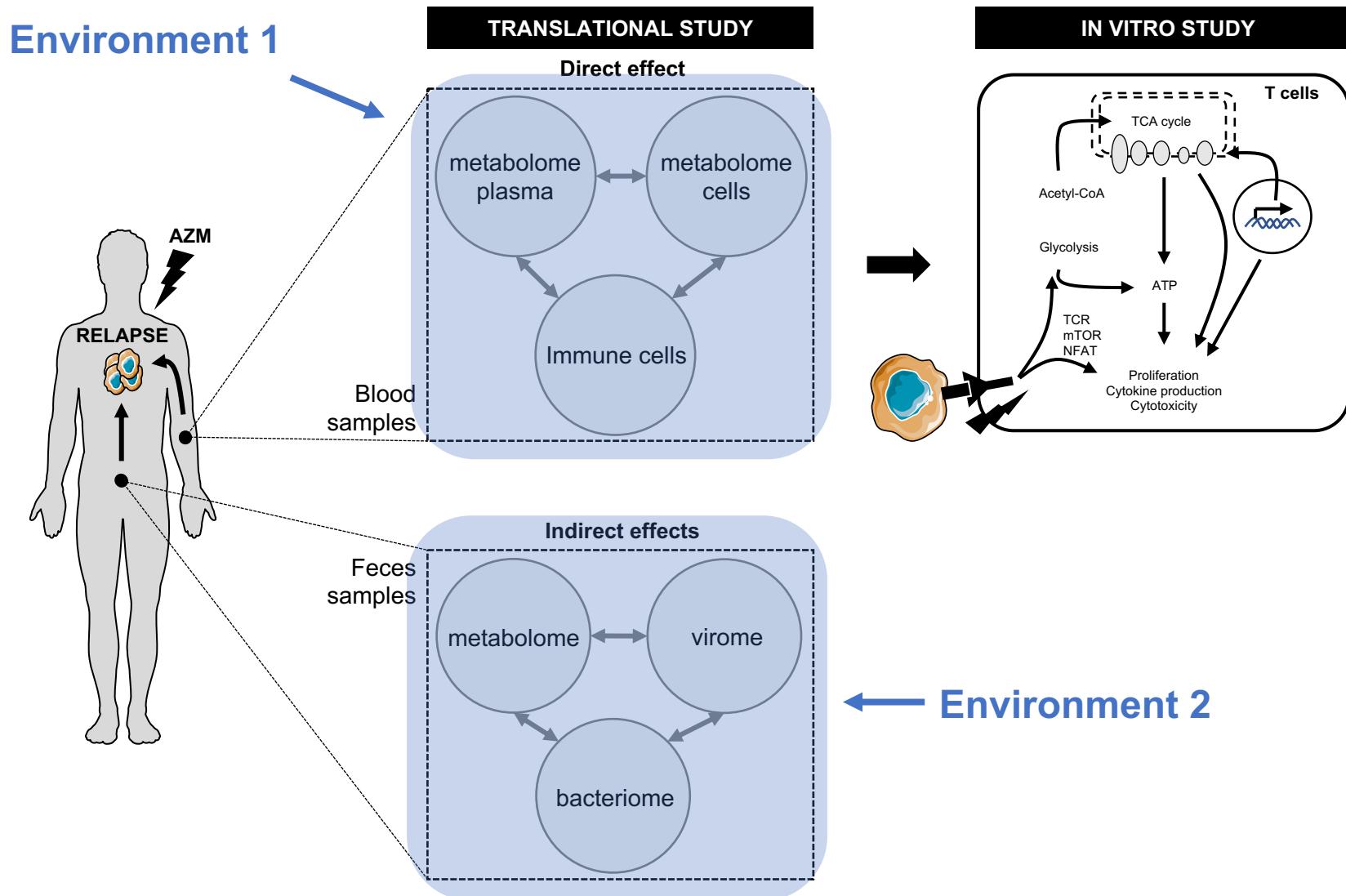
# Guix in our workflow



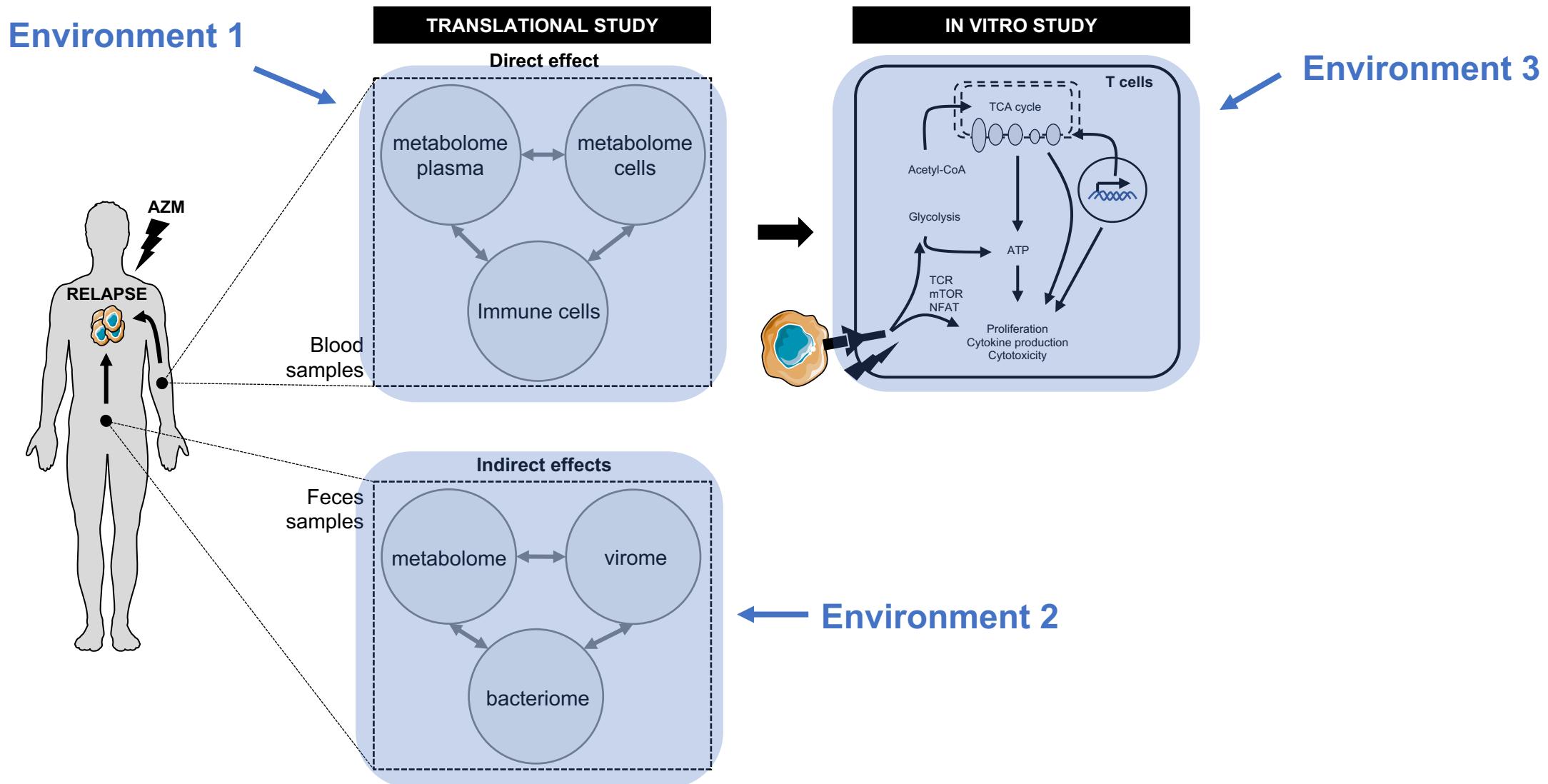
# Guix in our workflow



# Guix in our workflow



# Guix in our workflow



# Guix config directories in Git repositories

<https://gitlab.com/nivall/azimutfeces>  
<https://gitlab.com/nivall/azimut-in-vitro>  
<https://gitlab.com/nivall/azimut-blood>

master azimutfeces / guixconfig

Historique Rechercher un fichier

Nom	Dernière validation	Dernier
..		
my-pkgs	coda4microbiome added to guixconfig	
README.md	Add README files	
channels.scm	Updated Guix configuration	
manifest.scm	Added new packages (WIP)	
runguix.sh	first config guix for reproducibility \o/	
README.md		

## GUIX configuration

This folder contains all files necessary to generate the environment from GUIX See : <https://hpc.guix.info/> and <https://guix.gnu.org/>

- channels.scm : gets the commit number to get reproducible versions of the environment
- manifest.scm : gets the packages stored in GUIX
- my-pkgs.scm : gets the packges with reproducible versions that are not stored in GUIX

Run either the runguix.sh file or use the commande line below to load the environment

```
guix time-machine -C channels.scm -- environment -m manifest.scm -- R
```

Modifier

channels.scm 617 o

```
1 ;; This file point to the Guix channel.
2 (list (channel
3   (name 'guix)
4   (url "https://git.savannah.gnu.org/git/guix.git")))
```

manifest.scm 496 o

```
1 (specifications->manifest avannah.gnu.org/git/guix.git")
2 (list
3   ;;= upstream packages
4   "r"
5   "r-tidyverse"
6   "r-vegan"
7   "r-factoextra"
8   "r-ggplot2"
9   "r-cowplot"
10  "r-ggrepel"
11  "r-factominer"
12  "r-rstatix"
13  "r-rcolorbrewer"
14  "r-ape"
15  "r-phyloseq"
16  "r-complexheatmap"
17  "r-ggraph"
18  "r-igraph"
19  "r-cmprsk"
20  "r-prodlim"
21  "r-survminer"
22  "r-vennDiagram"
23  "r-viridis"
24  "r-nnet"
25  ;;= defined in my-pkgs
26  "r-khroma"
27  "r-ggalt"
28  "r-gtsummary"
29  "r-gt"
30  "r-visnetwork"
31  "r-riskregression"
32  "r-coda4microbiome"
33  ))
34
```

my-pkgs.scm 17.86 Kio

```
1 (define-module (my-pkgs)
2   #:use-module ((guix licenses) #:prefix license:)
3   #:use-module (gnu packages statistics)
4   #:use-module (gnu packages gcc)
5   #:use-module (gnu packages bioconductor)
6   #:use-module (gnu packages bioinformatics)
7   #:use-module (gnu packages cran)
8   #:use-module (gnu packages commencement)
9   #:use-module ((gnu packages compression) #:prefix compression:)
10  #:use-module (gnu packages geo)
11  #:use-module (gnu packages guile)
12  #:use-module (gnu packages pkg-config)
13  #:use-module (guix git-download)
14  #:use-module (guix packages)
15  #:use-module (guix build-system r)
16  #:use-module (guix download)
17  #:use-module (guix licenses)
18  )
19
20  ;;= khroma
21  (define-public r-khroma
22    (let ((commit "c7eaf45d5127a3807e3bc7a648dd463d27030361") (revision "1"))
23      (package
24        (name "r-khroma")
25        (version (git-version "1.9.0.9000" revision commit))
26        (source
27          (origin
28            (method git-fetch)
29            (uri (git-reference
30              (url "https://github.com/tesselle/khroma")
```

# Guix in our research papers

Data and code sharing: Raw data are available in the following public repositories: (1) mass cytometry: FlowRepository FR-FCM-Z5ZB and FR-FCM-Z5L7; (2) metabolomic: Metabolights MTBLS406; (3) single-cell RNA sequencing: GEO GSE197658 and GSE208399. Analysis pipelines are available in a Git repository: <https://gitlab.com/nivall/azimut-blood>; <https://gitlab.com/nivall/azimut-in-vitro>; <https://gitlab.com/nivall/azimutscma>.

## Computational environment

`manifest.scm` and `channels.scm` files are available in `guixconfig` directories of each git repositories to reproduce computational environment of FlowSOM clustering and single cell RNA sequencing analyses with GNU Guix (guix.gnu.org). Software: Manuscript figures were created from R outputs and combined with Inkscape (version 1.1.1) on macOS (version 11.5.1).

Vallet et al. Blood. 2022

Git repositories version at submission time are archived on Software Heritage

- (i) <https://archive.softwareheritage.org/swh:1:dir:16a829f98f9d8d707343b3b48bc13f5d641998d9>,
- (ii) <https://archive.softwareheritage.org/swh:1:dir:cc8aec0e0c85d7ea70979581e766353d3e2fec22>,
- (iii) <https://archive.softwareheritage.org/swh:1:dir:68ec62f3d8f0cc9f42a15449f75844df12f65934>

## Data and code availability

Raw data are available on a public repository: (i) metabolomic, Metabolights: MTBLS406; (ii) bacteriome, Bioproject: PRJNA902819; (iii) virome, Bioproject: PRJNA898682. Source codes, data and CSV files of interim analyses are available on the following Git repositories: <https://gitlab.com/nivall/azimutfeces>. Git repositories version at submission time are archived on Software Heritage: <https://archive.softwareheritage.org/swh:1:dir:9a24ab367cbe9519007f0dd407423fe47def5cfa>. Unless otherwise specified, data analyses were computed using R environment. Raw figures were made with the “ggplot2” R package. Computational environment may be reproduced using GNU Guix with the files “manifest.scm” and “channels.scm” in “guixconfig” directory of the git repository.<sup>86</sup> Manuscript figures were created from R outputs and combined with Inkscape (version 1.2.1) on macOS (version 12.5).

Vallet et al. Cell Host Microbe. 2023

# Guix in our research papers

Data and code sharing: Raw data are available in the following public repositories: (1) mass cytometry: FlowRepository FR-FCM-Z5ZB and FR-FCM-Z5L7; (2) metabolomic: Metabolights MTBLS406; (3) single-cell RNA sequencing: GEO GSE197658 and GSE208399. Analysis pipelines are available in a Git repository: <https://gitlab.com/nivall/azimut-blood>; <https://gitlab.com/nivall/azimut-in-vitro>; <https://gitlab.com/nivall/azimutscma>.

## Computational environment

`manifest.scm` and `channels.scm` files are available in `guixconfig` directories of each git repositories to reproduce computational environment of FlowSOM clustering and single cell RNA sequencing analyses with GNU Guix (guix.gnu.org). Software: Manuscript figures were created from R outputs and combined with Inkscape (version 1.1.1) on macOS (version 11.5.1).

Vallet et al. Blood. 2022

Git repositories version at submission time are archived on Software Heritage

- (i) <https://archive.softwareheritage.org/swh:1:dir:16a829f98f9d8d707343b3b48bc13f5d641998d9>,
- (ii) <https://archive.softwareheritage.org/swh:1:dir:cc8aec0e0c85d7ea70979581e766353d3e2fec22>,
- (iii) <https://archive.softwareheritage.org/swh:1:dir:68ec62f3d8f0cc9f42a15449f75844df12f65934>

## Data and code availability

Raw data are available on a public repository: (i) metabolomic, Metabolights: MTBLS406; (ii) bacteriome, Bioproject: PRJNA902819; (iii) virome, Bioproject: PRJNA898682. Source codes, data and CSV files of interim analyses are available on the following Git repositories: <https://gitlab.com/nivall/azimutfeces>. Git repositories version at submission time are archived on Software Heritage: <https://archive.softwareheritage.org/swh:1:dir:9a24ab367cbe9519007f0dd407423fe47def5cfa>. Unless otherwise specified, data analyses were computed using R environment. Raw figures were made with the “ggplot2” R package. Computational environment may be reproduced using GNU Guix with the files “manifest.scm” and “channels.scm” in “guixconfig” directory of the git repository.<sup>86</sup> Manuscript figures were created from R outputs and combined with Inkscape (version 1.2.1) on macOS (version 12.5).

Vallet et al. Cell Host Microbe. 2023

# Guix in our research papers

Data and code sharing: Raw data are available in the following public repositories: (1) mass cytometry: FlowRepository FR-FCM-Z5ZB and FR-FCM-Z5L7; (2) metabolomic: Metabolights MTBLS406; (3) single-cell RNA sequencing: GEO GSE197658 and GSE208399. Analysis pipelines are available in a Git repository: <https://gitlab.com/nivall/azimut-blood>; <https://gitlab.com/nivall/azimut-in-vitro>; <https://gitlab.com/nivall/azimutscrna>.

## Computational environment

`manifest.scm` and `channels.scm` files are available in `guixconfig` directories of each git repositories to reproduce computational environment of FlowSOM clustering and single cell RNA sequencing analyses with GNU Guix (guix.gnu.org). Software: Manuscript figures were created from R outputs and combined with Inkscape (version 1.1.1) on macOS (version 11.5.1).

Vallet et al. Blood. 2022

## Data and code availability

Raw data are available on a public repository: (i) metabolomic, Metabolights: MTBLS406; (ii) bacteriome, Bioproject: PRJNA902819; (iii) virome, Bioproject: PRJNA898682. Source codes, data and CSV files of interim analyses are available on the following Git repositories: <https://gitlab.com/nivall/azimutfeces>. Git repositories version at submission time are archived on Software Heritage: <https://archive.softwareheritage.org/swh:1:dir:9a24ab367cbe9519007f0dd407423fe47def5cfa>. Unless otherwise specified, data analyses were computed using R environment. Raw figures were made with the “ggplot2” R package. Computational environment may be reproduced using GNU Guix with the files “manifest.scm” and “channels.scm” in “guixconfig” directory of the git repository.<sup>86</sup> Manuscript figures were created from R outputs and combined with Inkscape (version 1.2.1) on macOS (version 12.5).

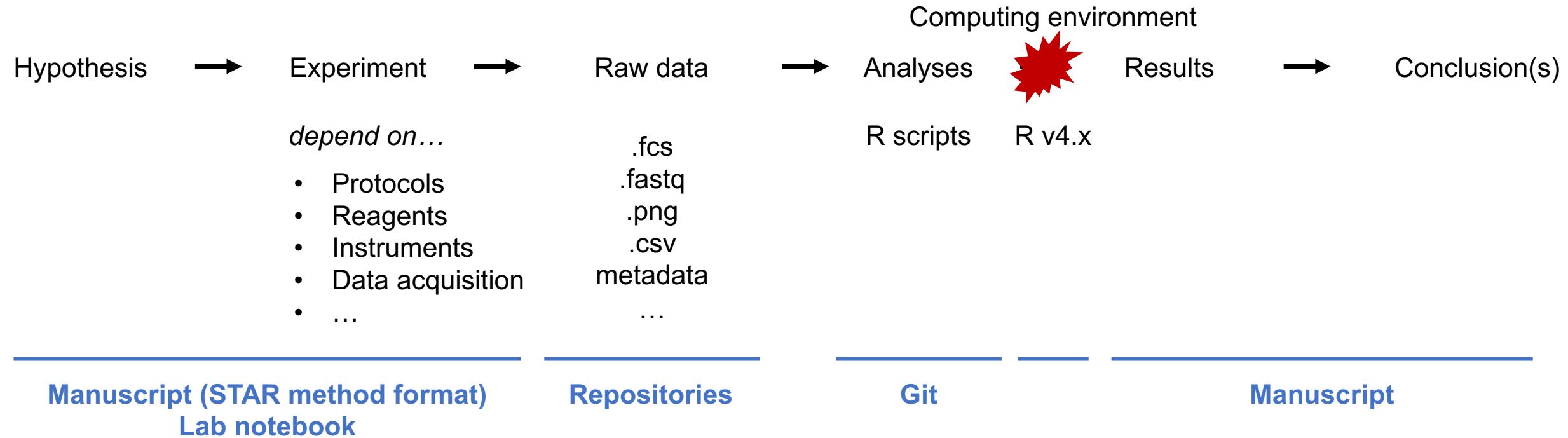
Vallet et al. Cell Host Microbe. 2023

## Long term preservation with Software Heritage

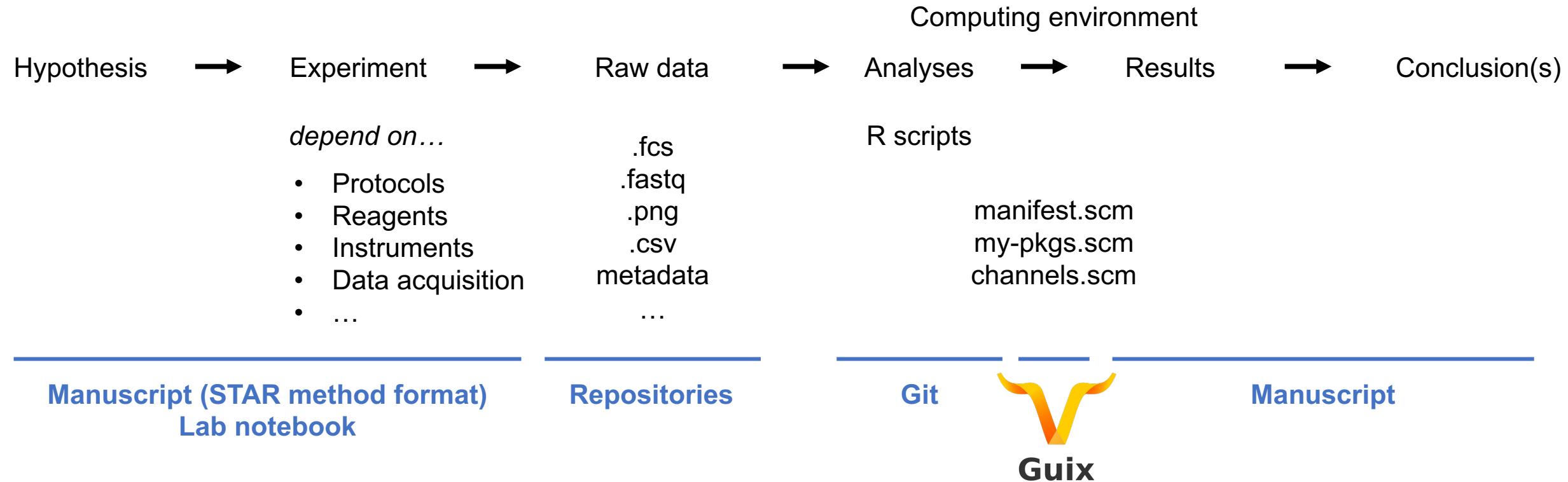
Git repositories version at submission time are archived on Software Heritage

- (i) <https://archive.softwareheritage.org/swh:1:dir:16a829f98f9d8d707343b3b48bc13f5d641998d9>,
- (ii) <https://archive.softwareheritage.org/swh:1:dir:cc8aec0e0c85d7ea70979581e766353d3e2fec22>,
- (iii) <https://archive.softwareheritage.org/swh:1:dir:68ec62f3d8f0cc9f42a15449f75844df12f65934>

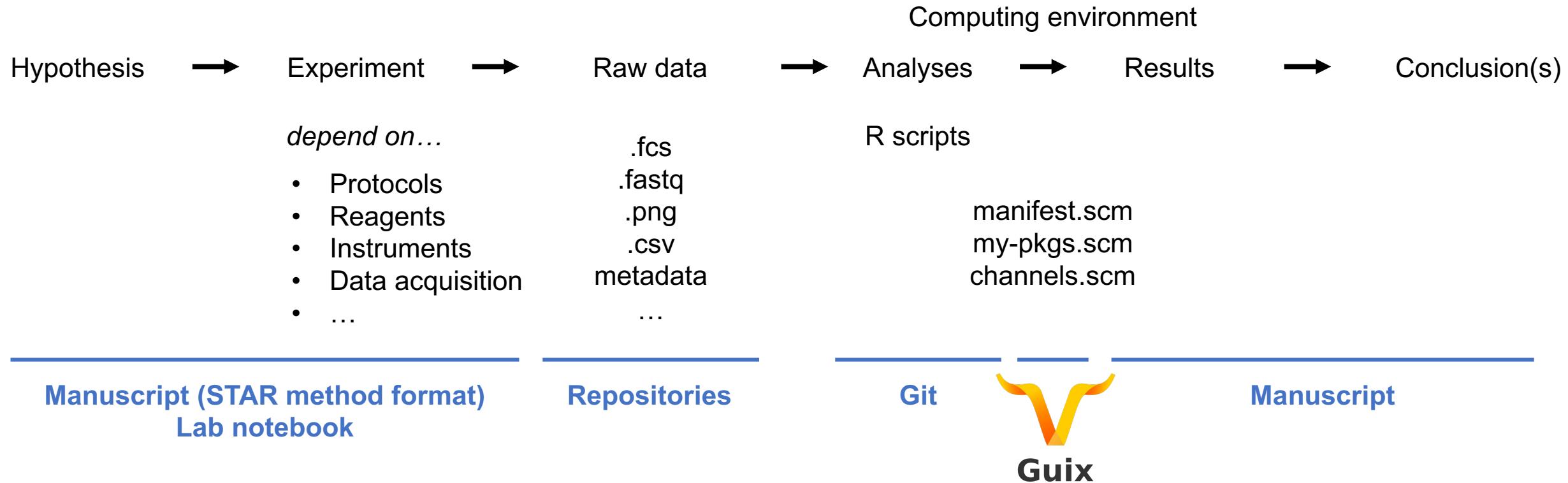
# Reproducibility planning from the beginning of the project



# Reproducibility planning from the beginning of the project

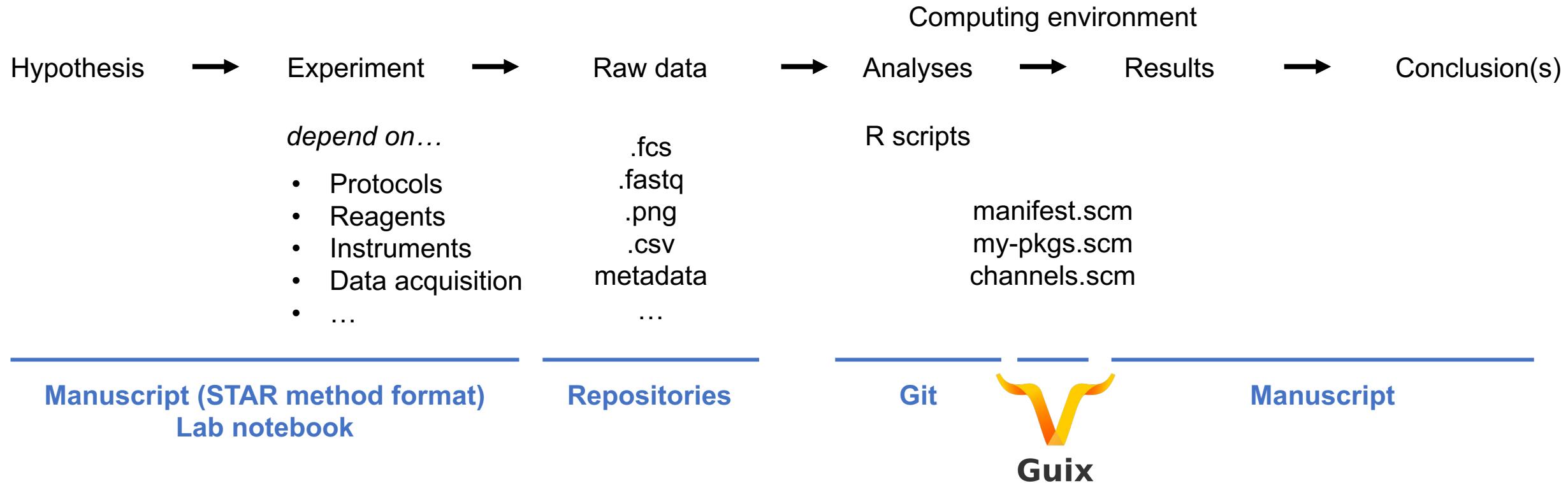


# Reproducibility planning from the beginning of the project



Will Guix effectively allow us to reproduce our analyses in the future?

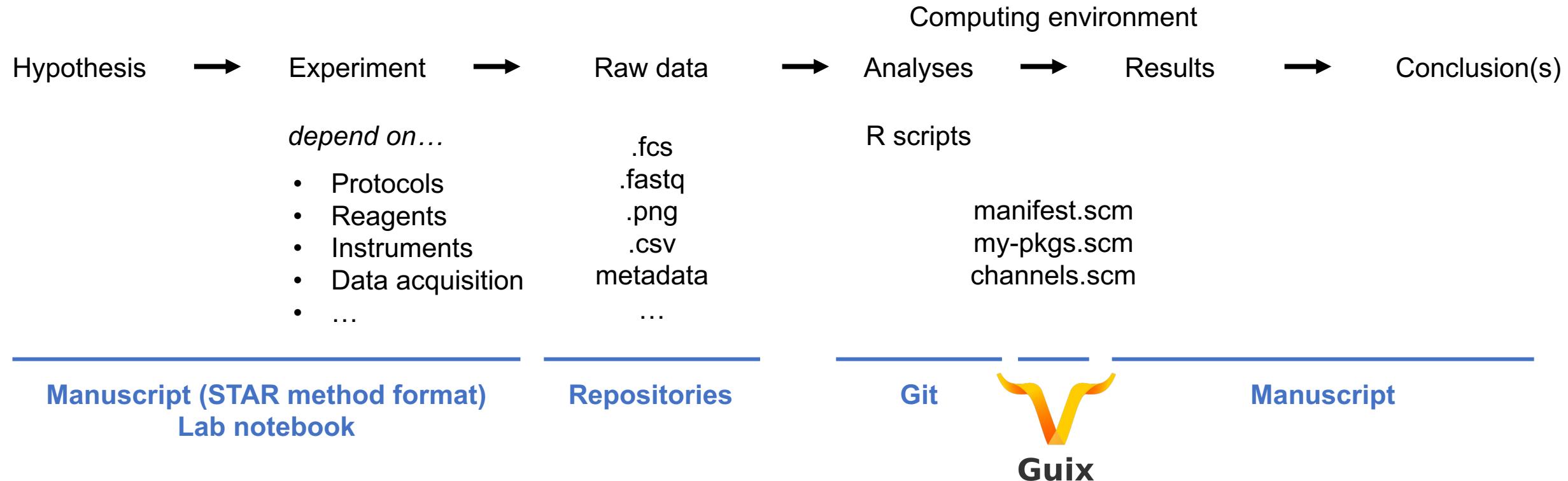
# Reproducibility planning from the beginning of the project



Will Guix effectively allow us to reproduce our analyses in the future?

Can we provide a proof of concept?

# Reproducibility planning from the beginning of the project



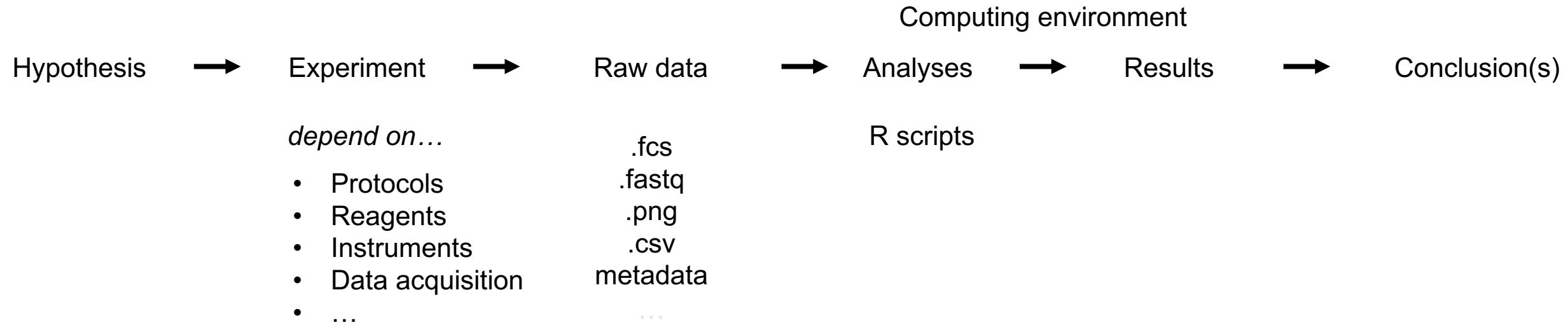
Will Guix effectively allow us to reproduce our analyses in the future?

Can we provide a proof of concept?

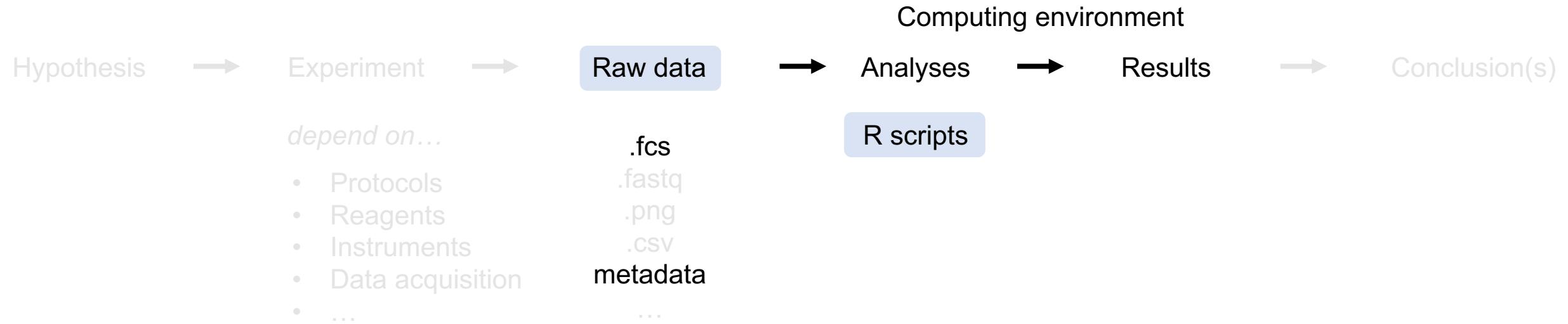
**Aim**

- Build an environment that can be deployed anywhere AND
- which reproduces analyses

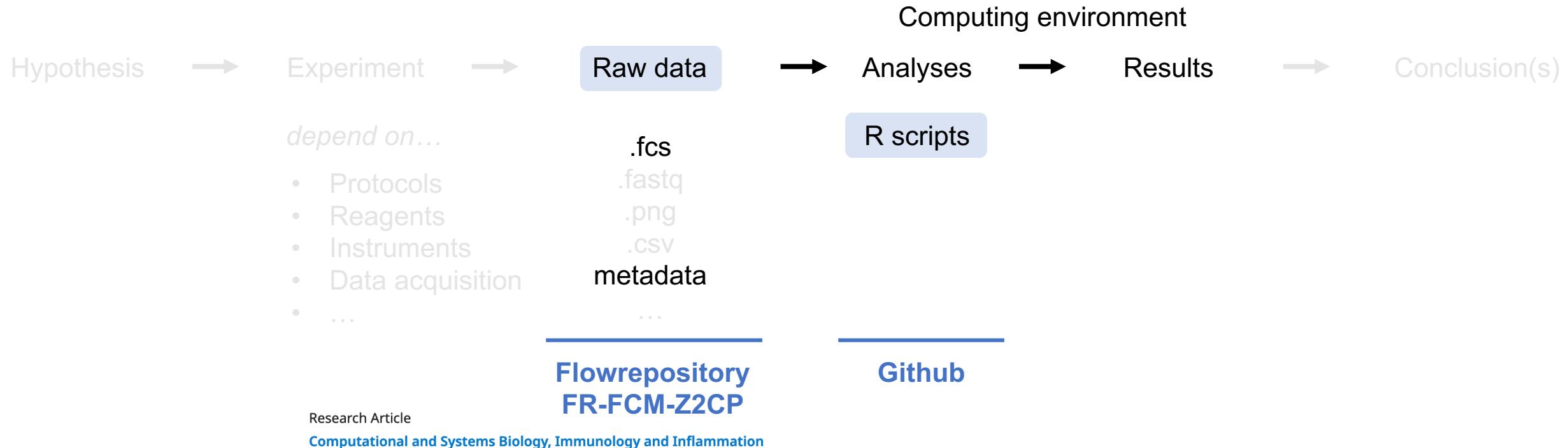
# Requirement to provide a proof of concept



# Requirement to provide a proof of concept



# Requirement to provide a proof of concept

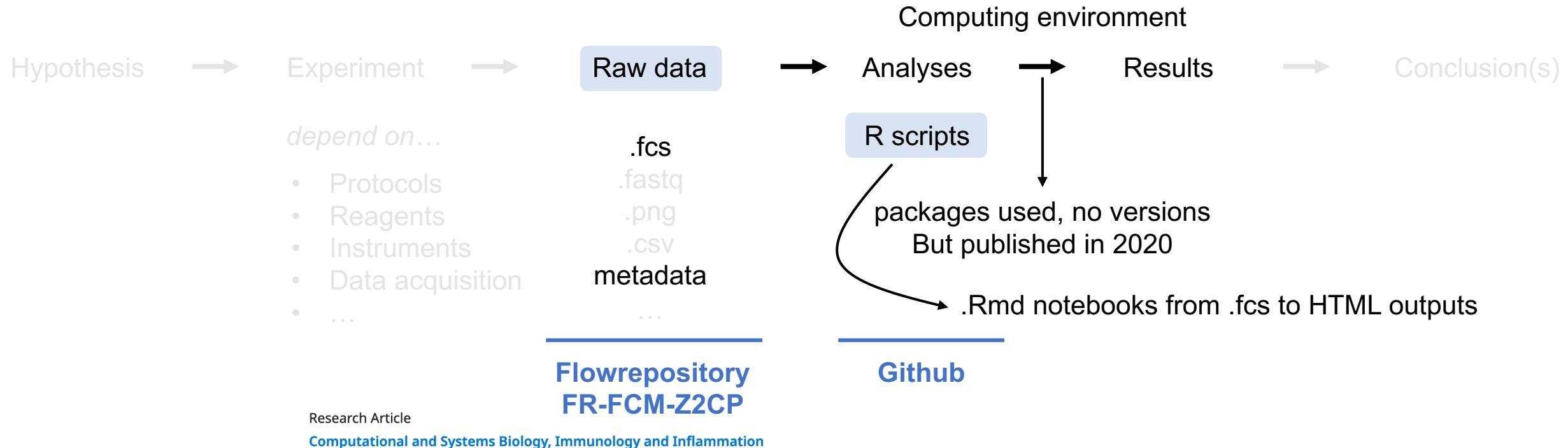


**Stimulation strength controls the rate of initiation but not the molecular organisation of TCR-induced signalling**

Claire Y Ma, John C Marioni , Gillian M Griffiths , Arianne C Richard 

Cambridge Institute for Medical Research, University of Cambridge, United Kingdom; Cancer Research UK Cambridge Institute, University of Cambridge, United Kingdom; EMBL-European Bioinformatics Institute, Wellcome Genome Campus, United Kingdom; Wellcome Sanger Institute, Wellcome Genome Campus, United Kingdom

# Requirement to provide a proof of concept



Research Article

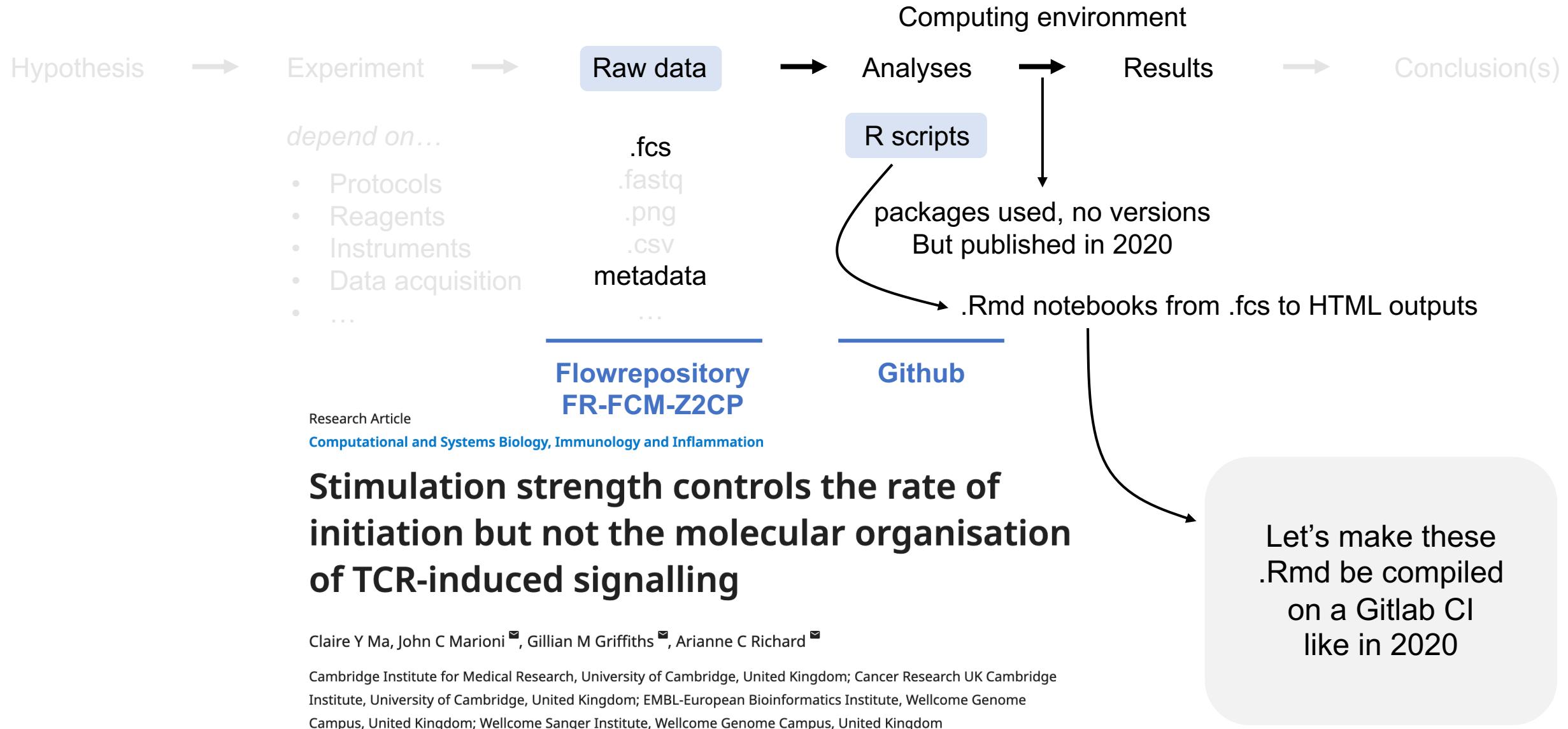
[Computational and Systems Biology, Immunology and Inflammation](#)

**Stimulation strength controls the rate of initiation but not the molecular organisation of TCR-induced signalling**

Claire Y Ma, John C Marioni □, Gillian M Griffiths □, Arianne C Richard □

Cambridge Institute for Medical Research, University of Cambridge, United Kingdom; Cancer Research UK Cambridge Institute, University of Cambridge, United Kingdom; EMBL-European Bioinformatics Institute, Wellcome Genome Campus, United Kingdom; Wellcome Sanger Institute, Wellcome Genome Campus, United Kingdom

# Requirement to provide a proof of concept



# Reproducing the analyzes

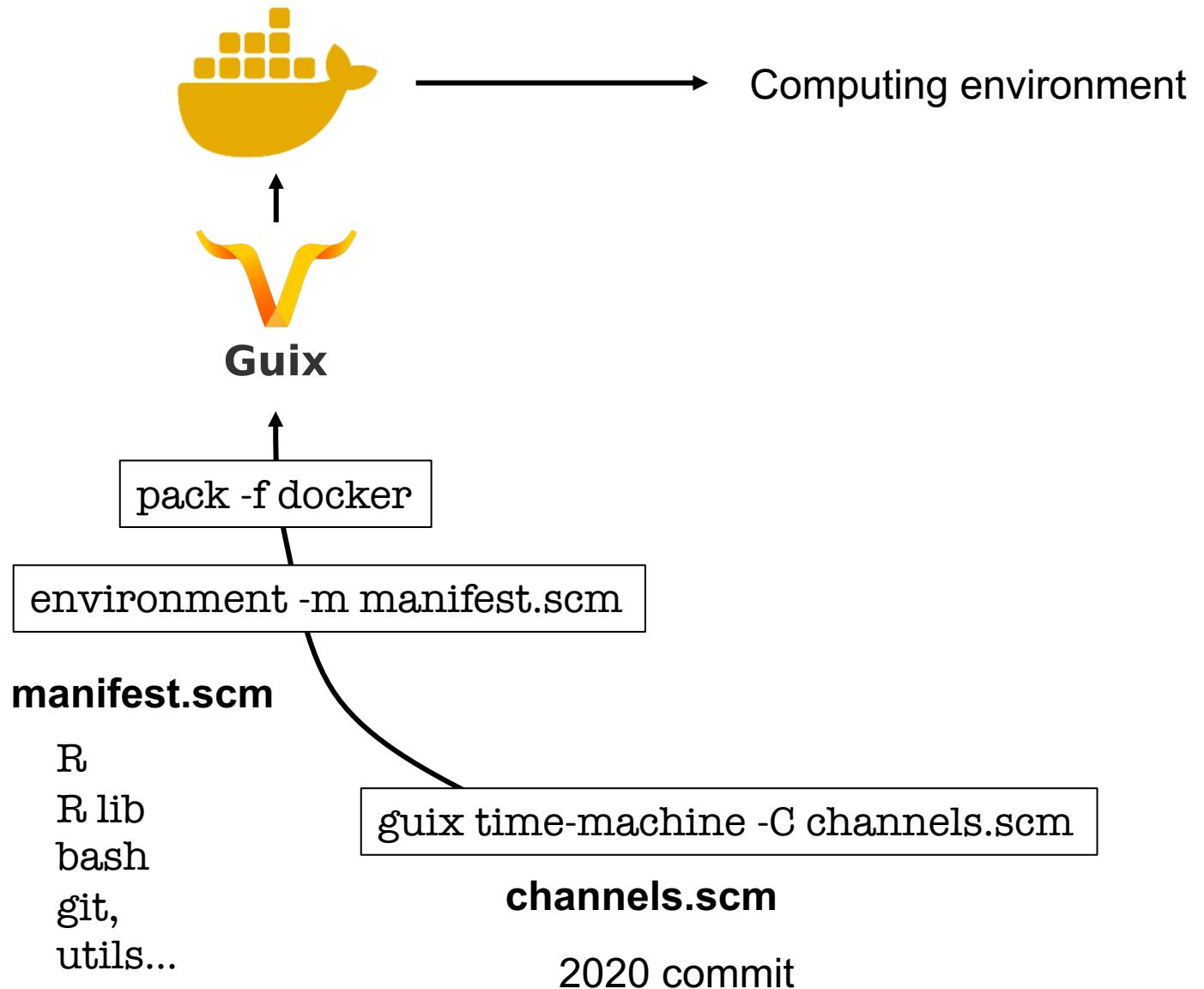
**manifest.scm**

R  
R lib  
bash  
git,  
utils...

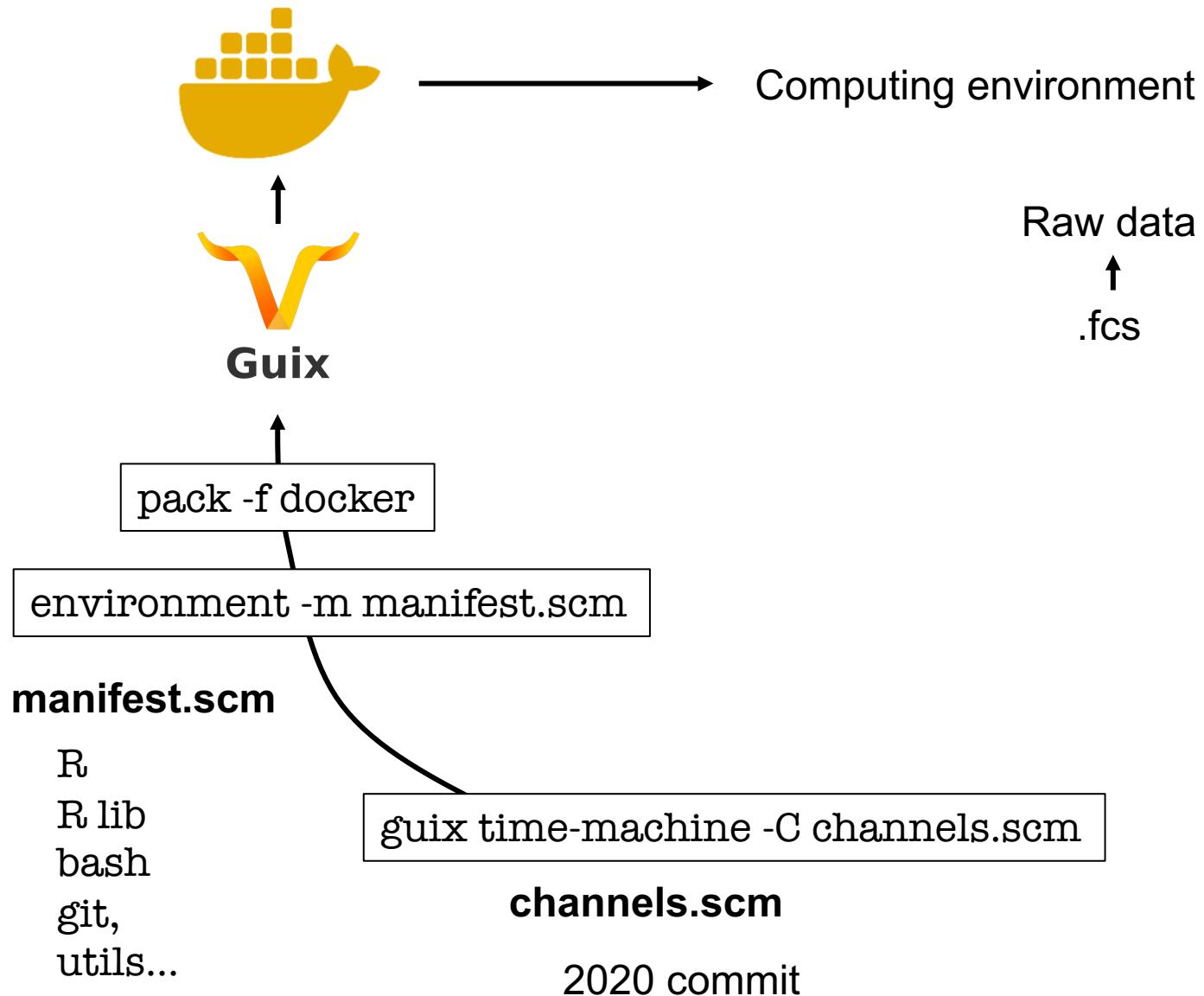
**channels.scm**  
2020 commit

<https://gitlab.com/nivall/guixreprodsci>  
Vallet N, Michonneau D, Tournier S Sci. Data 2022

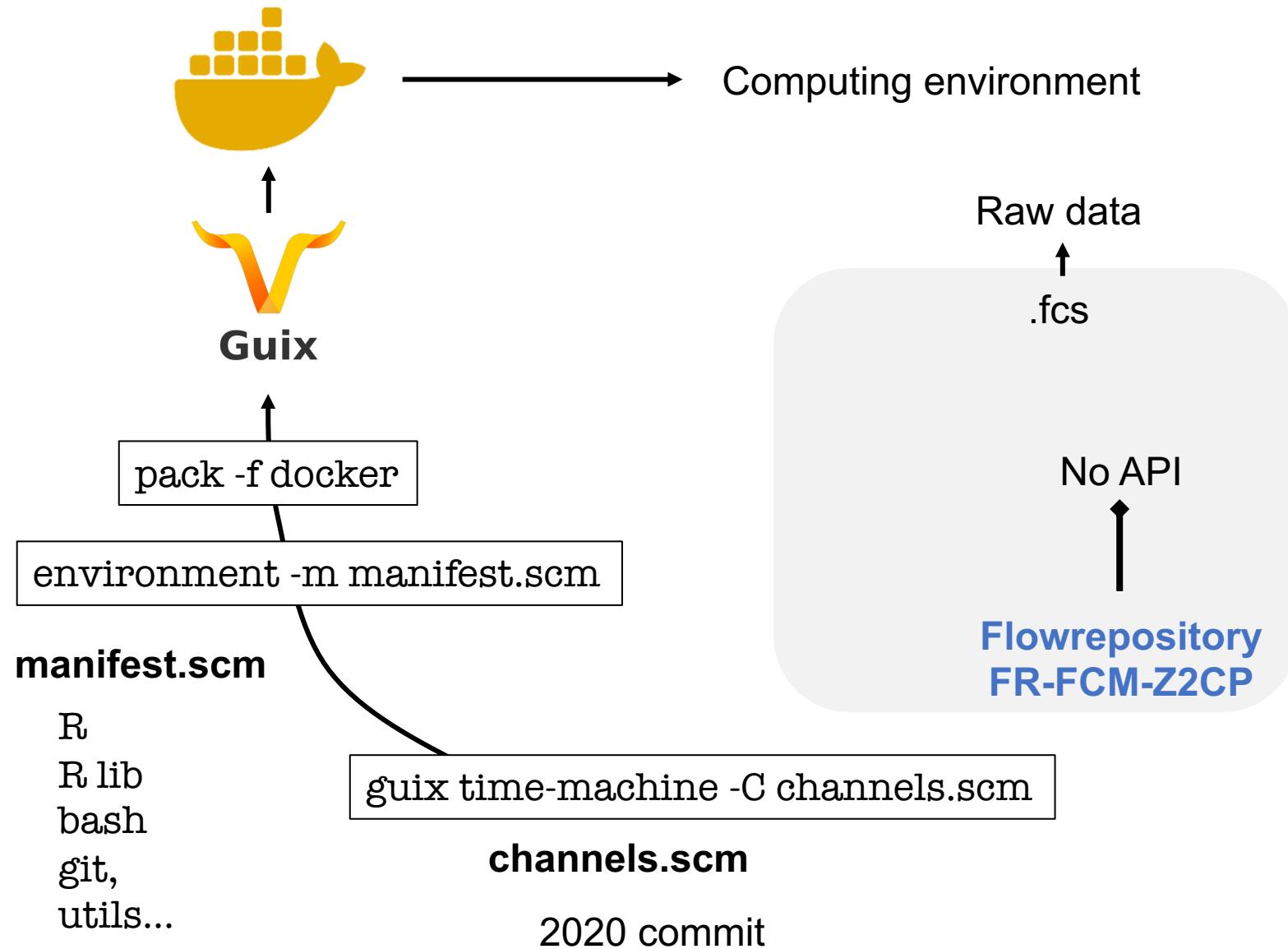
# Reproducing the analyzes



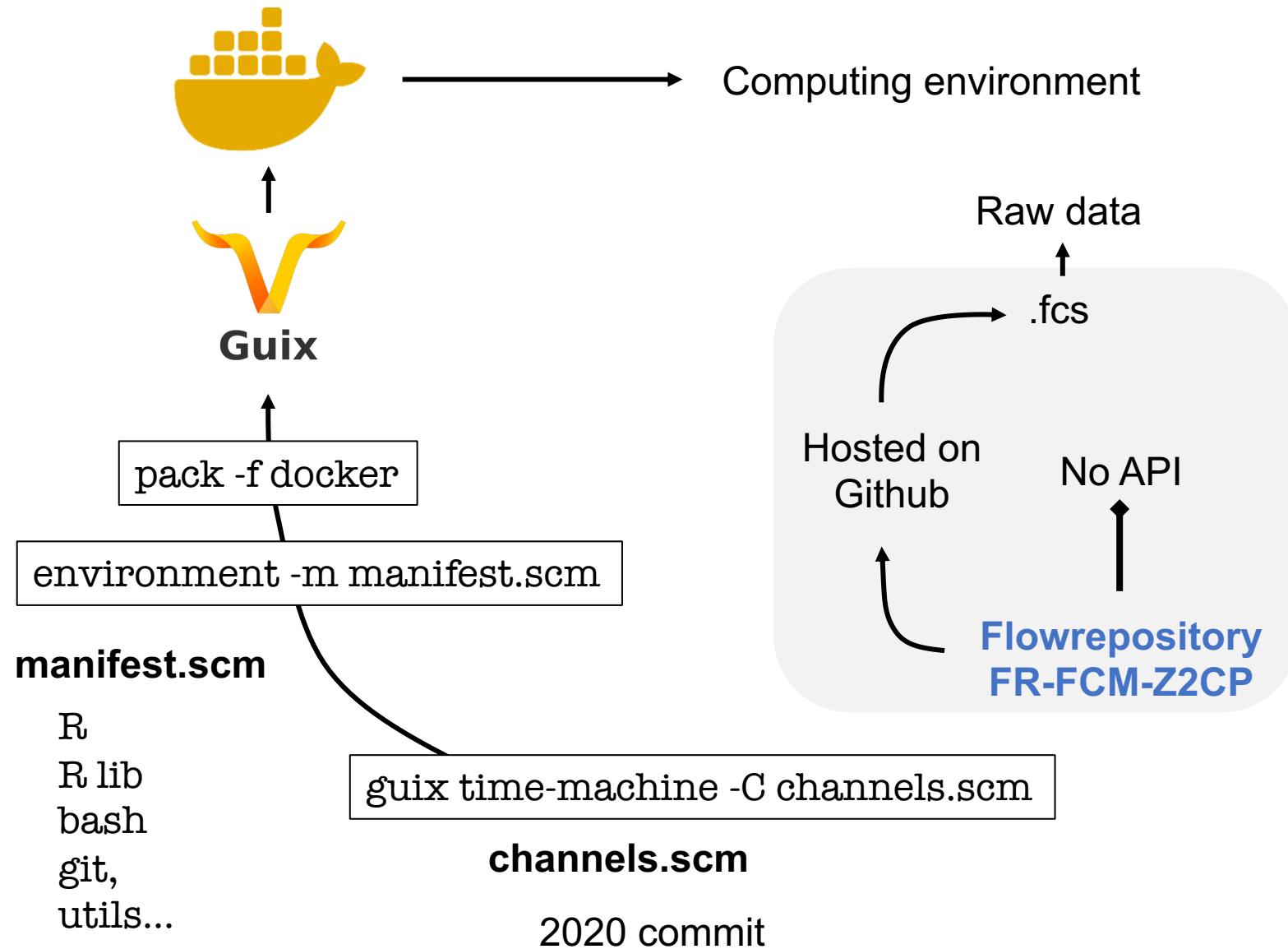
# Reproducing the analyzes



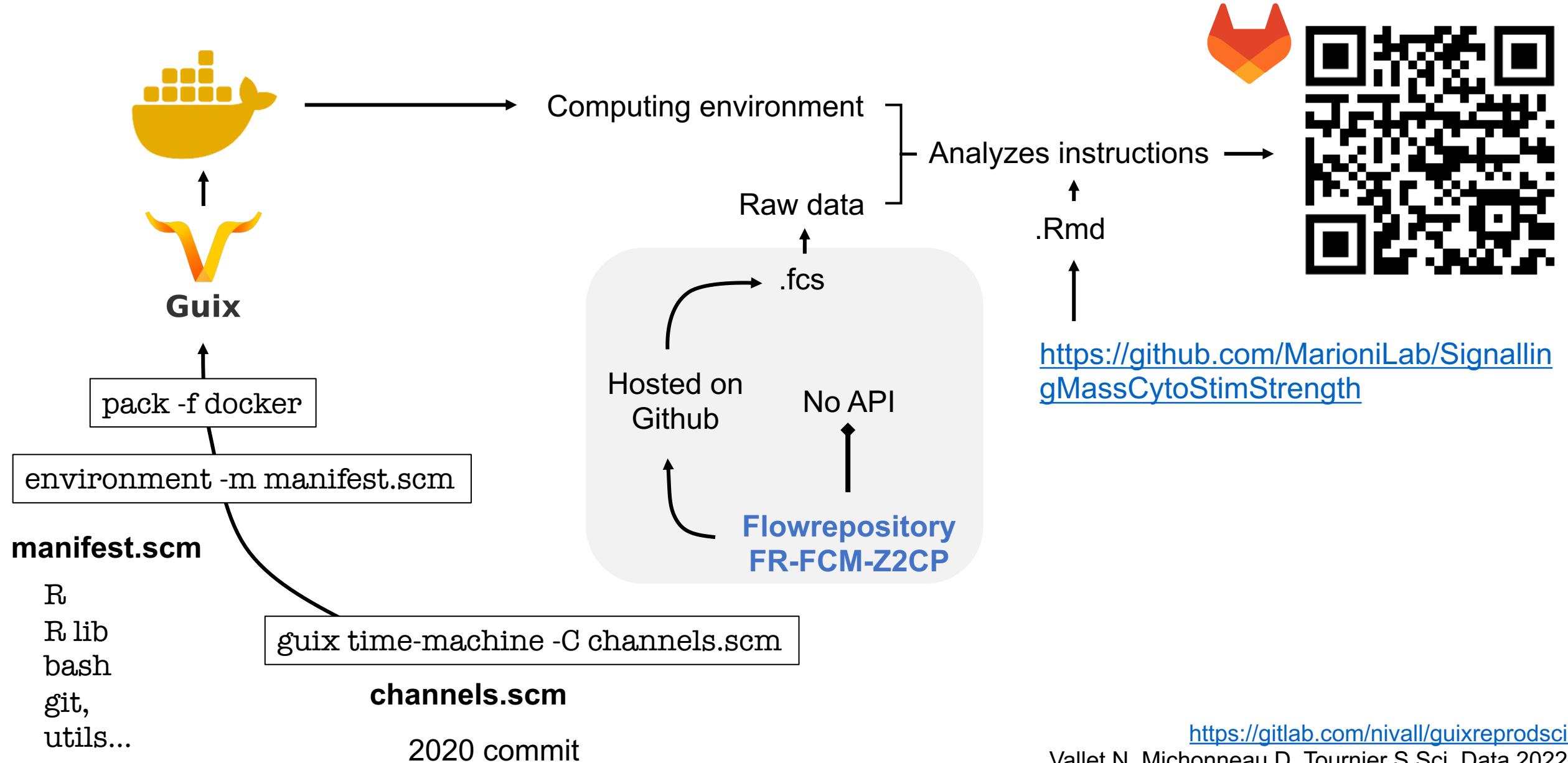
# Reproducing the analyzes



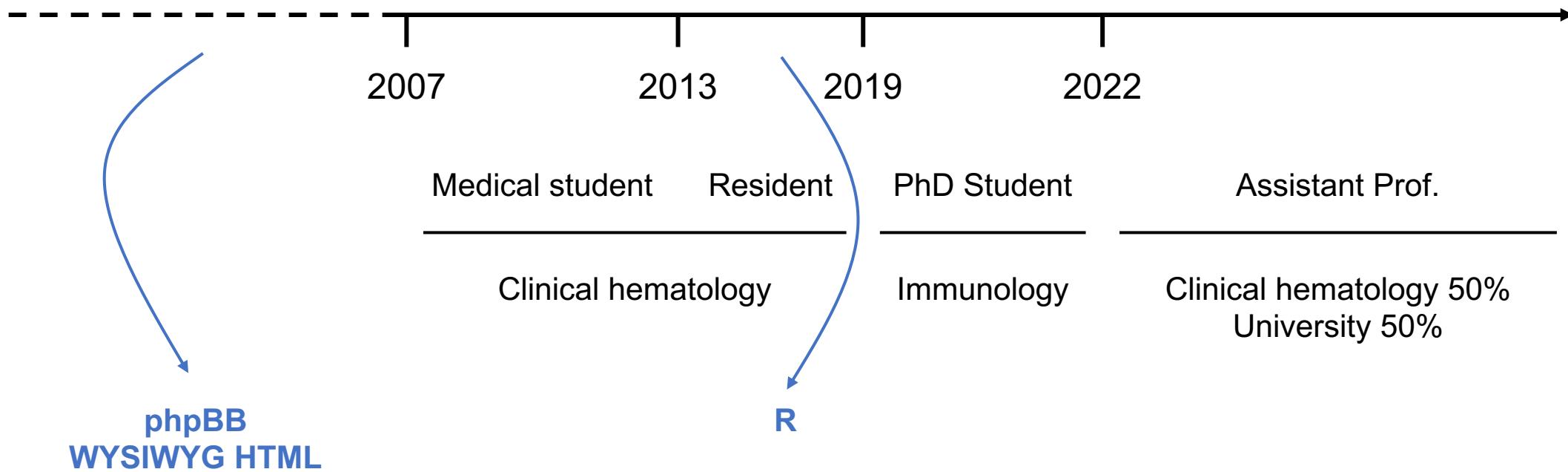
# Reproducing the analyzes



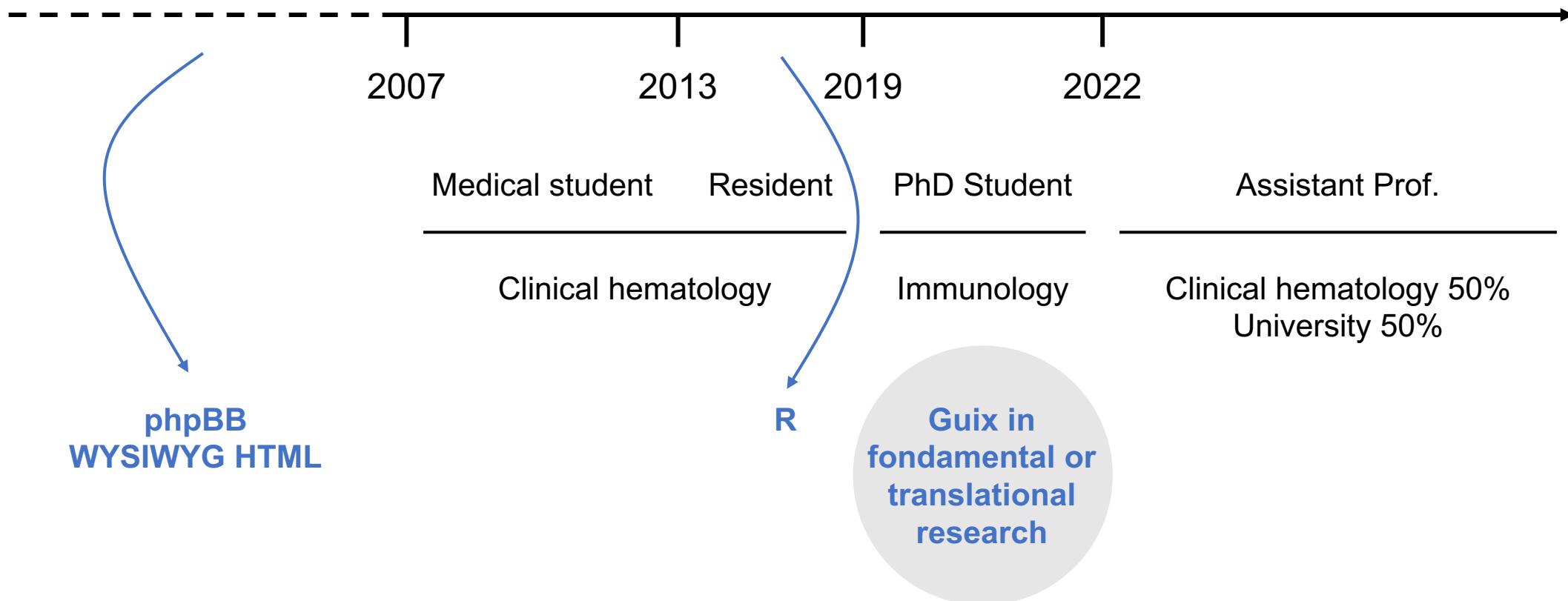
# Reproducing the analyzes



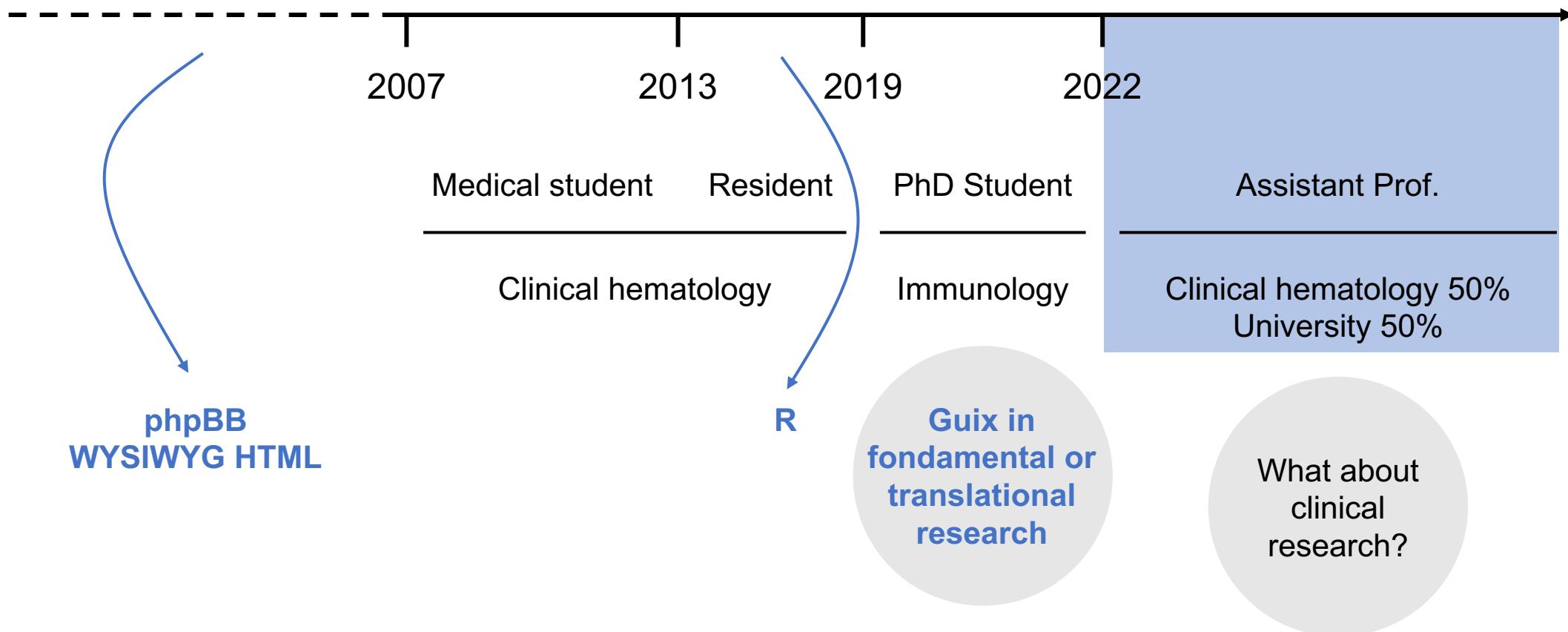
# The next step with clinical research



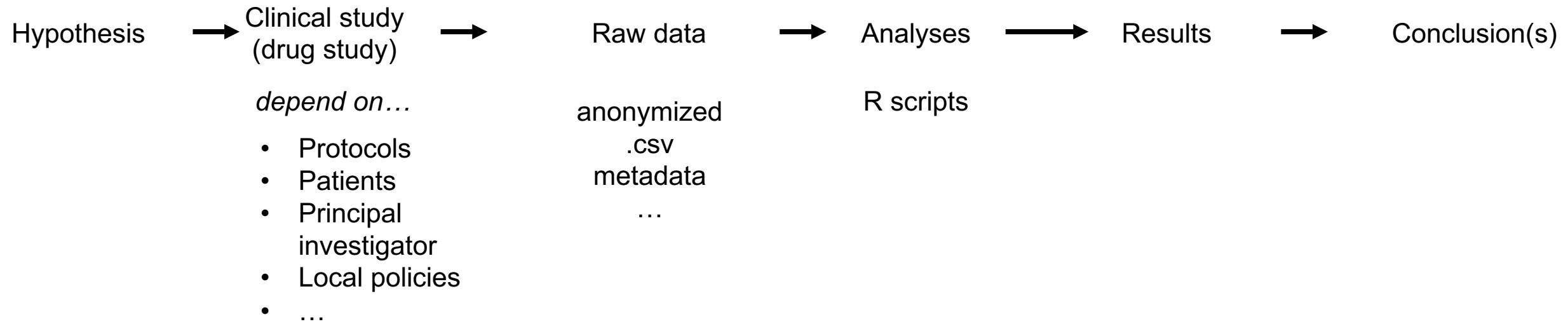
# The next step with clinical research



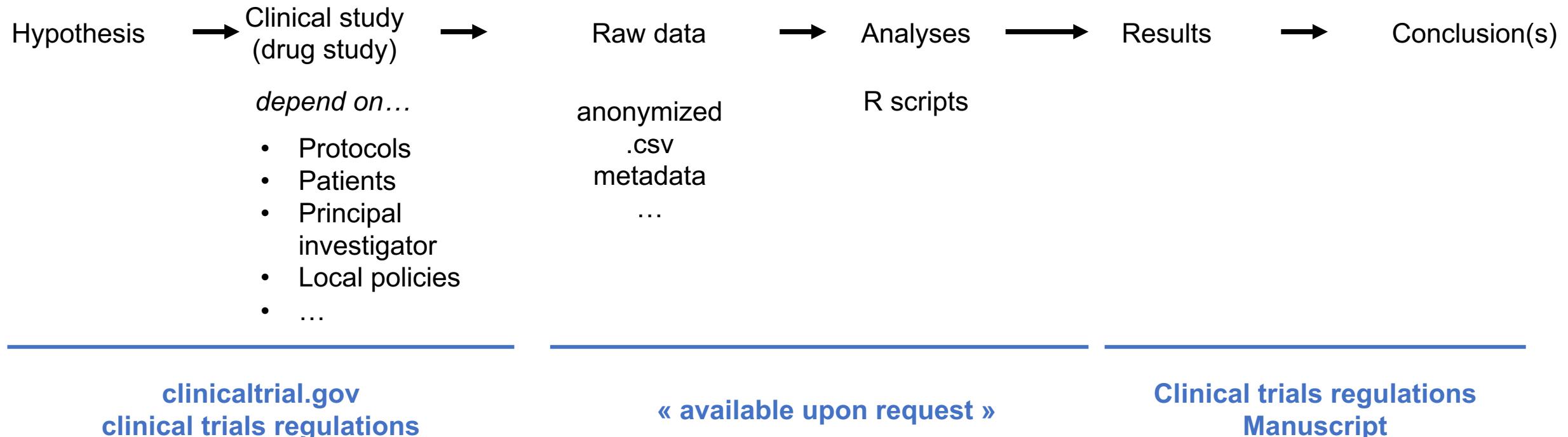
# The next step with clinical research



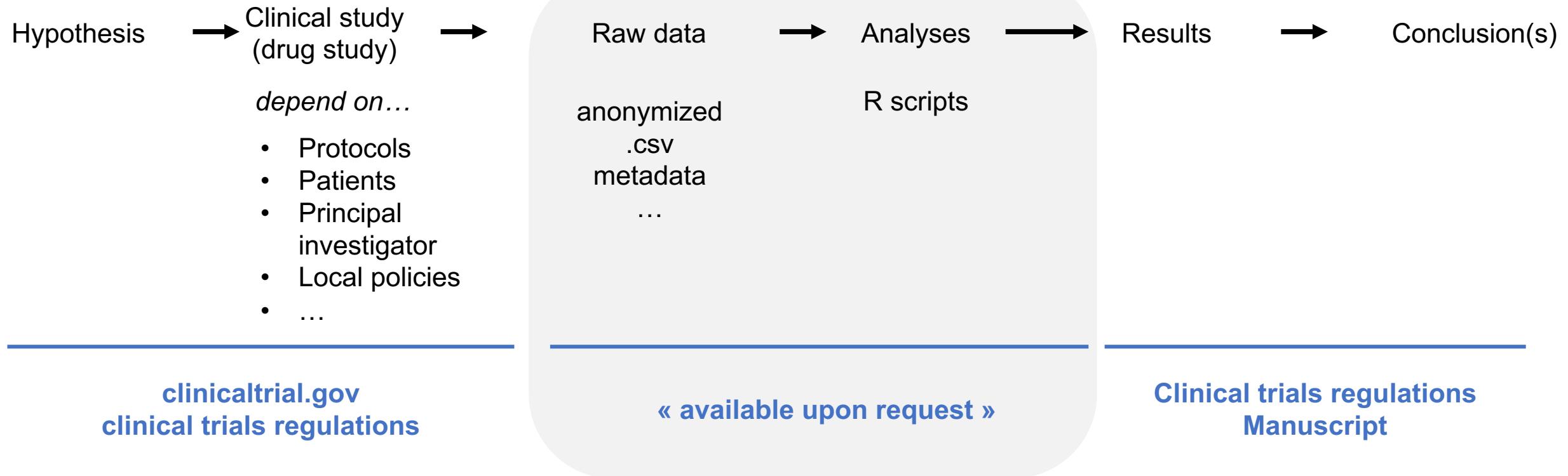
# Is clinical research reproducible / transparent



# Is clinical research reproducible / transparent

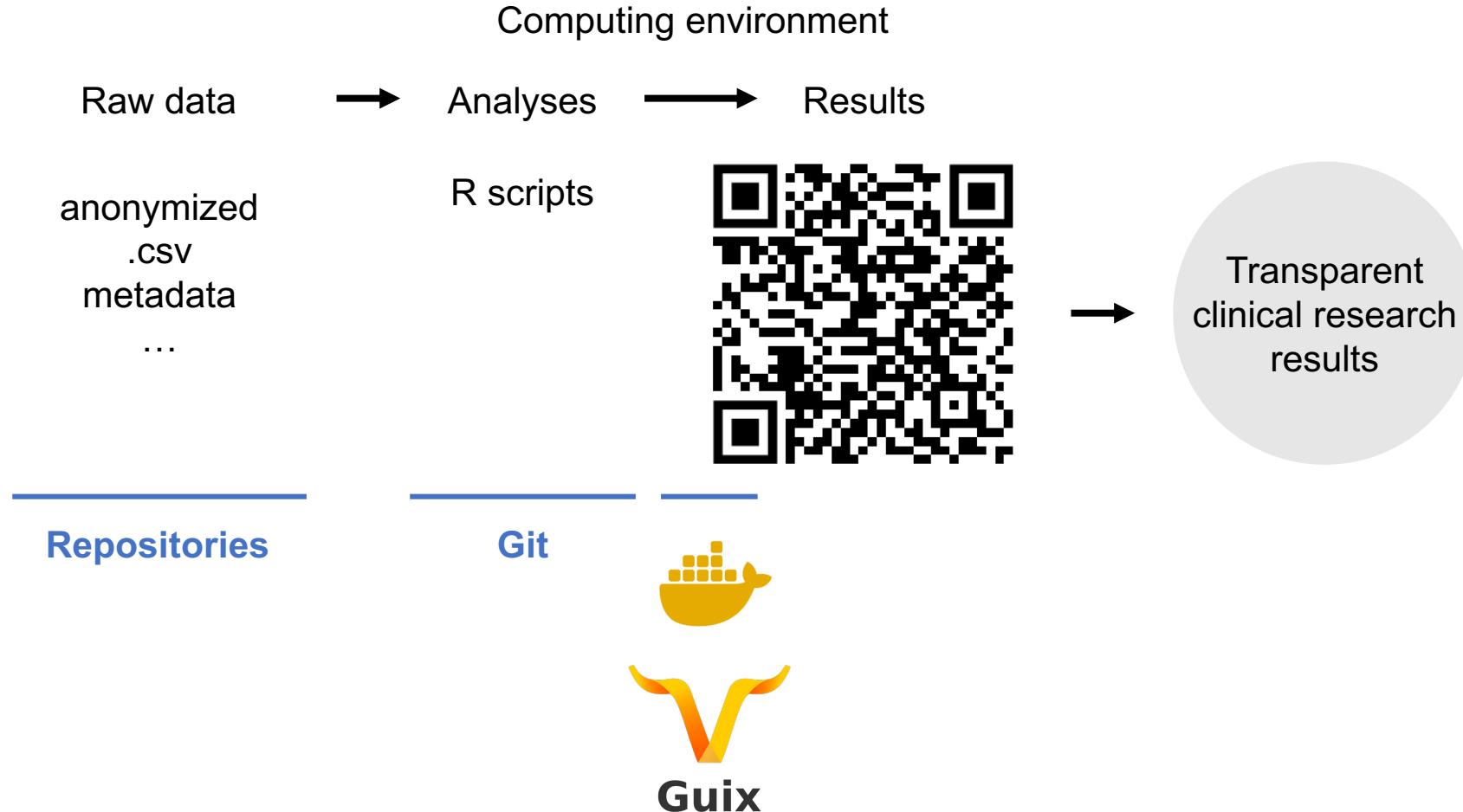


# Is clinical research reproducible / transparent

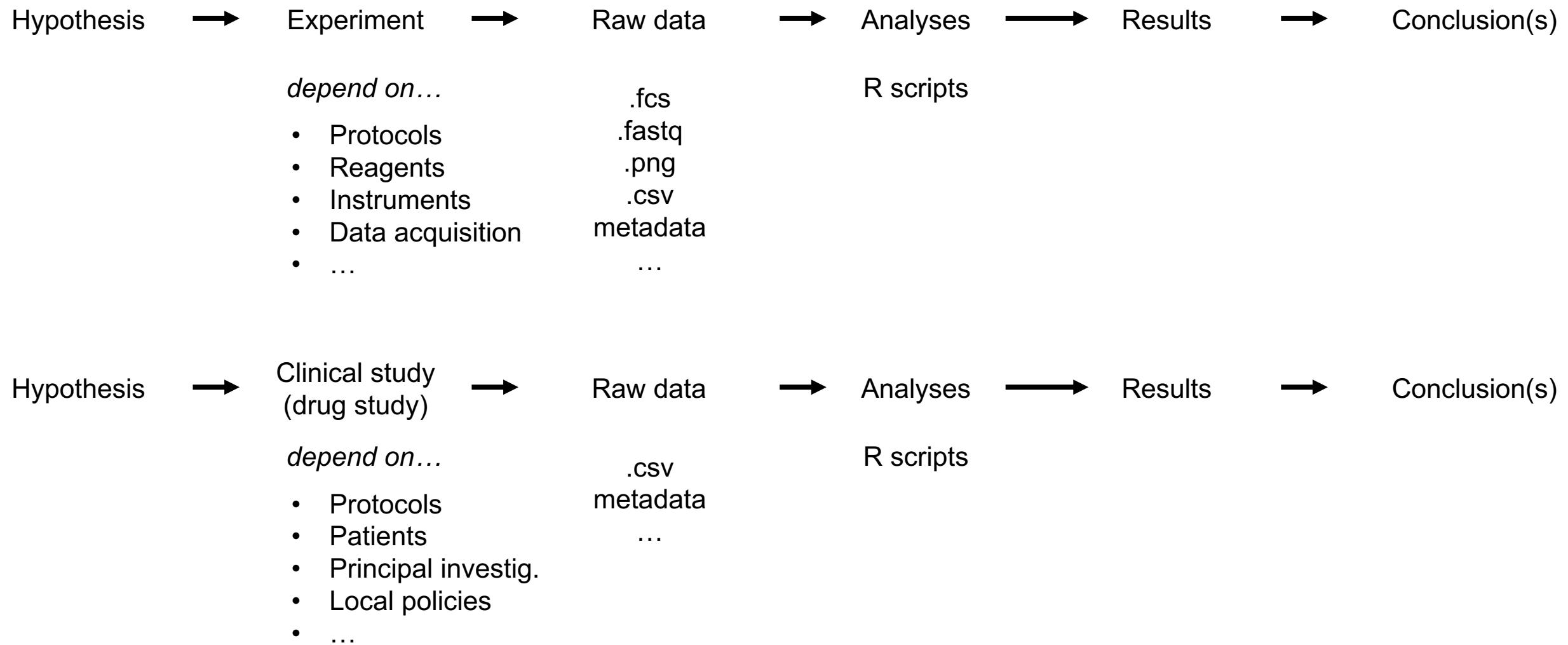


Can we improve our practices toward transparent and reproducible clinical research?

# Clinical research

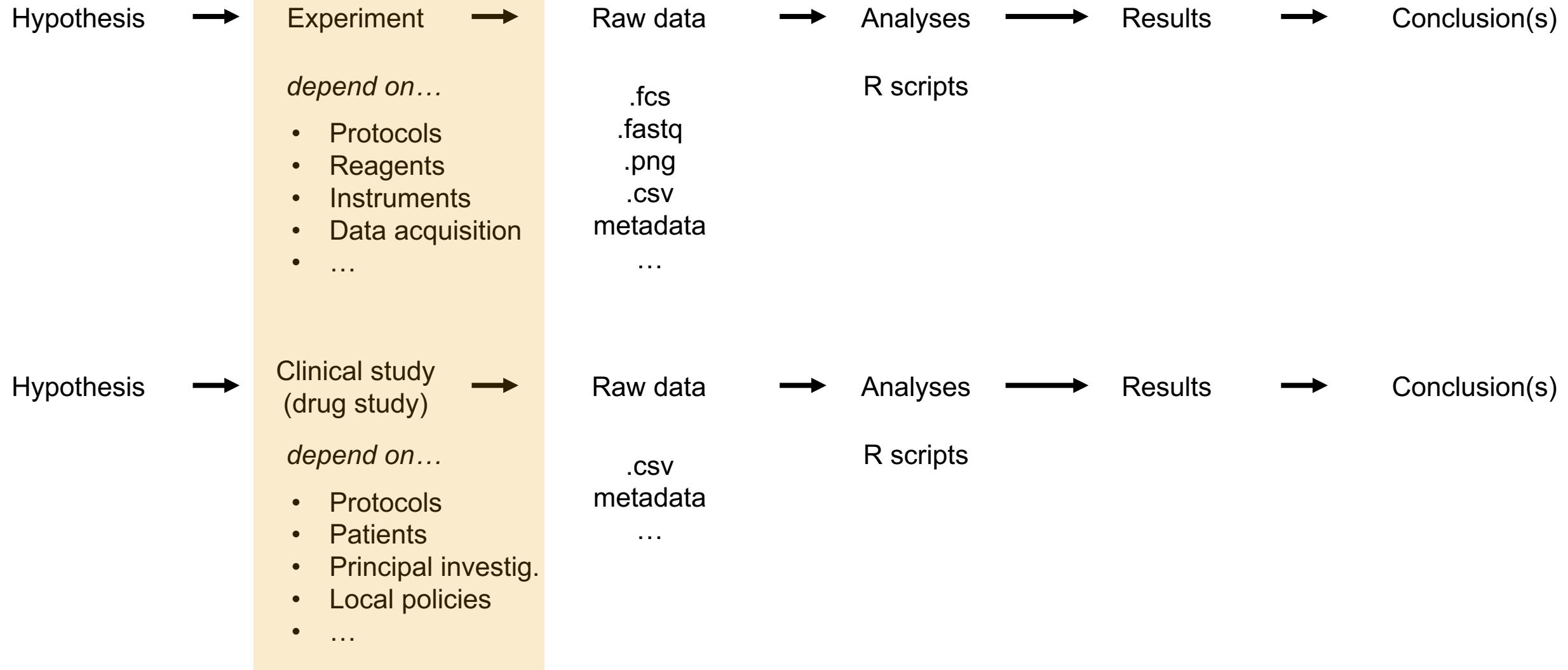


## To conclude



## To conclude

Unlikely to be 100% reproduced



## To conclude

Unlikely to be 100% reproduced

Hypothesis →

Experiment →

*depend on...*

- Protocols
- Reagents
- Instruments
- Data acquisition
- ...

Hypothesis →

Clinical study  
(drug study) →

*depend on...*

- Protocols
- Patients
- Principal investig.
- Local policies
- ...

Repositories

Raw data →

Analyses →

Results →

Conclusion(s)

.fcs  
.fastq  
.png  
.csv  
metadata  
...

R scripts

Raw data →

Analyses →

Results →

Conclusion(s)

.csv  
metadata  
...

R scripts

## To conclude

Unlikely to be 100% reproduced

Hypothesis →

Experiment →

*depend on...*

- Protocols
- Reagents
- Instruments
- Data acquisition
- ...

Hypothesis →

Clinical study  
(drug study) →

*depend on...*

- Protocols
- Patients
- Principal investig.
- Local policies
- ...

Repositories

Raw data →

.fcs  
.fastq  
.png  
.csv  
metadata  
...

Analyses →

R scripts

→

Results →

Conclusion(s)

**Computing environment  
is now the most  
reproducible and  
transparent step of  
biomedical research**

Raw data →

.csv  
metadata  
...

Analyses →

R scripts

→

Results →

Conclusion(s)

## To conclude

Unlikely to be 100% reproduced

Hypothesis →

Experiment →

*depend on...*

- Protocols
- Reagents
- Instruments
- Data acquisition
- ...

Hypothesis →

Clinical study  
(drug study) →

*depend on...*

- Protocols
- Patients
- Principal investig.
- Local policies
- ...

Repositories

Raw data →

.fcs  
.fastq  
.png  
.csv  
metadata  
...

Analyses →

R scripts

→

Results →

Conclusion(s)

**Computing environment  
is now the most  
reproducible and  
transparent step of  
biomedical research**

*Modulo the accessibility*

Results →

Conclusion(s)

# Acknowledgments



Emmanuel Gyan



Olivier Héault



Service d'Hématologie et Thérapie Cellulaire



David Michonneau



## Collaborations

Jean-Baptiste Delaye, Chantal Barin-Le Guellec, Hélène Blasco

(Service de Biochimie CHRU Tours)

Yoann Devisgnes (DRCI Tours)

Agnès Caille (U1246 SPHERE)

Martine Ropert (Biochimie Rennes)



Patricia Lepage (INRA MICALIS U1319)

Equipe de CyPS (Mass cytometry)

Y. Marie & D. Bouteiller (ICM)

Anne Bergeron (Pneumologie Genève)

Catherine Poirot (GRECOT)

CRYOSTEM  
Régis Peffault de Latour



CRYOSTEM



Guix HPC / IRSN  
Simon Tournier



Pour leur soutien  
France Leucémie Espoir  
Association pour Laurène  
SOS Oxygène  
ITMO Cancer Aviesan / Inserm  
Association CANCEN  
Novartis



NOVARTIS



Aviesan  
ITMO Cancer

