HD-HuB

Heidelberg Center for Human Bioinformatics
## General Overview: Training/Outreach & Technology

HD-HuB consortium [1,2,3,4,5,6]

Fkz 031A537A/B/C/D, 031L0101A/D

[1] European Molecular Biology Laboratory, Structural and Computational Biology Unit/Genome Biology Unit, Heidelberg, Germany; [2] Division Signaling and Functional Genomics/ Division Epigenomics and Cancer Risk Factors / Division of Applied Bioinformatics / Division of Theoretical Bioinformatics /Omics / Computational Genomics and Systems Genetics / IT & Data Management Core Facility, German Cancer Research Center (DKFZ), Heidelberg, Germany; [3] Centre for Digital Health, Charité / Berlin. Institute of Health (BIH), Digital Health Center, Berlin, Germany ; [4] Department for Bioinformatics and Functional Genomics / Advanced Biological Screening Facility, & Biomedical Computer Vision Group, BioQuant, Heidelberg University, Heidelberg, Germany; [5] Department of Genetics/Epigenetics, Saarland University, Saarbrucken, Germany; [6] Department of Computational Biology and Applied Algorithmics, Max Planck Institute for Informatics, Saarbrucken, Germany

Short description of HD-HuB
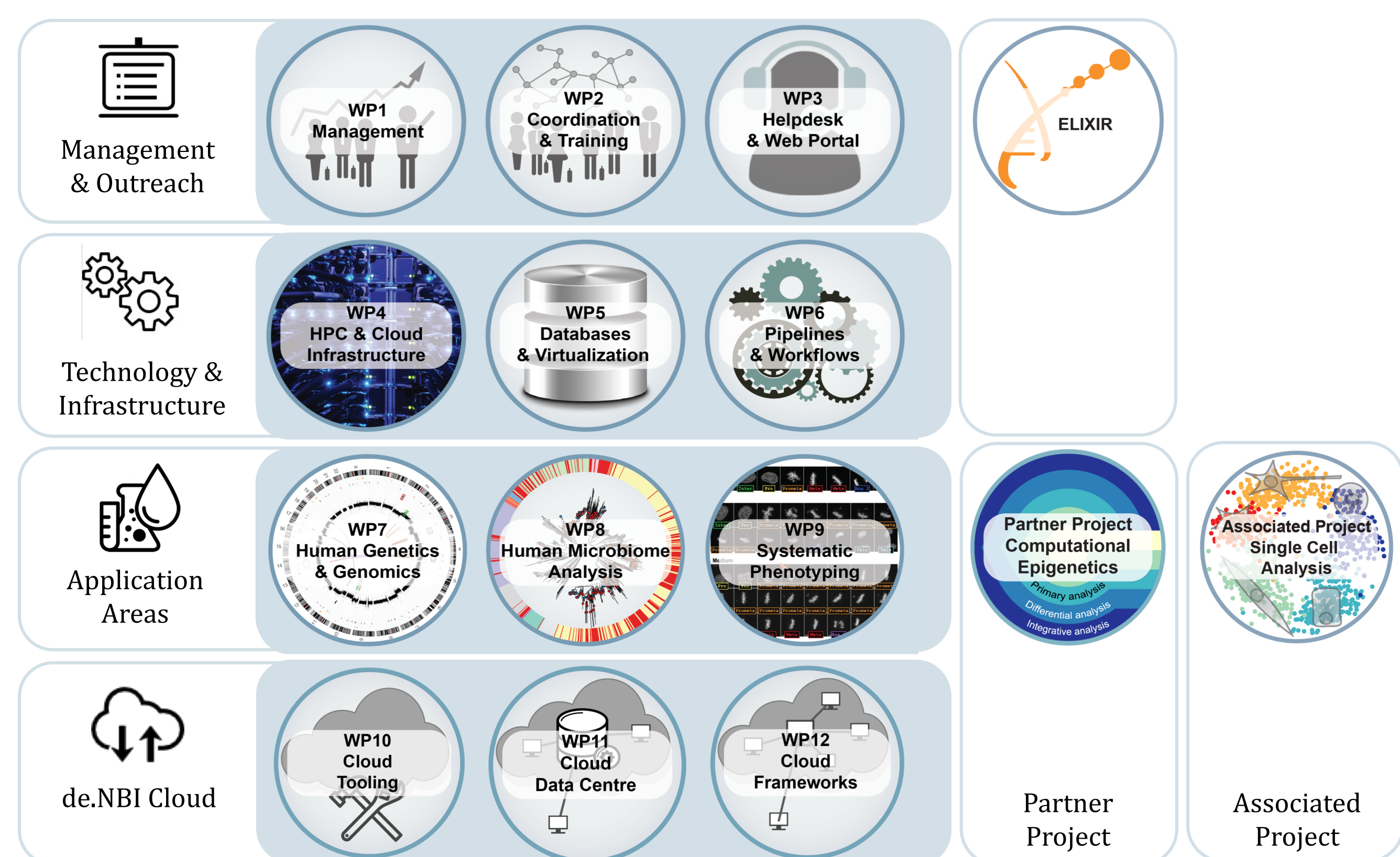

General information on HD-HuB

Who?
HD-HuB connects four established research institutions in Heidelberg and Berlin:
- **European Molecular Biology Laboratory** (EMBL; PIs: P. Bork, J. Korbel, W. Huber, G. Zeller)
- **German Cancer Research Center** (DKFZ; PIs: M. Boutros, I. Buchhalter)
- **Heidelberg University** (PIs: R. Russell, K. Rohr, H. Erfle)
- **Charite / Berlin Institute of Health** (BIH; PI: R. Eils)

The de.NBI-epi partner project consists of research groups from DKFZ (PI: B. Brors), Saarland University (PI: J. Walter) and the MPI for Informatics (PI: T. Lengauer).

Since January 2019, O. Stegle (DKFZ) has been an associated member (for single-cells analysis).

→ ~20 positions (~16 FTEs) and >60 "in kind" contributors (~12 FTEs)
→ Growth despite consolidated funding
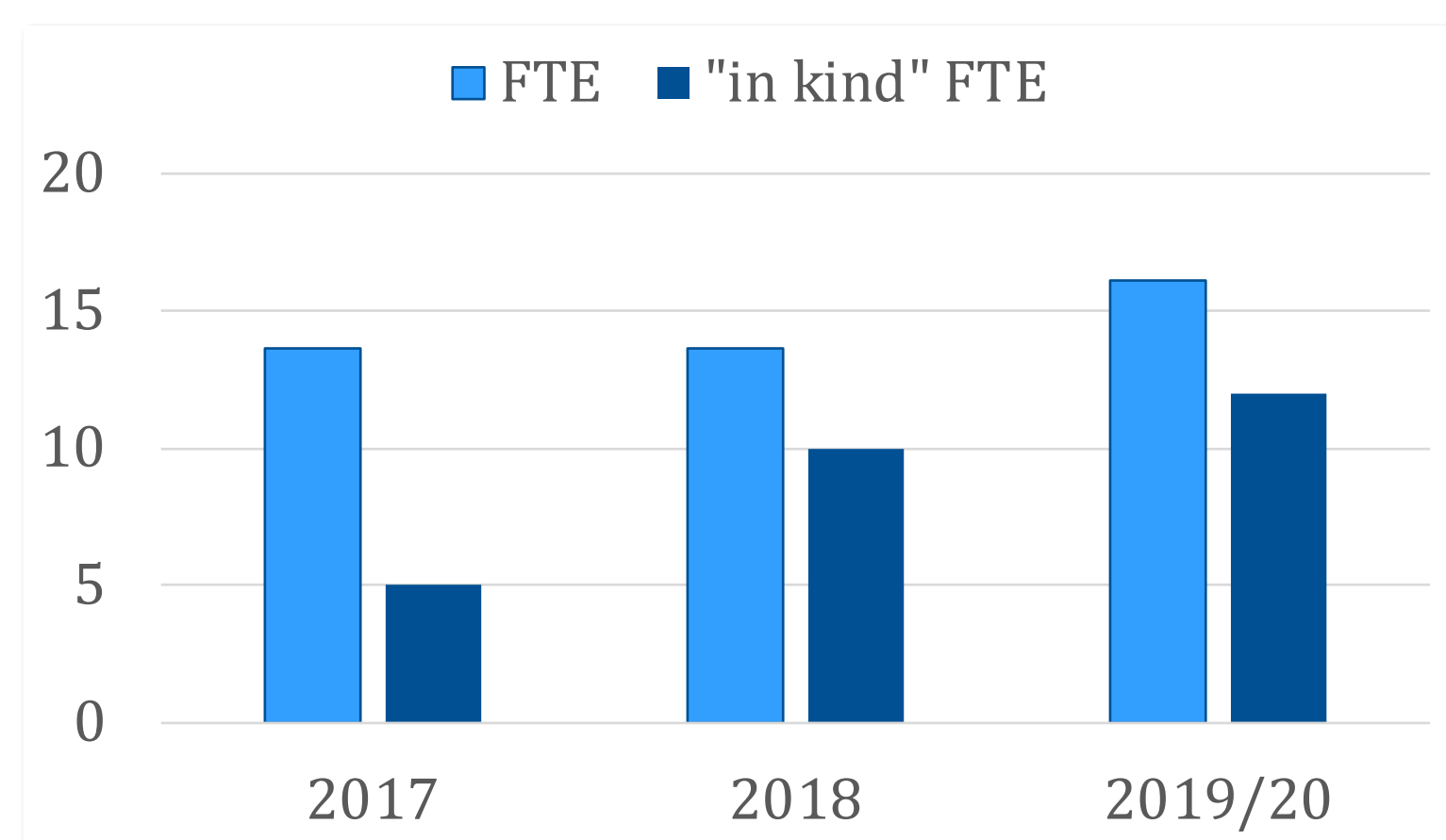
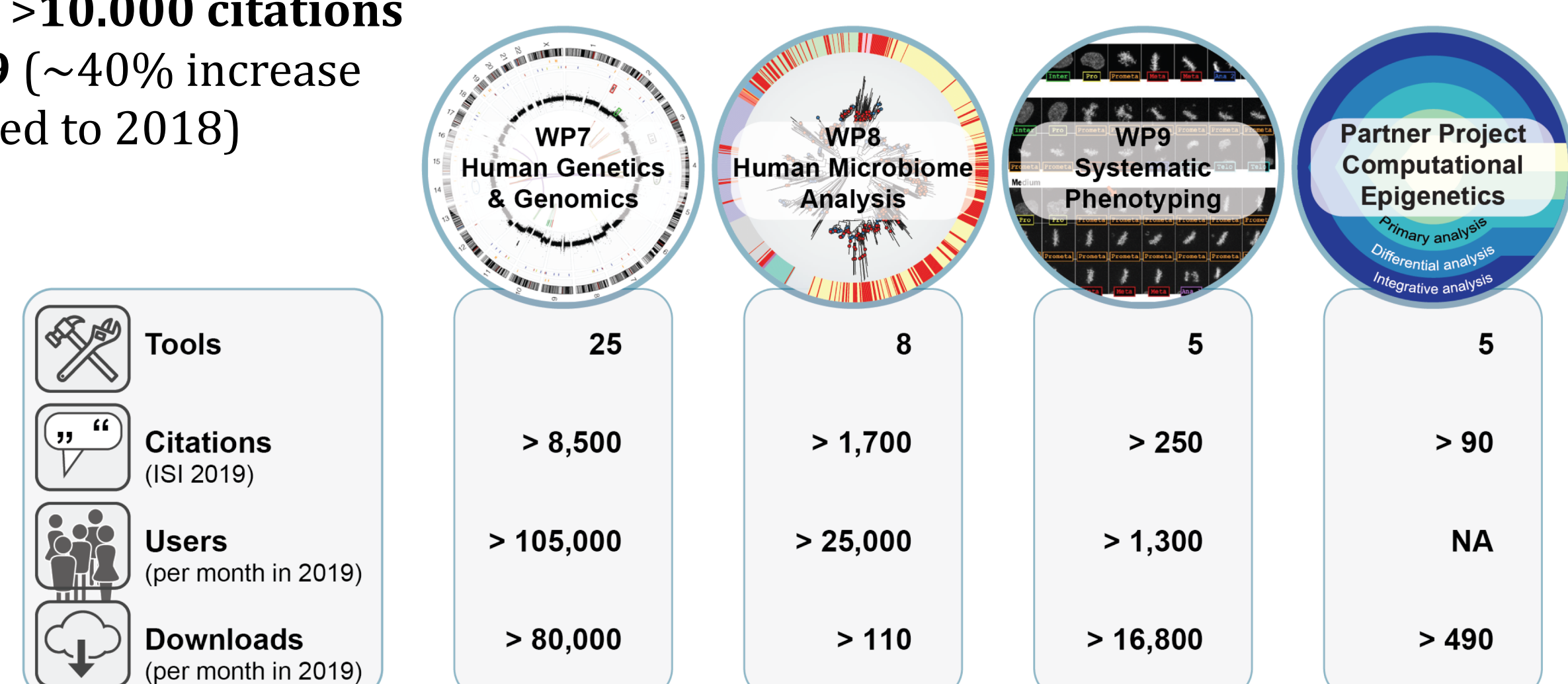### What?
Services for human bioinformatics are focusing on five application areas:
(1) **human genetics and genomics**,
(2) metagenomics and **human microbiome** analysis,
(3) **systematic phenotyping** of human cells,
(4) computational **epigenetics**,
(5) **single-cell** analysis.

Progress Report

- For all services, life cycle management und quality control has been implemented.
- KPI monitoring for all HD-HuB web tools has been re-implemented using Matomo.
- HD-HuB tools are widely used: >1.6 mio users, >1 mio downloads in total in 2019.
- In total, >**10.000 citations in 2019** (~40% increase compared to 2018)

	WP7 Human Genetics & Genomics	WP8 Human Microbiome Analysis	WP9 Systematic Phenotyping	Partner Project Computational Epigenetics
Tools	25	8	5	5
Citations (ISI 2019)	> 8,500	> 1,700	> 250	> 90
Users (per month in 2019)	> 105,000	> 25,000	> 1,300	NA
Downloads (per month in 2019)	> 80,000	> 110	> 16,800	> 490

De.NBI training and education

Title	Date	Location
4th Course on Bioimage Analysis	Dec 2018	Heidelberg
The Carpentries 'Train the trainer' Workshop	Dec 2018	Quilmes, Argentina
Software Carpentry: 'Computational Skills for Life Scientists'	Dec 2018	Quilmes, Argentina
Data Carpentry Workshop	Jan 2019	Heidelberg
Intermediate Linux Command Line and Basic Scripting	Feb 2019	Heidelberg
Interpretation of RNA-Seq and Bisulfite Sequencing Data in Cancer Research	Mar 2019	Heidelberg
Introduction to Python Programming	Apr 2019	Heidelberg
Single-Cell Omics Workshop	May 2019	Heidelberg
Version Control with Git and GitHub	May 2019	Heidelberg
Version Control with Git and GitHub	May 2019	Saarbruecken
Single-Cell RNA-Seq Analysis Workshop	May 2019	Espoo, Finland
Image Processing and Analysis with ilastik	Jun 2019	Heidelberg
CSAMA 2019: Statistical Data Analysis for Genome-Scale Biology	Jul 2019	Bressanone-Brixen, Italy
Microscopy Image Analysis Course	Sep 2019	Heidelberg
MOFA Workshop at the GCB Conference	Sep 2019	Heidelberg
Software Carpentry Workshop	Oct 2019	Heidelberg
Machine Learning using mlr	Nov 2019	Heidelberg

Since 2015, HD-HuB partners have organized and taught in **52 courses** attended by more than **1400 scientists in total** (~3/4 from Germany). Of the attendants, 81% rated these courses excellent or very good.

ELIXIR and outreach activities

HD-HuB has been **involved in** the following **ELIXIR activities:**
- **5 ELIXIR Communities:** (1) Human CNV, (2) Rare Diseases, (3) Galaxy, (4) Federated Human Data, (5) Single Cell Omics Community and (6) ELIXIR-GA4GH
- **2 ELIXIR Platforms:** (1) Tools (Bioconda/ Biocontainers, Galaxy) and (2) Compute platform.
- **2 ELIXIR implementation studies:**
  ELIXIR ID: 2019-hCNV : Human Copy Number Variation
  ELIXIR ID: 2019-Containers: Deploying Reproducible Containers and Workflows Across Cloud Environments
- HD-Hub personal co-leads a cloud work package in the **EOSC Life project**
- A HD-HuB staff member is **deputy training coordinator of ELIXIR-DE**
- Involvement in organization of **ELIXIR conferences and symposia** (together with other ELIXIR nodes) e.g. single RNA-Seq course in Espoo (Finland) and Carpentries Workshops in Germany, Belgium and Greece (see Table)

Title	Date	Location
ELIXIR: Software Carpentry	Jan 2019	Athens, Greece
ELIXIR / The Carpentries Train-the-trainer	Nov 2019	Heidelberg
ELIXIR: The Carpentries Instructor Training (hosted by ELIXIR Sweden)	Apr 2019	Heidelberg
ELIXIR: Carpentry instructor training	Apr 2019	Online
ELIXIR: Data Carpentry Genomics	May 2019	Ghent, Belgium
ELIXIR: Best practises in Open Source Software Registration	May 2019	Ghent, Belgium

Publications

Tool-related publications (2019/2020):
(1) Milanese, Mende et al., Microbial abundance, activity and population genomic profiling with mOTUs2. *Nat Commun.*
(2) Letunic and Bork, Interactive Tree Of Life (iTOL) v4: recent updates and new developments. *Nucleic Acids Res.*
(3) Mende et al., proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. *Nucleic Acids Res.*
(4) Rausch et al., Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. *Bioinformatics.*
(5) Föll et al., Accessible and reproducible mass spectrometry imaging data analysis in Galaxy. *Gigascience.*
(6) Childs et al., Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. *Mol Cell Proteomics.*
(7) Huerta-Cepas et al., eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. *Nucleic Acids Res.*
(8) Yakneen et al., Butler enables rapid cloud-based analysis of thousands of human genomes. *Nat Biotechnol.*

Selected Research Publications using HD-HuB tools (2019/2020):
(9) Pan-Cancer Analysis of Whole Genomes. *Nature Special Issue*, containing 6 articles with HD-HuB contributions
(10) Wirbel, Pyl et al., Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. *Nat Med.*
(11) Zhan et al. MEK inhibitors activate Wnt signalling and induce stem cell plasticity in colorectal cancer. *Nat Commun.*