



# **BioInfra.Prot1: Bioinformatics Services for Proteomics** at the Ruhr University Bochum FKZ 031 A 534A

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## **Short description of the project**

The project **Biolnfra.Prot1**, which is part of the service center Biolnfra.Prot, the German Network for Bioinformatics Infrastructure (de.NBI) and ELIXIR, provides a comprehensive portfolio of bioinformatics services for proteomics. This includes data standardization, data conversion and data publication services as well as computational and statistical consultancy and data analysis (esp. protein inference and expression analysis), software tools, hardware sharing and training courses. Altogether a comprehensive proteomics workflow is offered. The relatively high usage of these free and high-quality services confirms the strong need for bioinformatics infrastructure in proteomics research.

# de.NBI services



### **Progress report**

#### **Standard workflows:**

Workflows for typical proteomics task (e.g., QC, identification, quantification & protein *inference) were implemented* & *are available.* 



#### **Most important ELIXIR activities:**

- Tools platform (BioContainers initiative).
- Proteomics community.
- Intrinsically Disordered Protein Community.
- Curation of ProteomeXchange uploads into PRIDE & processing of related user requests.
- *Implementation studies:* • *'Mining the proteome: Enabling* 
  - 2 automated processing (...)'
- 'Crowd-sourcing the annotation of GERMANY public proteomics datasets (...)
- 'Comparison, benchmarking and dissemination of proteomics data analysis pipelines'





- for provision important proteomics tasks Tool (tool names in brackets):
- Protein inference and protein list comparison (PIA and ProLiC)
- Analysis of protein microarrays (PAA)
- Format conversion and data upload (ProCon)
- Multi-omics analysis (CrossPlatformCommander)



**Protein Inference Algorithms (PIA):** 

PIA's import and export of PSI standard formats



#### **BIONDA:**



#### de.NBI cloud activities:

BioInfra.Prot1 uses the de.NBI cloud:

- Porting some of our software into de.NBI cloud (i.e., PIA and PAA).
- PRIDE export into the de.NBI cloud is currently in progress.

## de.NBI training and education

Date	Course title	Location	Particip. (appl.)	Organized by	25	Cumu	ılative	numb	er o
28.03.19	Tool Training for Proteomics at Proteomic Forum 2019	Potsdam	54 (55)	BioInfra.Prot1&2, EuBIC	30				
02.09.19	de.NBI Summer School 2019 - (Bio)Data Science	Gatersle- ben		BioInfra.Prot & other de.NBI partners	25				
28.10.19	3rd Tool-Training for Proteomics	Bochum	8 (10)	BioInfra.Prot1	20				1!
18.11.19	4th Differential analysis of quantitative proteomics data using R	Bochum	17 (33)	BioInfra.Prot1	10		E	10	
19.11.19	Advanced analysis of quantitative proteomics data using R	Bochum	18 (30)	BioInfra.Prot1	5 0	2	5		

Table 1: BioInfra.Prot1 training activities in 2019. We have taught 316 participants (~87% satisfied) out of 405 applications.

**Cumulative number of participants** 

Figure 2: Cumulative number of participants

since 2015. We have taught 413 participants

(~87% satisfied). \*With our average number of

80 participants per year there may be ~573

700

# of training events 30 25 20

2015 2016 2017 2018 2019 2020\* 2021\*

Figure 1: Cumulative number of training events since 2015. \*We plan 5 training events in each year 2020 & 2021.

633

533

**Cumulative number of applications** 733

405



Data

### **Computational & statistical analysis:** Our services comprise consulting regarding statistics and bioinformatics for proteomics. Furthermore, we provide hardware and toolbox sharing (i.e. the offer of preinstalled tools and free third-party software on our hardware infrastructure).

#### Usage metrics highlights (2015-03-01 to 2019-12-15)

- 10,581 service tickets from all services.
- 9,946 tickets from data standardization & conversion service.
- **509 tickets** from bioinformatical & statistical consulting & analysis.
- 8,867 software tool downloads (distinct IPs). • 52 publications.

# **Publications**



	Poor	Below	Average	Above	Excellent
		average		average	
Quality	0%	0%	1%	14%	85%
Responsi-	0%	0%	3%	16%	81%
veness					
Usability	0%	0%	3%	23%	74%

Data

Standardization

and Conversion

Service

Table 2: User satisfaction with BioInfra.Prot1. Results of the de.NBI user satisfaction survey are shown.



2015 2016 2017 2018 2019 2020\* 2021\* Figure 3: Cumulative number of applications since 2015. We have recorded 533 applications. \*With our average number of 100 applications per year there may be ~733 applications in 2021.

Figure 4: Cumulative number of BioInfra.Prot1 publications since 2015. We have already 52 scientific articles published where BioInfra.Prot1 staff is included in the author list and de.NBI is mentioned (incl. grant number). \*With our average number of 12 articles per year there may be ~76 publications in 2021.

### **General information on the project**

#### **BioInfra.Prot1 staff in 2019:**

• No. of staff paid from de.NBI grant (FTE): 4 scientists & 1 technician.

• Other staff involved: 1 PI & 2 scientists.



participants in 2021.



800

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