



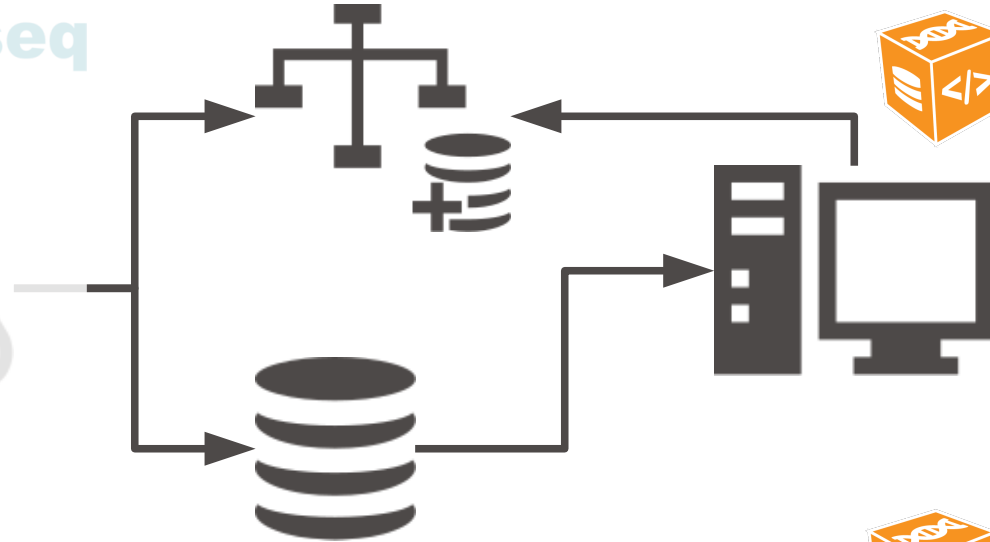
# Data Storage Platforms



Korbinian Bösl  
Data management coordinator  
ELIXIR Norway/Digital Life Norway  
9th of March 2021

# NeLS

Norwegian e-Infrastructure for Life Sciences



sensitive  
data



# NeLS



Feide ola@uib.no



My Projects



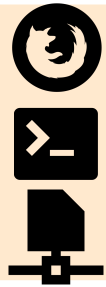
NeLS



Norwegian e-Infrastructure for Life Sciences

Data curation

# NeLS



 **Feide** ola@uib.no  
**My Projects**

**NeLS**

Norwegian e-Infrastructure for Life Sciences

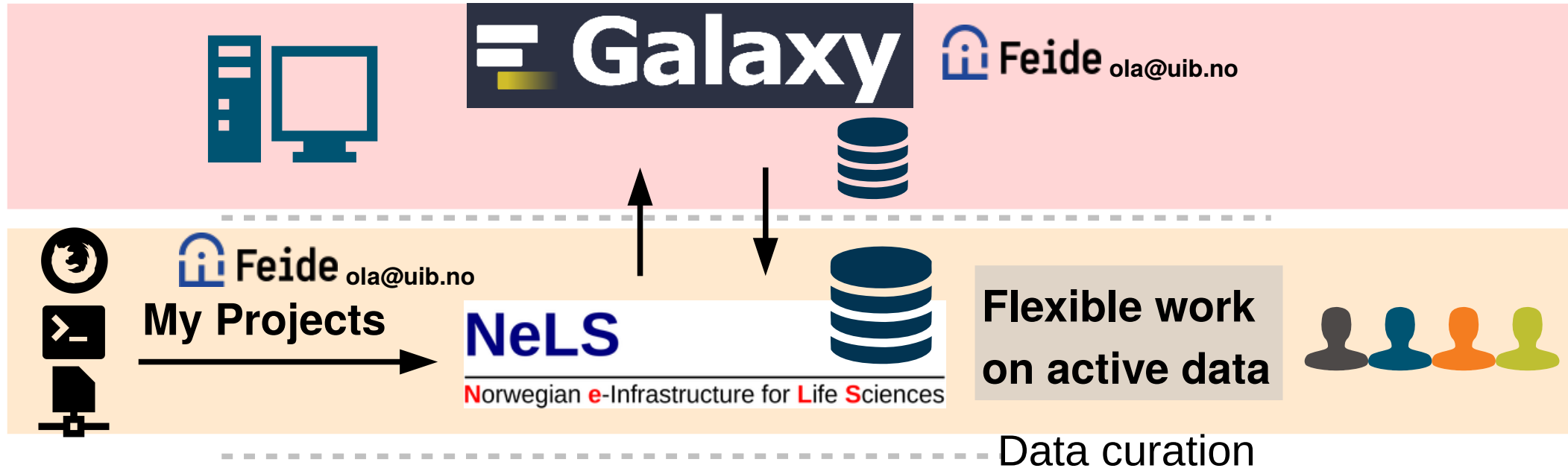


**Flexible work  
on active data**

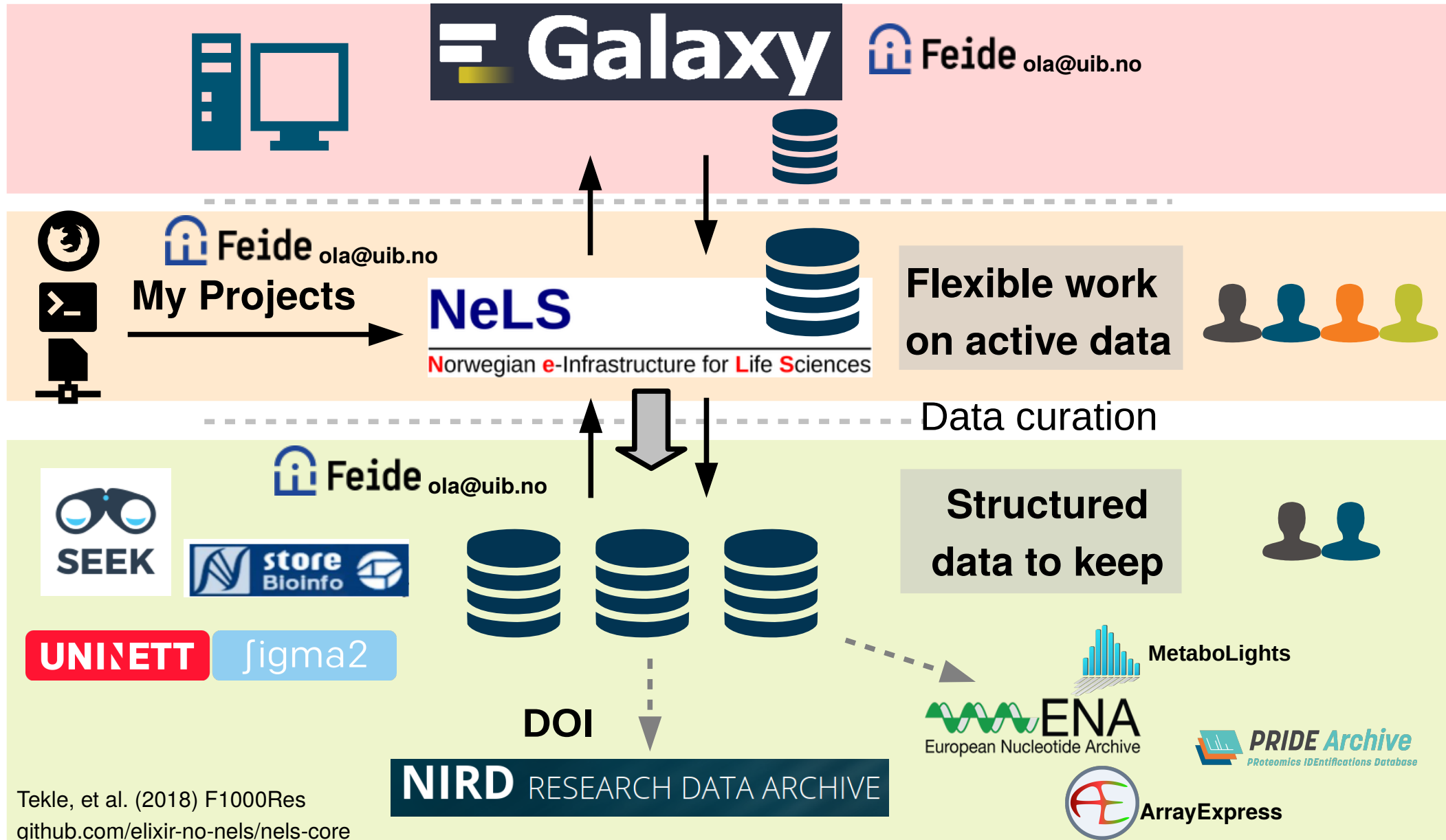


Data curation

# NeLS



# NeLS



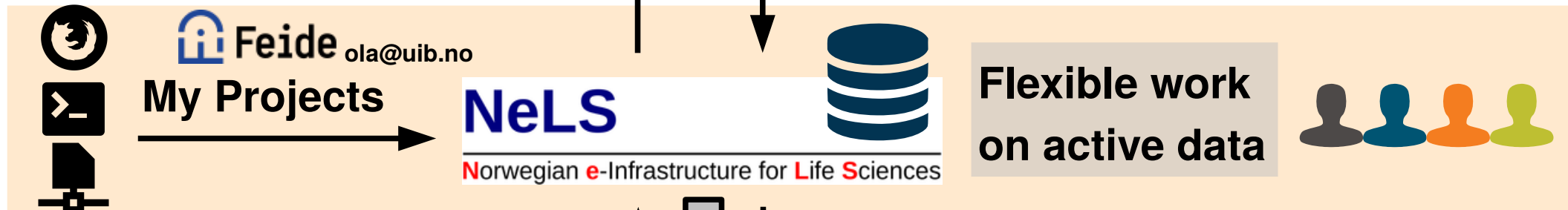
 **nor seq**

# NeLS

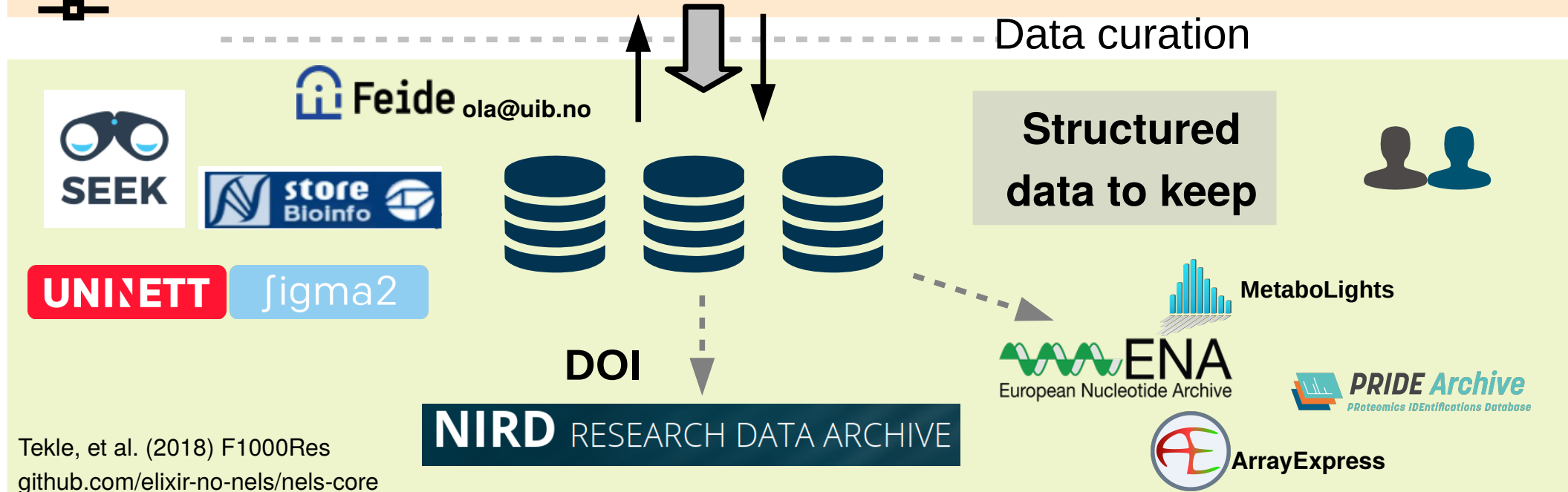
Days - weeks



 **nor seq**  
Months



Years



Decades

<https://nels.bioinfo.no/>

Tekle, et al. (2018) F1000Res  
[github.com/elixir-no-nels/nels-core](https://github.com/elixir-no-nels/nels-core)

# NeLS - Accessibility

small datasets



ola@uib.no



# NeLS - Accessibility

small datasets



ola@uib.no

larger datasets



ssh-key



git



sFTP

# Data Analysis in NeLS

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated↓
16S Workflow with Mothur program ▾		kjetil-klepper	★★★★★		Oct 17, 2020
NGS Pipeline for Paired End Reads (R1 and R2) ▾		kjetil-klepper	★★★★★		Oct 17, 2020
miRNA differential expression (miRBase, hg38) ▾		kjetil-klepper	★★★★★	nels	Oct 15, 2020
miRNA differential expression (MirGeneDB, hg38) ▾		kjetil-klepper	★★★★★	nels	Oct 14, 2020
COVID-19: PE Variation ▾		kjetil-klepper	★★★★★	nels	Oct 13, 2020
Pre-process COVID-19 PE collections ▾		kjetil-klepper	★★★★★	nels	Oct 13, 2020
Pre-process COVID-19 PE single sample ▾		kjetil-klepper	★★★★★	nels	Oct 13, 2020

# NeLS - Getting Access

## NeLS

Norwegian e-Infrastructure for Life Sciences

Typically > 1TB data

Free < 10TB & <15 mill. NOK

Allocation through Helpdesk: [contact@bioinfo.no](mailto:contact@bioinfo.no)

Direct upload through Nourseq facilities

<https://nels.bioinfo.no/pages/user-terms.xhtml>



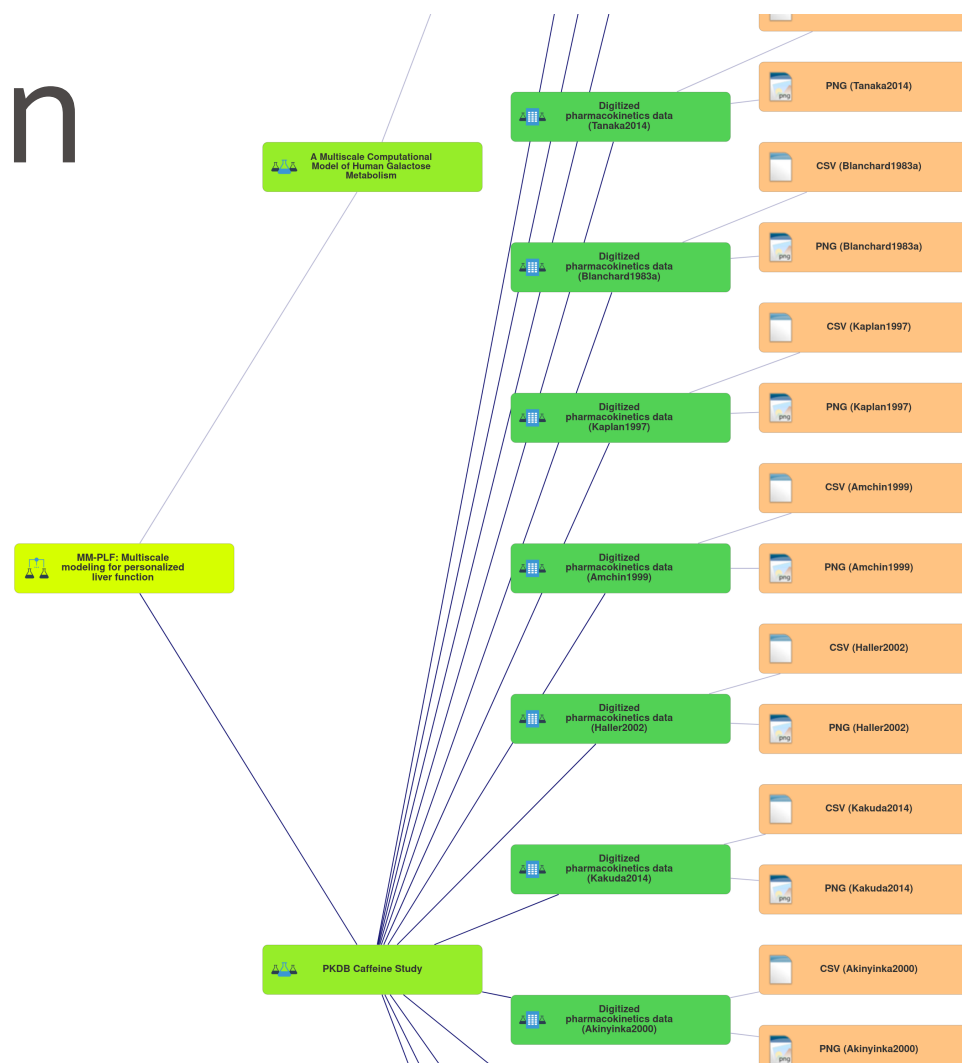
# SEEK





# SEEK

# Investigation Study Assay



# RightField



File Edit Sheet Help

	A	B	C	D	E	F
1	# This is an excel template...					
2	# Use this template for ...					
3	# Click the Metadata Ex...					
4	# Field names (in blu...					
5	# CLICK HERE for the F...					
6						
7	<b>SERIES</b>					
8	# This section describes ...					
9						
10	<b>title</b>					
11	<b>summary</b>					
12	<b>summary</b>					
13	<b>overall design</b>					
14	<b>contributor</b>					
15	<b>contributor (SEEK ID)</b>					
16	SEEK Project	Project				
17	<b>Experiment Class (a...</b>	transcriptomics				
18	<b>Experiment Design t...</b>	ExperimentDesignT...				
19	<b>Technology type</b>	microarray				
20	<b>quality control type</b>	QualityControlDesc...				
21						
22	<b>SAMPLES</b>					
23	# The Sample name...					
24	# CLICK HERE to find t...					
25						
26	<b>Sample name</b>	<b>title</b>	<b>CEL file</b>	<b>source name</b>	<b>organism</b>	<b>characteristics:...</b>
27	<b>SAMPLE 1</b>				organism	
28	<b>SAMPLE 2</b>				organism	
29	<b>SAMPLE 3</b>				organism	
30	<b>SAMPLE 4</b>				organism	
31	<b>SAMPLE 5</b>				organism	
32	<b>SAMPLE 6</b>				organism	
33	<b>SAMPLE 7</b>				organism	
34	<b>SAMPLE 8</b>				organism	
35	<b>SAMPLE 9</b>				organism	
36	<b>SAMPLE X</b>				organism	
37						
38						
39	<b>PROTOCOLS</b>					
40	# This section includes pr...					
41	# Protocols which are ap...					
42						
43	<b>growth protocol</b>					
44	<b>treatment protocol</b>					
45	<b>extract protocol</b>					
46	<b>label protocol</b>					

Selected cells: B17:B17

ONTOLOGY HIERARCHIES

MGEDOntology.owl x

JERMOntology x

- ExperimentClassType
  - fluxomics
  - genomics
  - interactomics
  - metabolomics
  - proteomics
  - reactomics
  - single\_cell
  - transcriptomics
- InformaticsAnalysisType
- ModelAnalysisType
- CultureGrowth
- FactorsStudied
  - concentration
  - expression

TYPE OF ALLOWED VALUES

☐ Free text

☐ Direct subclasses

☒ Subclasses

☐ Instances

☐ Direct instances

ALLOWED VALUES

- Comparative genomic hybridization
- RNAi
- gene expression profiling
- methylation profiling
- microRNA profiling
- tiling path

Apply

Metadata Template Matrix Template Metadata Example Matrix Example 1 Matrix Example 2

**NeLS**

Norwegian e-Infrastructure for Life Sciences



# Integration



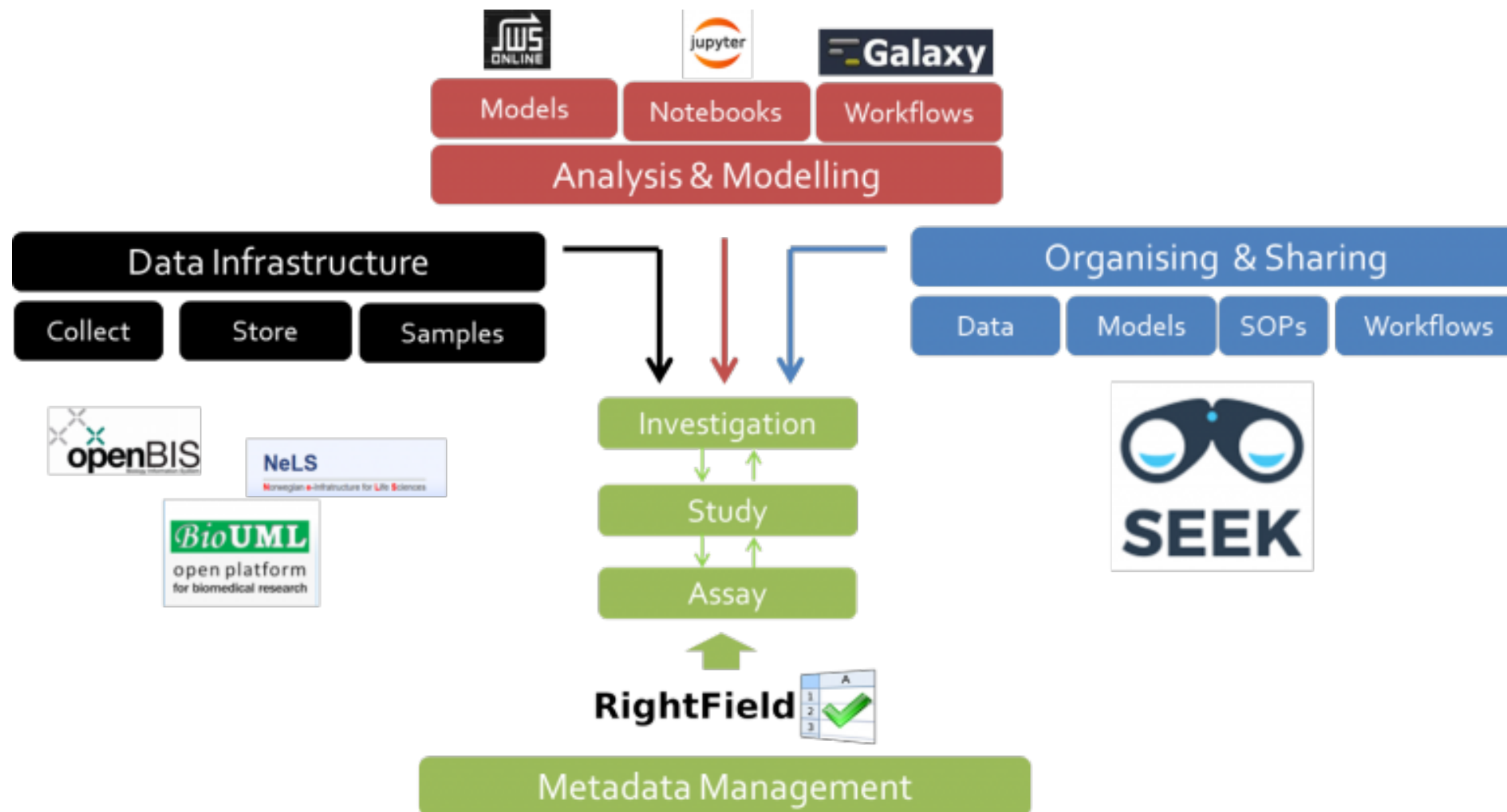
**Reference data in NeLS in SEEK**



**Access data in NeLS through SEEK**



**Save Metadata to SEEK through NeLS**





# National HPC infrastructure

**UNINETT**

sigma2



Advanced Storage Needs

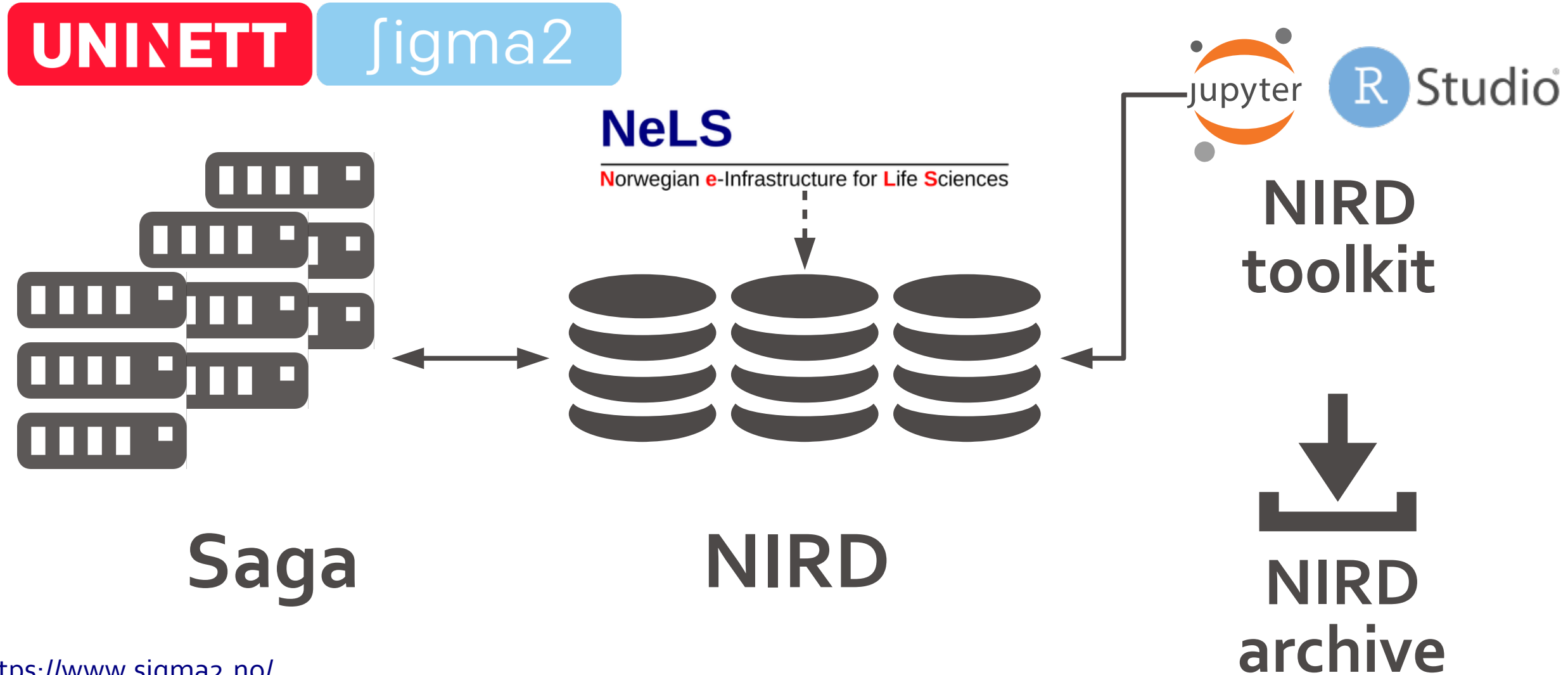


Advanced Computing Resources



Free Analysis Toolkit (Rstudio, Jupyternotebook)

# National HPC infrastructure



# HPC infrastructure

**UNINETT**

sigma2

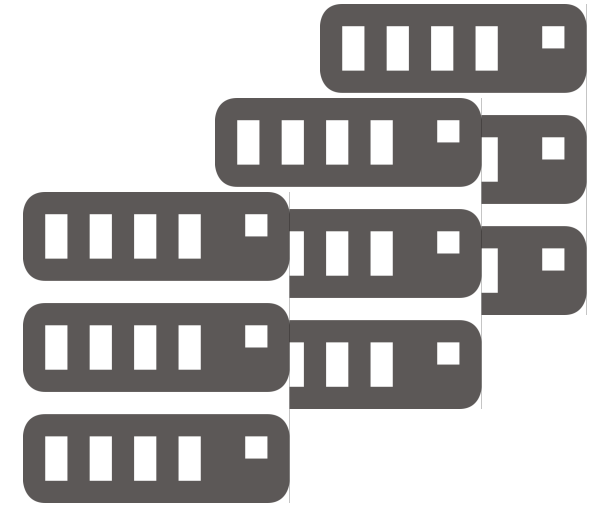
Saga

244 nodes – 9824 cores – 32 GPUs

Total 75TB RAM – 186-3066GB/node

89TB + 60TB NVMe+SSD

1PB file system



# Storage infrastructure - NIRD

**UNINETT**

sigma2

Geo replicated

Nightly snapshots

12 PB (→ 36 PB next 3 yrs)



# Sigma2 - Getting Access



**Bi-annual calls (January & July) – Reapplication (!)**

**User contribution model (projects > 15 mill. NOK)**

**Application for small grants continually**

# TSD – National sensitive data service



Maximum classification



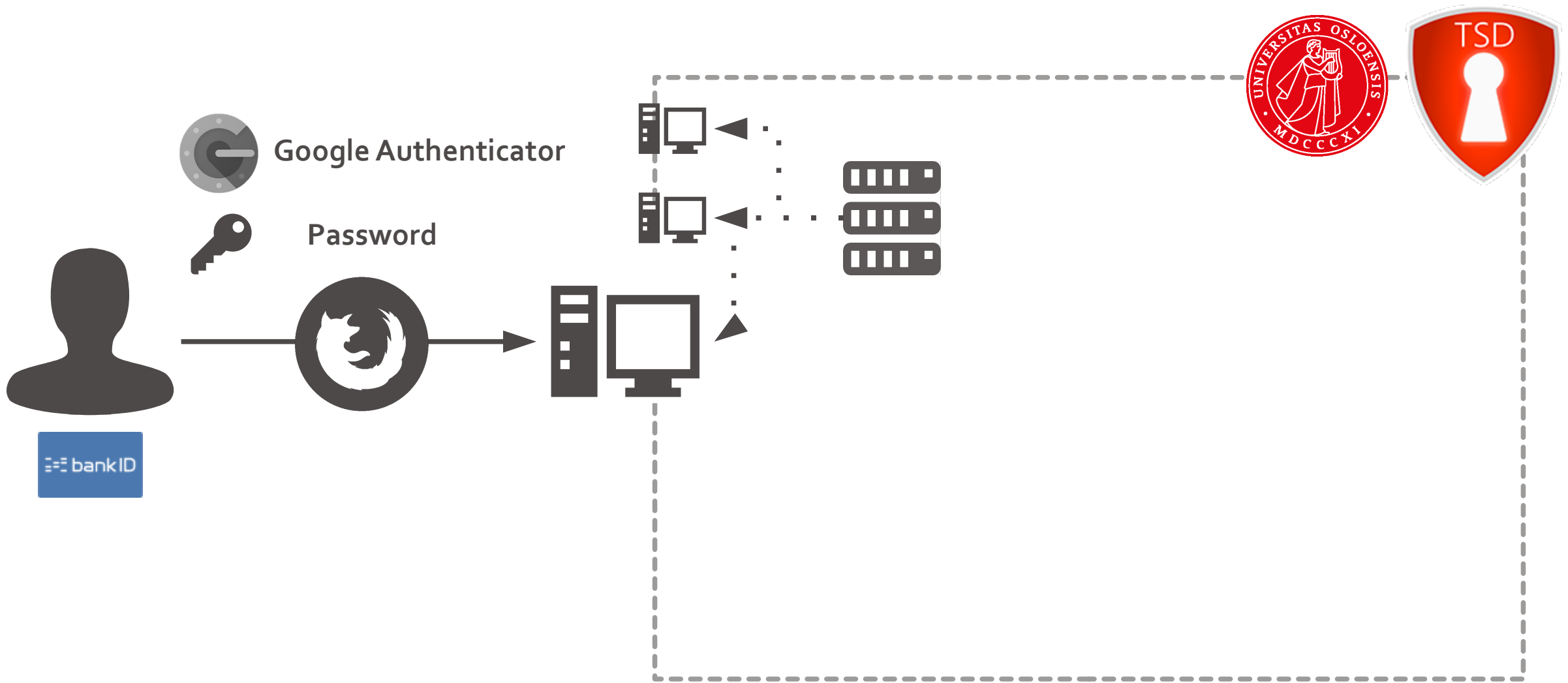
2-factor authentication

Attached HPC resources

# TSD – National sensitive data service

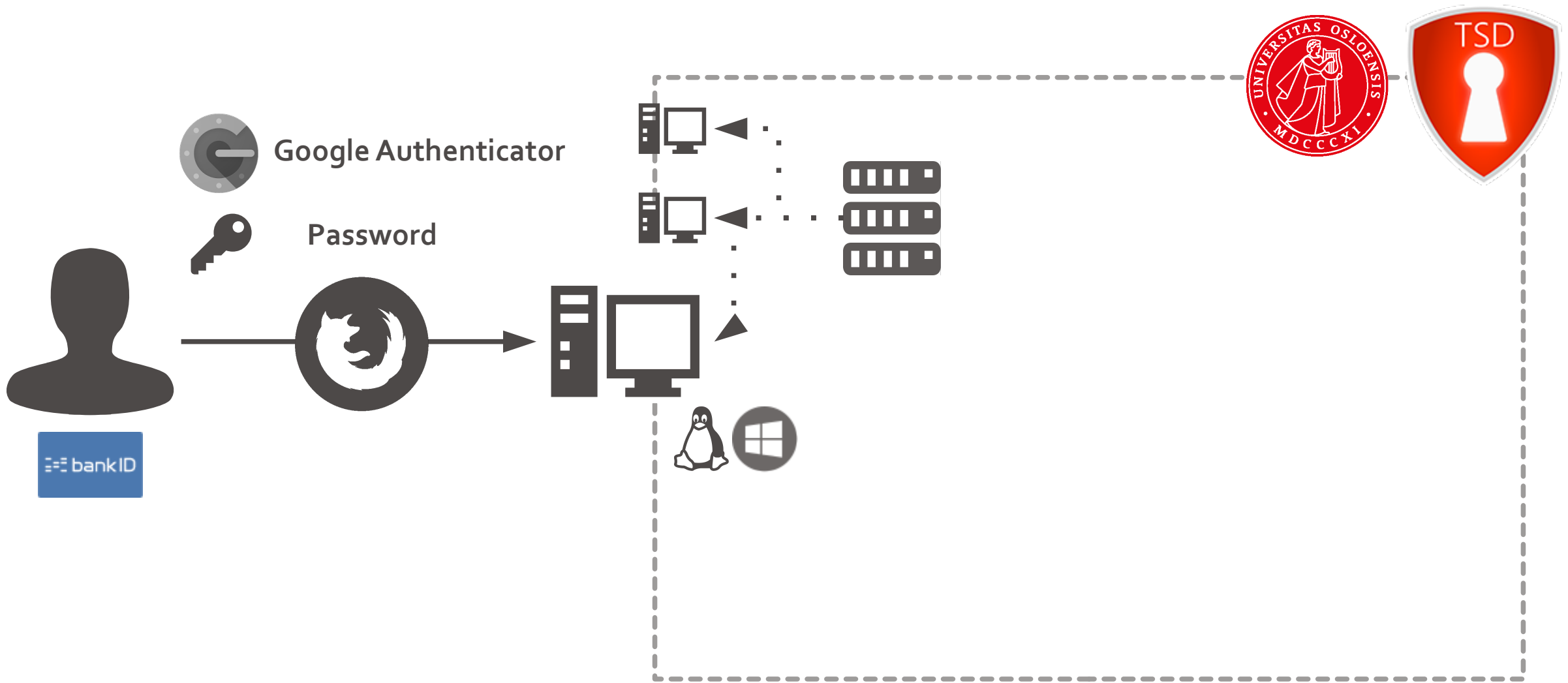


# TSD – National sensitive data service

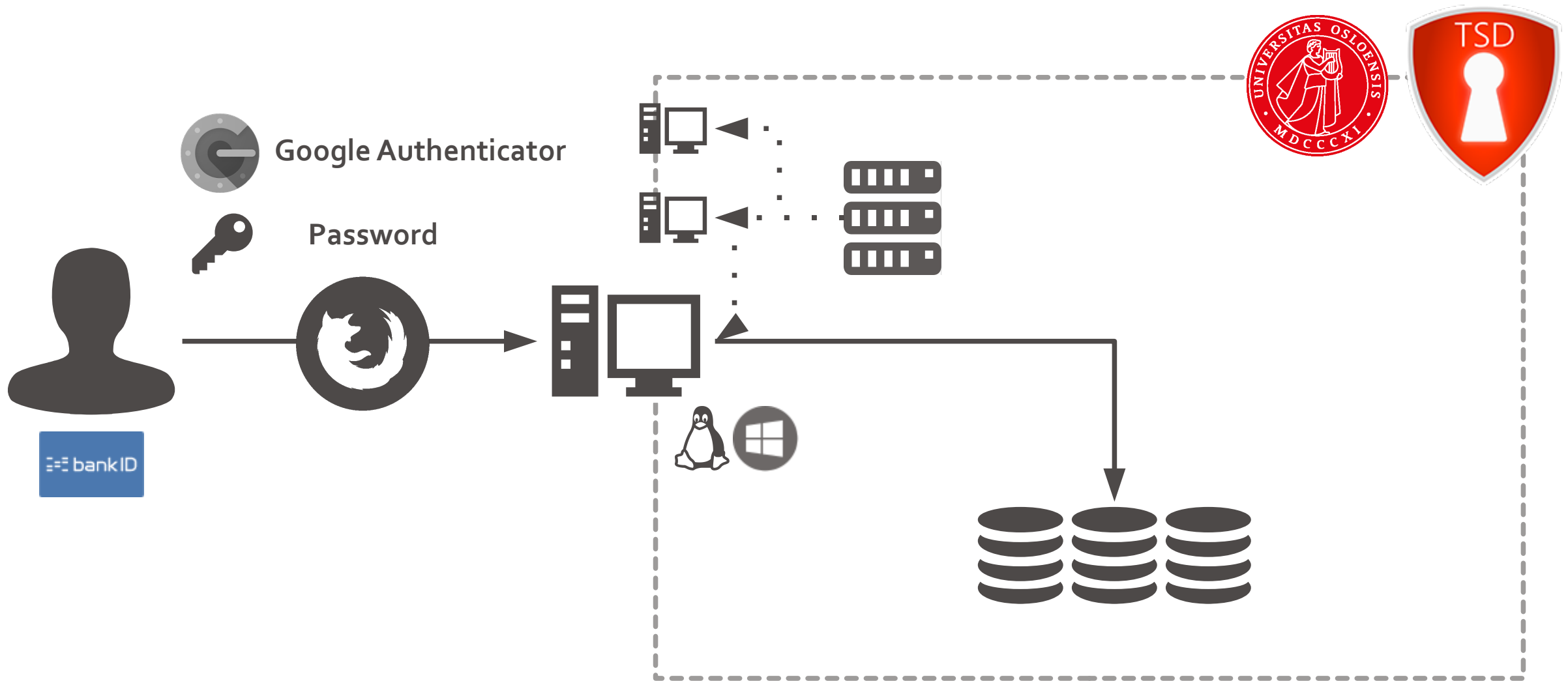




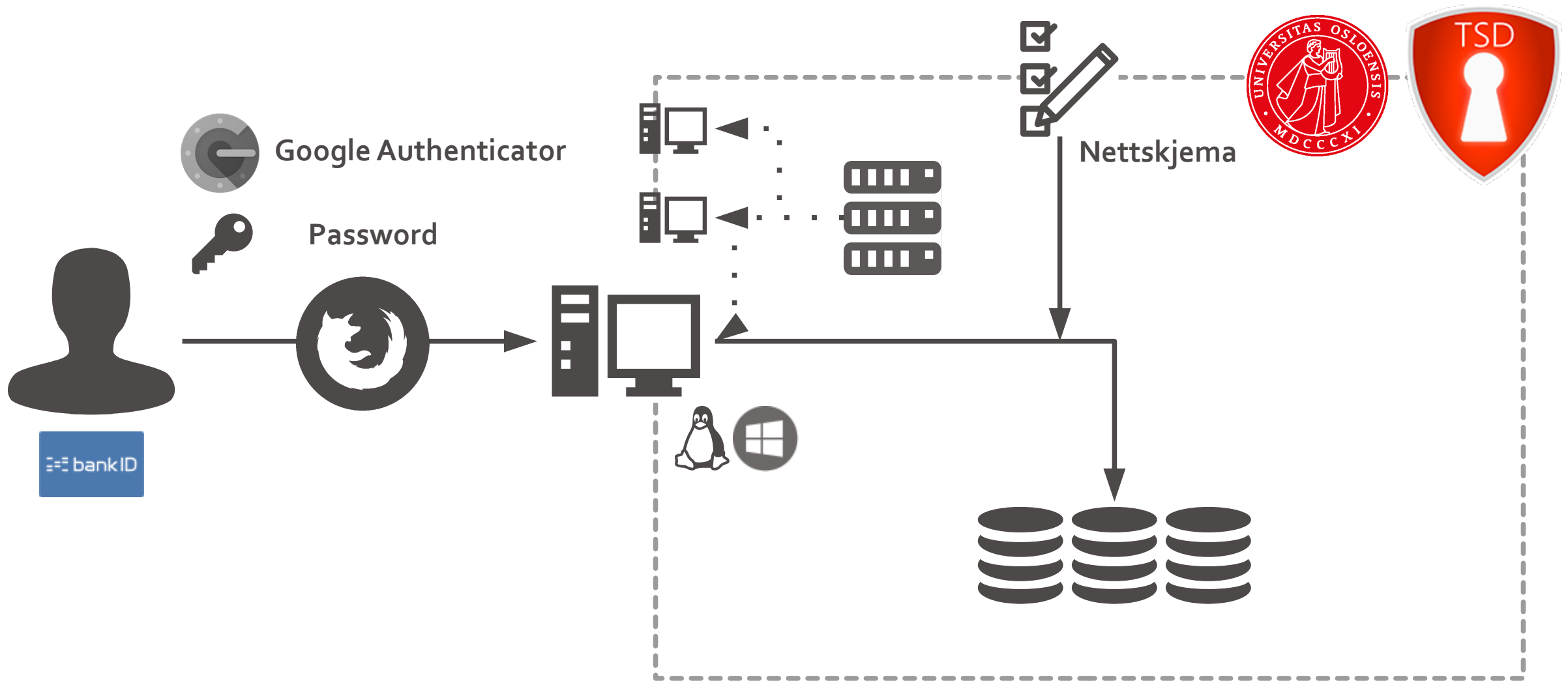
# TSD – National sensitive data service



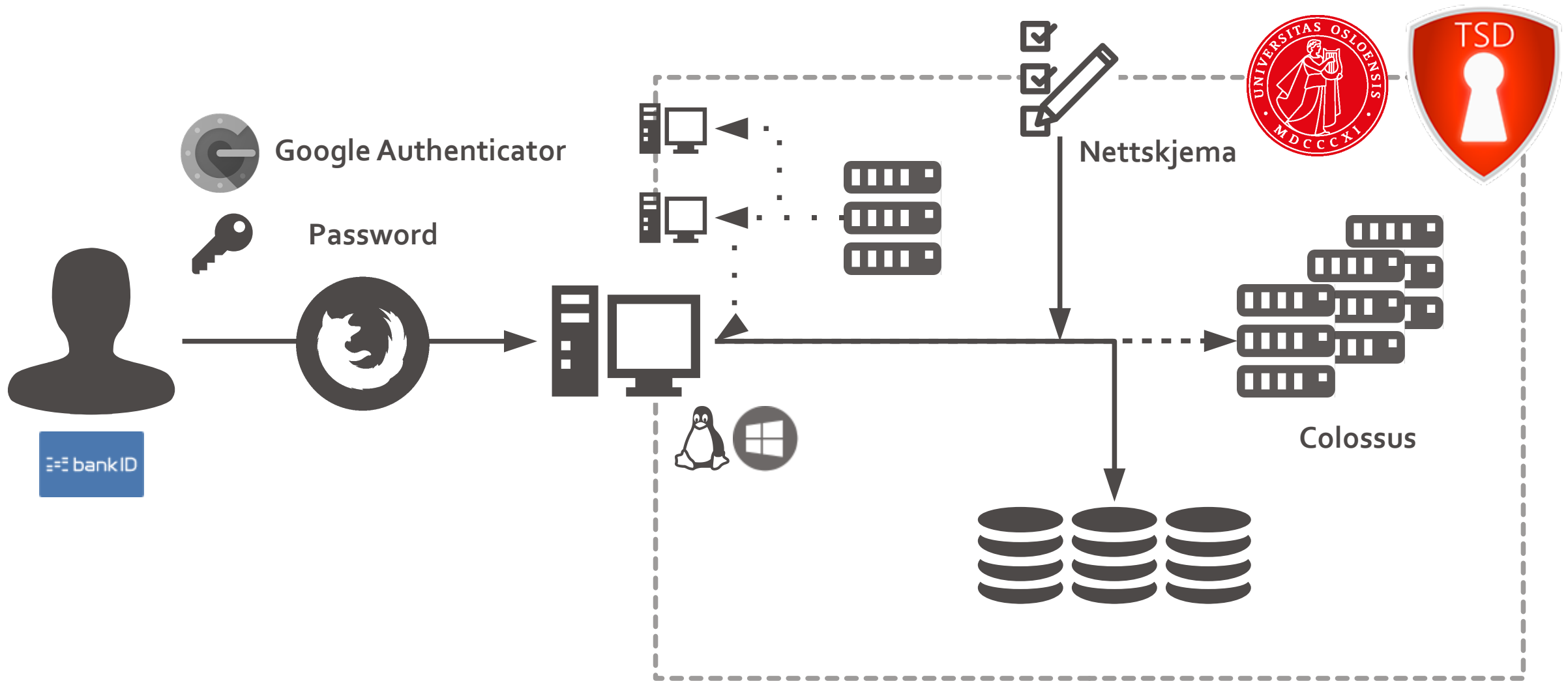
# TSD – National sensitive data service



# TSD – National sensitive data service



# TSD – National sensitive data service



# TSD – Getting Access



**Subsidized access through Sigma2 calls**

**User contribution model (non UiO: min 15kNOK/a)**

**Free storage quotas through NeLS**