



Heidelberg Center for Human Bioinformatics HD-HuB **Metagenomics**

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Human Microbiome

Analysis

Short description of the project

The metagenomics work package of the Heidelberg Center for Human Bioinformatics (HD-HuB) aims to provide **state-of-the-art computa-tional** tools and services for human microbiome research, a field which is rapidly growing and heavily relying on bioinformatics analyses.

Progress report

Pre

Software tools were improved and extended, in particular their robustness, interoperability, documentation and user support enabled by



We maintain, further develop, and support methods that are tailored for clinical microbiome studies which help to define the role of human microbiomes in host health and disease. We also offer **training and user support** in metagenomic data analysis.

> Meta-data (external factors)

de.NBI services

nt		
a	Raw shotgun	Reference
at	metagenomic	genome
3 Ū	read data	sequences

EMBL Microbiome Tools

MOCAT

m©TUs

eggNOG

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microbiome association testing and modelling SIAMCAT

de.NBI funding. As examples of improved HD-HuB metagenomics tools,





mOTUs2.5 was recently released and published Algorithm and database resulted in high-precision taxonomic profiling for known species (as evaluated on <u>CAMI</u> data, see Fig.) and reference genome is not available (as benchmarked With mOTUs2.5 we also participated in the CAMI2





HD-HuB provides meta-genomics analysis tools addressing a diversity of tasks encountered in a typical human microbiome research project.

A preprint describing **SIAMCAT** was recently released [2]. The tool (<u>siamcat.embl.de</u>) enables novice users to easily run machinelearning analyses on metagenomic data to extract microbial disease biomarkers as demonstrated in a large-scale metaanalysis of published data sets (see Fig.). New versions of iTOL [3], eggNOG [4] and proGenomes [5] have also been published in





Recently specI functionality was migrated to the **proGenomes database**, which is now also offered as a new de.NBI/HD-HuB service.

Tool	Avg. users / year	Citations / year
iTol	>215 000	1016
eggNOG	>45 000	470
iPATH	>11 000	32
Enterotyping	>5 000	454
mOTUs	>3 000	46
MOCAT	>3 000	34
proGenomes	>1 800	14
SIAMCAT	>450	NA

These tools serve a large and fast-growing user community. In 2019 more than 280,000 visitors were counted (cumulated monthly visits). In total, these **tools were** cited >2,000 times in **2019**, an increase of ~38% compared to 2018.

Pub	licati	ons

2019 and 2020.

1] mOTUs2:	Milanese, Mende et al., <i>Nat. Commun.</i> 2019
2] SIAMCAT v1:	Wirbel et al., <i>bioRxiv preprint</i> 2020
3] iTOL v4:	Letunic and Bork, <i>Nucleic Acids Res.</i> 2019
4] proGenomes2:	Mende et al., <i>Nucleic Acids Res.</i> 2020
5] eggNOG v5.0:	Huerta-Cepas et al., <i>Nucleic Acids Res.</i> 2019





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