

# HD-HuB de.NBI-DKFZ: Human Bioinformatics

(According to the former  
de.NBI project phase)

Contract Nr. W-de.NBI-013

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## Short description of the project

de.NBI-DKFZ is offering services in the following areas: Cellular phenotyping and analysis of high-throughput genetic perturbation/interaction screens (Boutros); analysis of epigenetic data (Brors, Lutsik, Scherer); analysis of multi-omics single-cell sequencing data (Stegle); and analysis of large-scale human genome sequencing data (Hübschmann/Buchhalter/Brors). In addition, de.NBI-DKFZ operates one of the de.NBI cloud centers.

## de.NBI services

Services: 16 tools, 6 workflows, 3 databases, including:

- one touch pipeline (OTP) for large-scale sequencing data
- circlize (R package, circos plots, visualization)
- ComplexHeatmap (R package, visualization)
- EnrichedHeatmaps (R package, visualization)
- YAPSA (SNV signature analysis, R Package)
- LIMIX (linear mixed models, genetic variation/gene expression)
- slalom (single-cell RNA sequencing data analysis)
- MOFA/MOFA+ (multiomics factor analysis)
- E-CRISPR (sgRNA design, genomic perturbation screens)
- GenomeCRISPR (database, genomic perturbation screens)
- GenomeRNAi (RNAi phenotypes, genomic perturbation screens)
- BiocompR (R package, visualization)
- Methview.qc (QC of array-based methylation data)

## KPIs (2023)

|                     | Citations | Downloads/<br>month | Visits/<br>month | Executions/<br>month |
|---------------------|-----------|---------------------|------------------|----------------------|
| all services        | 1800      |                     |                  |                      |
| Tools               |           | 25,000              |                  |                      |
| Web<br>applications |           |                     | 1,500            |                      |
| Workflows           |           |                     |                  | 43,000               |

## Progress report

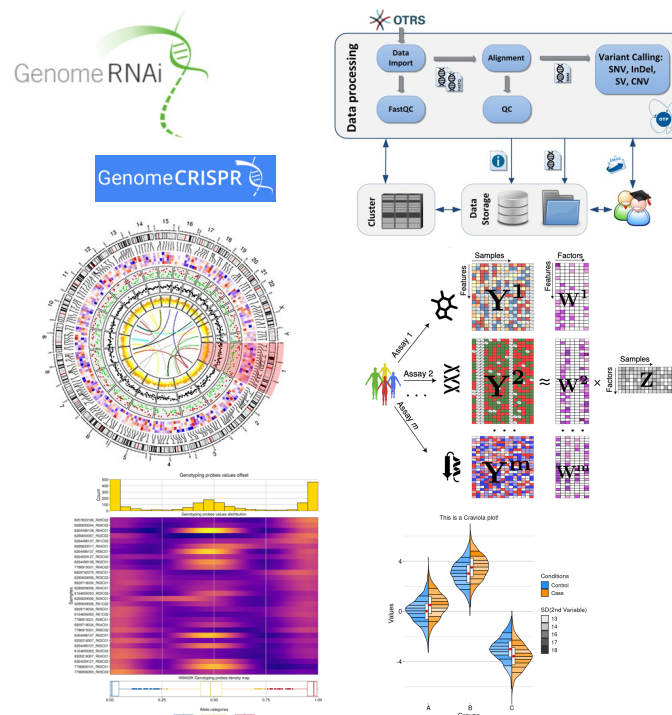
Additional services listed for ELIXIR:

- BiocompR
- methview.qc
- MOFA
- slalom
- LIMIX

E-CRISPR: work on database (improve security, technical improvements.)

Cloud (see additional poster):

- managed Kubernetes (KKP/Kubermatic)
- interaction with GHGA
- ISMS / ISO27001 certification (under way)



## de.NBI Training and education

Will resume training courses in 2025 (2 courses)

## References

1. Heigwer, F. et al. Cell Systems 14:346-262 (2023)
2. Jeong, Y. et al. Brief Bioinf 23:bbac248 (2022)
3. Jeong, H. et al. Nat Biotechnol 41:832-844 (2023)
4. <https://github.com/YoannPa/BiocompR>
5. <https://github.com/YoannPa/methview.qc>
6. <https://github.com/bioFAM/>
7. <https://www.dkfz.de/en/signaling/comptools.html>

## General information on the project

- Paid from de.NBI grant:
- 3 FTE
- Other staff involved:
- 3.5 FTE