

# GCBN

# German Crop BioGreenformatics Network at the IPK Gatersleben

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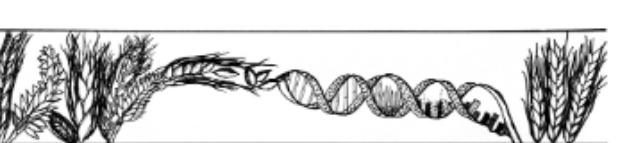
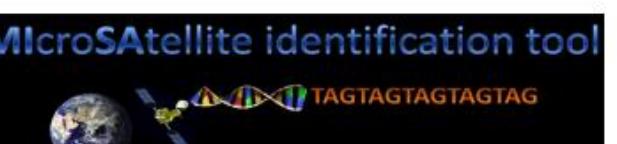
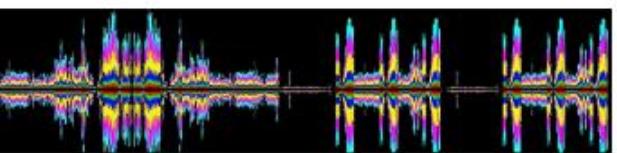
Sebastian Beier, Daniel Arend, Patrick König, Stephan Weise, Markus Oppermann, Matthias Lange, Uwe Scholz

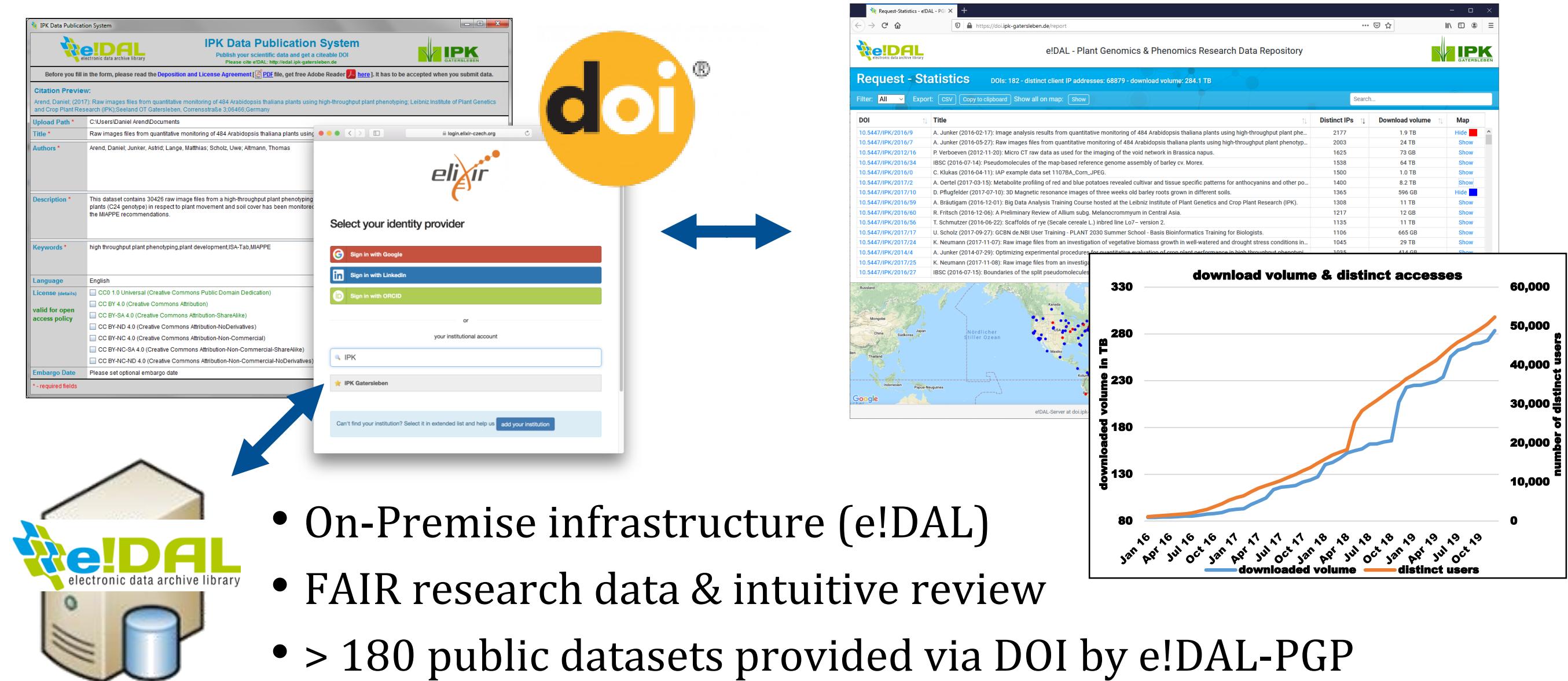
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Corrensstraße 3, 06466 Seeland, Germany

# Short project description

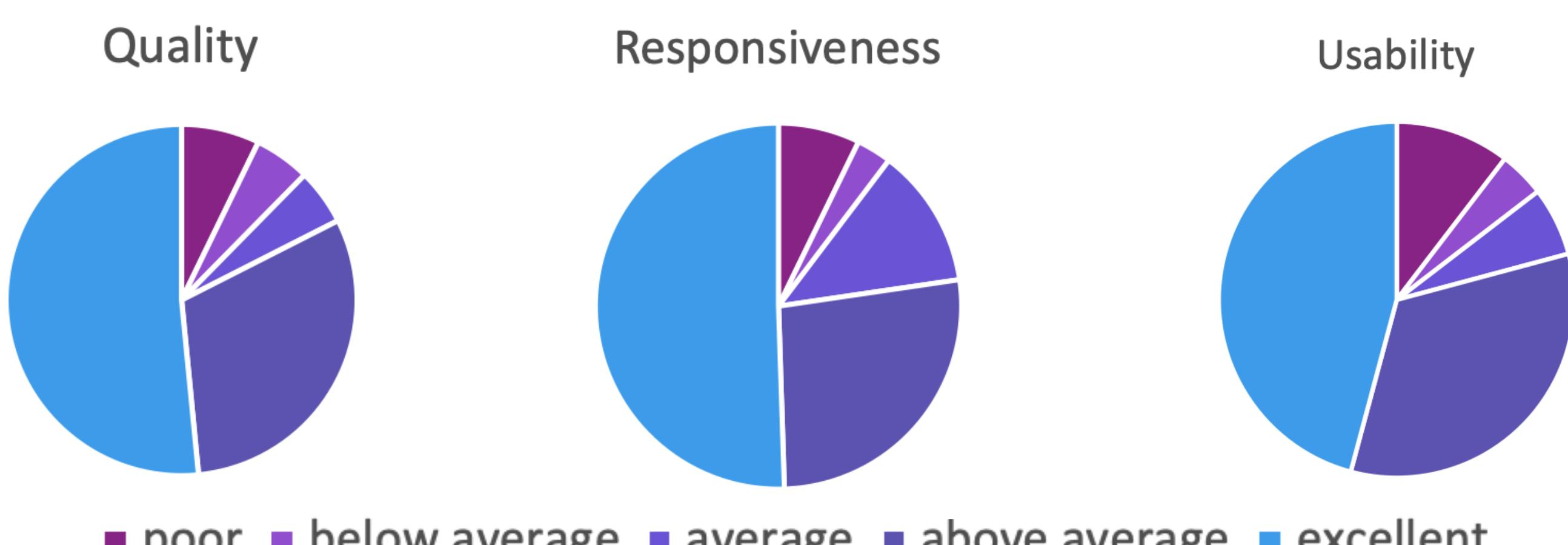
The service centre **GCBN** - German Crop BioGreenformatics Network – provides services for plant bioinformatics, like tailored plant-specific data and infrastructure. GCBN consists of the Leibniz Institute of Plant Genetics and Crop Plant Research in Gatersleben (IPK, BIT, Uwe Scholz), the Helmholtz Center Munich (HMGU, PGSB, Klaus Mayer) and Forschungszentrum Jülich (FZJ, IBG-2 Plant Sciences, Björn Usadel). The main service domains are: (1) **transparent access to germplasms and germplasm metadata**, (2) **improved workflows for plant gene annotation**, and (3) **bridging of multiple genotypes to phenotypes**. As GCBN partner the IPK Gatersleben contributes to the objectives (1) and (3).

de.NBI services provided by IPK Gatersleben

- Web Applications:
    - Crop Analysis Tool Suite - CATS
  - Databases:
    - Genebank Information System - GBIS
    - EURISCO – Database
  - e!DAL – Plant Genomics & Phenomics Research Data Repository



# User feedback for all GCBN services



The service unit GCBN collected user feedback for all offered services using the central de.NBI survey tool environment. As of December 2019, 97 responses have been received. This represents around 5% of all responses collected (2090 in total). The relatively small service unit GCBN offered 10 services (for de.NBI the total number in December 2019 was 131). In relation to the number of all de.NBI services offered, the number of responses collected is comparable (5% vs. 8%).

**The overall user satisfaction of 4.1 (max. 5) is considered a sign that the GCBN services are of high quality**

# General information on the project

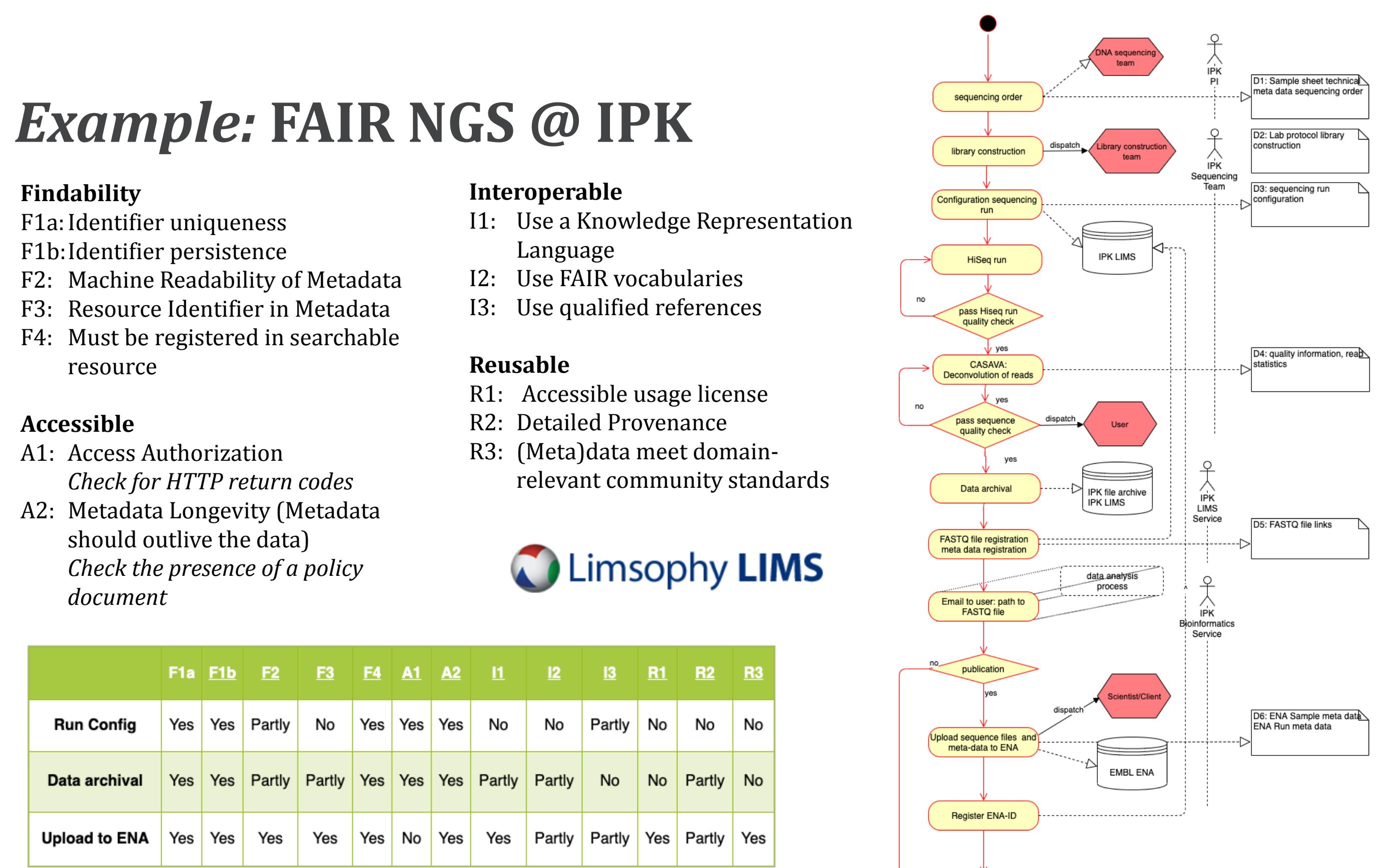
- Since Nov 2019 (**2 FTEs**) financed by de.NBI
  - Other staff involved: estimated **3 FTE**:
    - **1.5 scientists** §
    - **1.5 technicians** #

§ **0.2 FTE** PI (U. Scholz)  
**0.4 FTE** Co-PI & database management (M. Lange)  
**0.5 FTE** scientist EURISCO  
**0.1 FTE** scientist GBIS  
**0.3 FTE** scientist e!DAL/PGP

# **1.0 FTE** linux and network administrator  
**0.5 FTE** database management and HSM

# Progress report

- FAIR-IPK: Implementation of  BrAPI for IPK plant genetic resources
  - Extension of the GALAXY infrastructure at IPK
  - Preparation of DOI assignment to IPK Genebank accessions
  -  elixir activities especially in the Plant Community
    - Contribute to the MIAPPE 1.1 standard
    - ELIXIR implementation study FONDUE:  
FAIR-ification of Plant Genotyping Data and its linking to Phenotyping using ELIXIR Platforms
    - Application of EURISCO as ELIXIR Deposition Database



**de.NBI training, education and symposia**



# Publications (since 2019)

**Mathias Wilhelm**  
*Technical University of Munich, Germany*

**Doris Wedlich**  
*Karlsruhe Institute of Technology, Germany*

- Beier S, Ulpinnis C, Schwalbe M, Münch T, Hoffie R, Koeppel I, Hertig C, Budhagatapalli N, Hiekel S, Pathi K M, Hensel G, Grosse M, Chamas S, Gerasimova S, Kumlehn J, Scholz U, Schmutzer T. Kmasks - a tool for assessing complex sequence space in plant species. *Plant J.* (2019) accepted. dx.doi.org/10.1111/tpj.14645

Bolger A M, Poorter H, Dumschott K, Bolger M E, Arend D, Osorio S, Gundlach H, Mayer K F, Lange M, Scholz U, Usadel B. Computational aspects underlying genome to phenotype analysis in plants. *Plant J.* 97 (2019) 182-198. dx.doi.org/10.1111/tpj.14179

Ghaffar M, Schüler D, König P, Arend D, Junker A, Scholz U, Lange M. Programmatic access to FAIRified digital plant genetic resources. *J. Integr. Bioinform.* 16 (2019) 20190060. dx.doi.org/10.1515/jib-2019-0060

Mascher M, Schreiber M, Scholz U, Graner A, Reif J C, Stein N. Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. *Nat. Genet.* 51 (2019) 1076-1081. dx.doi.org/10.1038/s41588-019-0443-6

Mayer G, Quast C, Felden J, Lange M, Prinz M, Pühler A, Lawerenz C, Scholz U, Glöckner F O, Müller W, Marcus K, Eisenacher M. A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. *Brief. Bioinform.* 20 (2019) 1215-1221. dx.doi.org/10.1093/bib/bbx140

Milner S G, Jost M, Taketa S, Mazón E R, Himmelbach A, Oppermann M, Weise S, Knüppfer H, Basterrechea M, König P, Schüler D, Sharma R, Pasam R K, Rutten T, Guo G, Xu D, Zhang J, Herren G, Müller T, Krattinger S G, Keller B, Jiang Y, González M Y, Zhao Y, Habekuß A, Färber S, Ordon F, Lange M, Börner A, Graner A, Reif J C, Scholz U, Mascher M, Stein N. Genebank genomics highlights the diversity of a global barley collection. *Nat. Genet.* 51 (2019) 319-326. doi.org/10.1038/s41588-018-0266-x

Monat C, Padmarasu S, Lux T, Wicker T, Gundlach H, Himmelbach A, Ens J, Li C, Muehlbauer G J, Schulman A H, Waugh R, Braumann I, Pozniak C, Scholz U, Mayer K F X, Spannagl M, Stein N, Mascher M. TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. *Genome Biol.* 20 (2019) 284. dx.doi.org/10.1186/s13059-019-1899-5

Selby P, Abbeloos R, Backlund J E, Basterrechea Salido M, Bauchet G, Benites-Alfaro O E, Birkett C, Calaminos V C, Carceller P, Cornut G, Vasques Costa B, Edwards J D, Finkers R, Yanxin Gao S, Ghaffar M, Glaser P, Guignon V, Hok P, Kilian A, König P, Lagare J E B, Lange M, Laporte M-A, Larmande P, LeBauer D S, Lyon D A, Marshall D S, Matthews D, Milne I, Mistry N, Morales N, Mueller L A, Neveu P, Papoutsoglou E, Pearce B, Perez-Masias I, Pommier C, Ramírez-González R H, Rathore A, Raquel A M, Raubach S, Rife T, Robbins K, Rouard M, Sarma C, Scholz U, Sempéré G, Shaw P D, Simon R, Soldevilla N, Stephen G, Sun Q, Tovar C, Uszynski G, Verouden M, The BrAPI consortium. BrAPI—an application programming interface for plant breeding applications. *Bioinformatics* 35 (2019) 4147-4155. dx.doi.org/10.1093/bioinformatics/btz190

Wibberg D, Batut B, Belmann P, Blom J, Glöckner F, Grüning B, Hoffmann N, Kleinböltig N, Rahn R, Rey M, Scholz U, Sharan M, Tauch A, Trojahn U, Usadel B, Kohlbacher O. The de.NBI / ELIXIR-DE training platform – Bioinformatics training in Germany and across Europe within ELIXIR [version 1; peer review: awaiting peer review]. *E1000Research* 8 (2019) dx.doi.org/10.12688/e1000research.20244.1