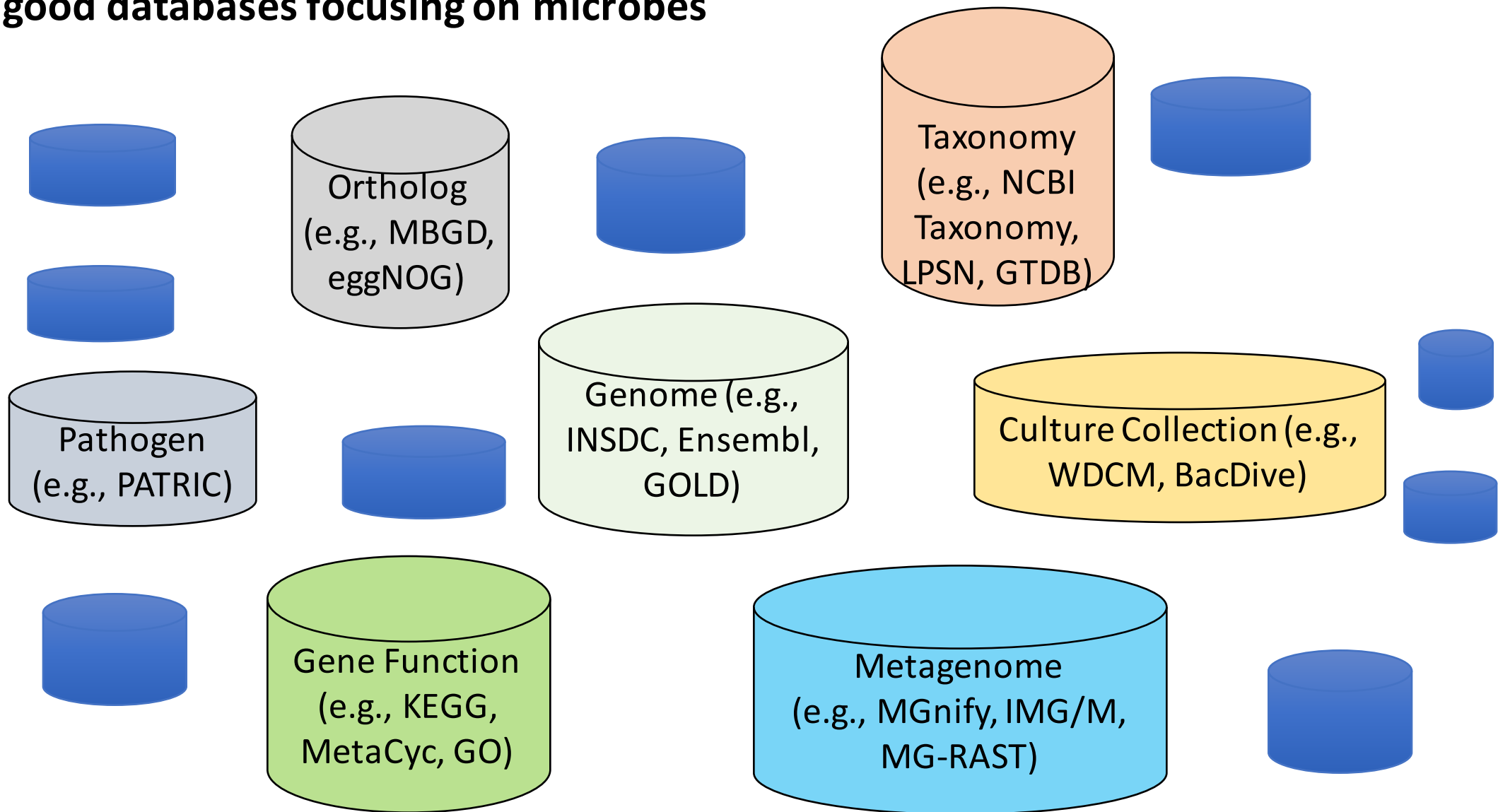


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4. 東京工業大学生命理工学院

Many good databases focusing on microbes



Integration of data is necessary especially for beginners

<https://microbedb.jp/>



MicrobeDB.jp

Integrating and representing genome, metagenome, taxonomy resources and the analysis datasets with Semantic Web Technologies.

[Learn more >>](#)

Features

Data sources of MicrobeDB.jp ver. 3

Metagenome and Microbes Environmental Ontology 2401

Taxonomy 129342

Ortholog Groups 4203173

Microbial Phenotype Ontology 277

Genome and Metagenome Sample 1920339

Culture collections in Japan 38414

Pathogenic Disease Ontology 387

Human Microbiome Associated Disease Ontology 305

KEGG Orthology 22421

Last Modified date: 2020-02-16

🔍 Keyword Search

MicrobeDB.jp provides a keyword search function with a simple interface. The keyword search gives the user free-text access to the literal fields of all RDF/OWL resources on MicrobeDB.jp. Click

Text search

MicrobeDB.jp version 3 data

Data category	Data sources	Ontologies
Genome Metadata	INSDC BioSample, NCBI Assembly report	MEO, HMADO, NCBITAX
Ortholog	MBGD	ORTH
Culture collection	JCM (RDF-Portal)	MCCV, MPO, MEO, PDO, CSSO
Culture collection	NBRC (RDF-Portal)	MCCV, MPO
Metagenome	INSDC DRA	NCBITAX, KEGG Orthology
Metagenome metadata	INSDC BioSample	MEO, HMADO, SIO

MicrobeDB.jp version 3 data

Data category	Number of entry
Prokaryote genome metadata (from RefSeq)	290,208 genomes
Culture collection strain metadata from JCM/NBRC (from RDF-Portal)	38,414 strains
Microbiome metadata (from INSDC BioSample)	1,631,611 samples
Microbiome taxonomic composition data	96,766 samples
Microbiome functional composition data	4,784 samples

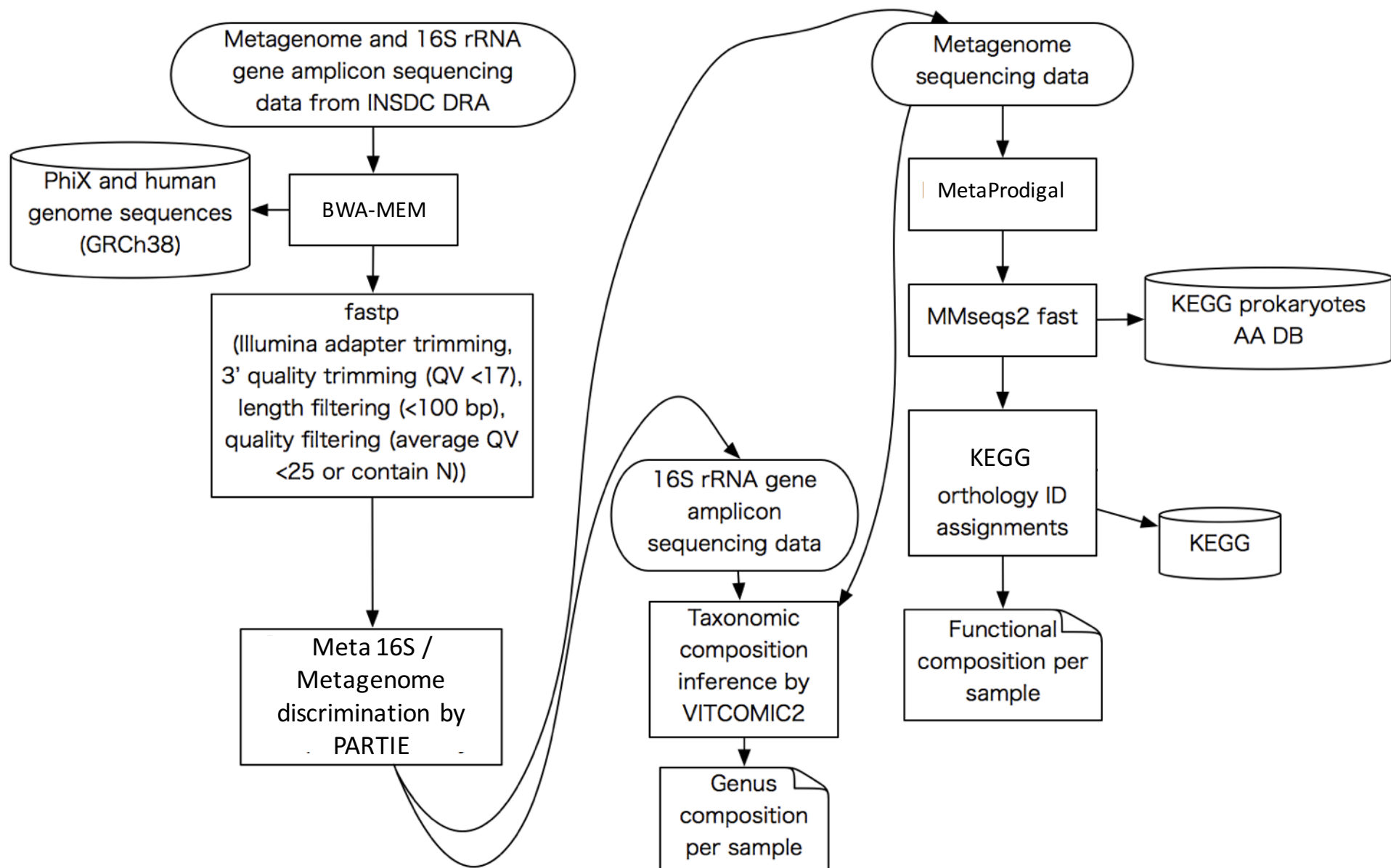
Version2と比べて、ゲノムは約20倍、メタゲノムは約10倍

INSDC DRA/ERA/SRAで公開されたマイクロバイームサンプル数 (2020年8月時点)

	サンプル数
マイクロバイーム	約 2,300,000
ヒト	約 650,000
マウス	約 120,000
土壌	約 280,000
水環境	約 240,000
人工環境	約 160,000
植物共生	約 150,000

230万サンプルはヒトや土壌等マイクロバイームサンプルの総数

MeGAP3 (MetaGenome Analysis Pipeline for MicrobeDB.jp ver. 3)



Search and compare microbiome samples from soil

MicrobeDB.jp
Home Document Analysis - e.g. hot spring, Enterococcus faecalis, psbA Search Sign Up Sign In

facet_metagenome_public 1531

hasMetagenomeAnalysis 8531

taxonomy

function 119

Search id ...

attribute name

Search attribute name ...

attribute value

Search attribute value ...

hasMEO (Text)

soil x

hasMEO: Component

Component for environment 8102

hasMEO: Env

Environment for microbes 7117

taxonomy (Text)

Search taxonomy terms ...

taxonomy

root 8531

hasHostTaxonomy (Text)

Search HostTaxonomy...

hasHostTaxonomy

root 1410

pH

0 14

Temperature

-100 150

HMADO (Text)

Search HMADO terms ...

HMADO

Human microbiome associated 87 disease

HostEthnicity

Search HostEthnicity ...

Metagenomic samples

8531 results found in 155ms

hasMetagenomeAnalysis: taxonomy x hasMEO (Text): soil x Clear all filters

Previous **1** 2 3 4 ... Next

10 Select All Deselect All

Select	MDB SampleID	title	organism.name	organism.identifier	BioProjectID	SRAID	SRRID	BioSampleID	publishedDate
Remove	SAMD00003586	Urease gene-containing Archaea dominate autotrophic ammonia oxidation in two acid soils	soil metagenome	410658	PRJDB1924	DRS001577	DRR002212	SAMD00003586	2012-07-04T00:00:00.000
Remove	SAMD00009749	Active ammonia oxidizers in an acid soil are phylogenetically closely related to neutrophilic Nitrososphaera viennensis	soil metagenome	410658	PRJDB2274	DRS012638	DRR014314	SAMD00009749	2013-10-30T00:00:00.000
Add	SAMEA1559038	RMR_Sample_16S	soil metagenome	410658	PRJEB3363	ERS184934	ERR186224	SAMEA1559038	2012-11-01T00:00:00.000
Remove	SAMEA1559037	RMR_Sample_16S	soil metagenome	410658	PRJEB3363	ERS184936	ERR186222	SAMEA1559037	2012-11-01T00:00:00.000
Add	SAMEA1559036	RMR_Sample_16S	soil metagenome	410658	PRJEB3363	ERS184935	ERR186225	SAMEA1559036	2012-11-01T00:00:00.000
Add	SAMEA1559035	RRR_Sample_16S	soil metagenome	410658	PRJEB3363	ERS184933	ERR186223	SAMEA1559035	2012-11-01T00:00:00.000
Remove	SAMD00018981	MIMARKS Survey related sample from rhizosphere metagenome	rhizosphere metagenome	939928	PRJDB2986		DRR021946 DRR021947 DRR021948	SAMD00018981	2015-01-16T00:00:00.000
Add	SAMN02054434	MIMARKS Survey related sample from Soil metagenome		410658	PRJNA198445	SRS416341	SRR835396 SRR835397 SRR835398	SAMN02054434	2013-04-23T00:00:00.000
Add	SAMN02054433	MIMARKS Survey related sample from Soil metagenome		410658	PRJNA198445	SRS416342	SRR835399 SRR835400 SRR835401	SAMN02054433	2013-04-23T00:00:00.000
Add	SAMN02054432	MIMARKS Survey related sample from Soil metagenome		410658	PRJNA198445	SRS416340	SRR835402 SRR835403 SRR835404	SAMN02054432	2013-04-23T00:00:00.000

Metagenome sample comparison analysis Compare

Taxonomic composition (bar) Taxonomic composition (heatmap) Diversity index Hierarchical clustering PCoA Functional composition (bar) Functional composition (heatmap)

Samples Taxonomic Composition

Composition rate

SampleID SAMD00003586 SAMD00009749 SAMD00018981 SAMEA1559037

- unclassified Anaerolineaceae
- Gemmatimonas
- unclassified Xanthomonadac...
- unclassified Veillonellaceae
- Stenotrophomonas
- Geobacter
- unclassified Pseudomonadac...
- Sideroxydans
- unclassified Bradyrhizobiaceae
- Azomonas
- unclassified Ignivibacteriaceae
- Nitrospira
- Geothrix
- unclassified Rhodospirillaceae
- unclassified Acetobacteraceae
- Thermosporothrix
- unclassified Planctomycetac...
- unclassified Sinobacteraceae

MicrobeDB.jp ver. 3の使い方

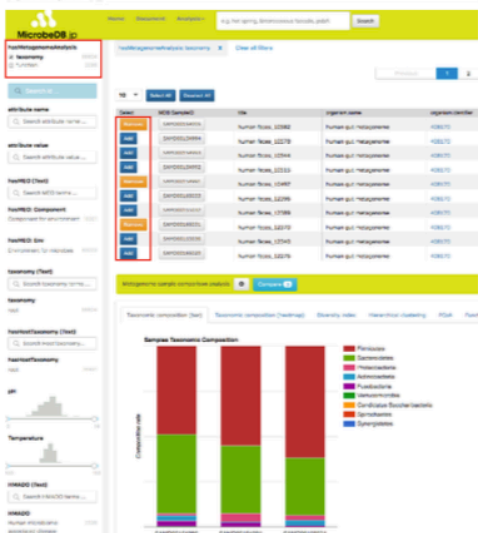


マイクロバイオームサンプルの絞り込み検索

1. Webブラウザで下記にアクセス
<https://microbedb.jp>
2. 最上段のAnalysis →
Metagenomic samples を選択

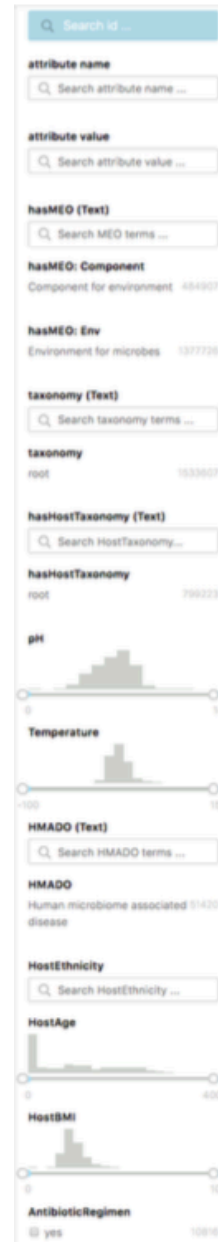


3. サンプル (BioSample) の絞り込み検索画面が表示
4. 左側のファセット検索用の選択窓でサンプルを絞り込む (詳細は裏ページ)



5. 絞り込んだサンプルのうち、左上のhasMetagenomeAnalysisでtaxonomy (系統組成) かfunction (遺伝子機能組成) を選択し、それらのデータが計算済みのサンプルのみ表示する
6. サンプルリストから、比較解析したいサンプルを複数選択し、Compareを押す
7. 系統組成等のグラフが表示される

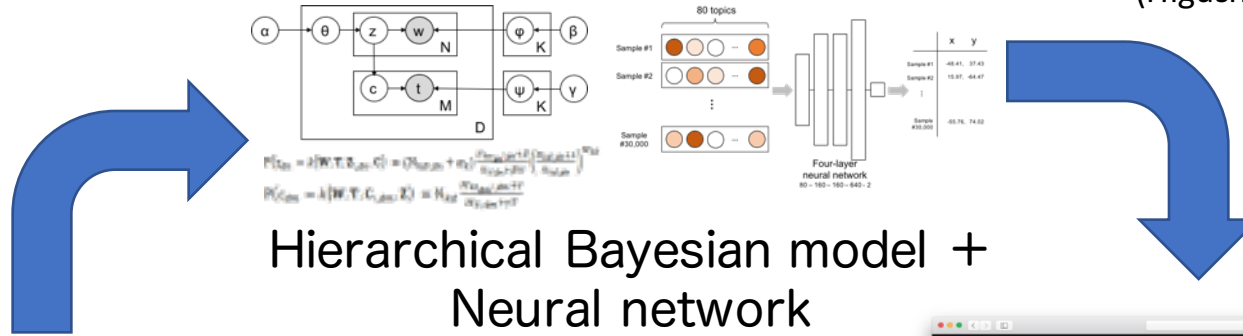
ファセット検索用の検索窓の説明



1. Search id: BioSample IDでサンプルを検索
2. attribute name: RDFの述語名で検索 (玄人向け)
3. attribute value: RDFの目的語で検索 (玄人向け)
4. hasMEO (Text): 微生物の生息環境オントロジーであるMEOに対するテキスト検索 (例: soil)
5. hasMEO: Component: MEOの階層構造からMEO Componentクラスを選択して検索
6. hasMEO: Env: MEOの階層構造からMEO Environmentクラスを選択して検索
7. taxonomy (Text): メタゲノムのNCBI Taxonomyに対するテキスト検索 (例: soil metagenome)
8. taxonomy: NCBI Taxonomyのクラスを選択して検索
9. hasHostTaxonomy (Text): 宿主の系統についてNCBI Taxonomyをテキスト検索 (Homo sapiens)
10. hasHostTaxonomy: 宿主の系統についてNCBI Taxonomyのクラスを選択して検索
11. pH: サンプルが由来した環境のpHを範囲指定
12. Temperature: サンプルが由来した環境の温度を範囲指定
13. HMADO (Text): 微生物が関係するヒトの病気の病名オントロジーであるHMADOに対するテキスト検索 (例: cancer)
14. HMADO: HMADOのクラスを選択して検索
15. HostEthnicity: サンプルが由来したヒトのethnicityに対するテキスト検索 (例: Japanese)
16. HostAge: サンプルが由来した宿主のageを範囲指定
17. HostBMI: サンプルが由来した宿主のBMIを範囲指定
18. AntibioticRegimen: サンプルが由来したヒトの抗生物質投与の有無を選択

Latent Environment Allocation (LEA)

(Higashi K et al. 2018, PLoS Comp Biol)



Hierarchical Bayesian model +
Neural network

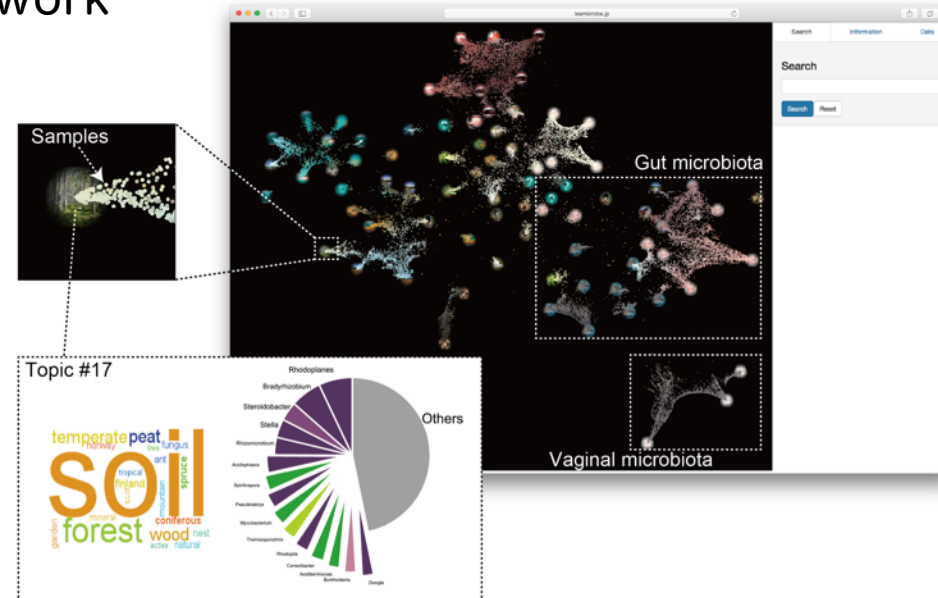
<http://leamicrobe.jp/>

Natural language data related to environments

Taxonomic composition calculated from DNA sequence

MicrobeDB.jp

Study Detail	
Title	Metatranscriptomic analysis for eu...
Study Type	Metatranscriptomics
Abstract	To explore the eukaryotic functiona... enriched forest soil sample. A total...
Description	The aim of this study is the explor... approach. This method is widely a...
Center Name	AIST



Visualization of microbial
community compositions with
environment topics



How to map your metagenome data on LEA

(Mori H et al. 2018, BMC Syst Biol)

VITCOMIC2
(<http://vitcomi.org/>)

LEA
(<http://leamicrobe.jp/>)

