

CLC Genomics Workbench Premiumを利用した メタトランスクリプトーム解析

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次世代シーケンス解析用ソフトウェア

◆ リシーケンシング解析

- ・ リファレンスゲノムへのマッピング
- ・ 変異検出

◆ トランスクリプトミクス解析

- ・ RNA-seq解析
- ・ small RNA解析

◆ エピゲノミクス解析

- ・ ChIP-seq解析
- ・ バイサルファイトシーケンス解析

◆ De Novo シーケンス解析

- ・ De Novo Assembly
- ・ BLAST解析

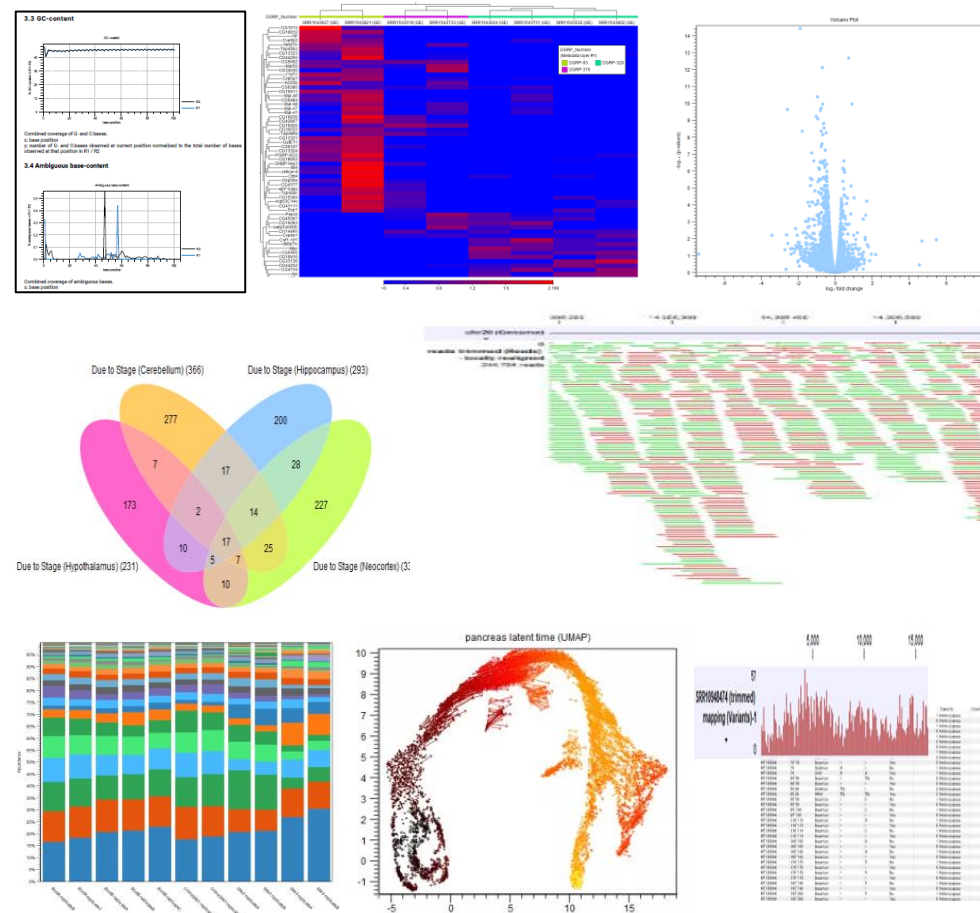
◆ 菌叢解析

◆ ゲノムフィニッシング解析

◆ シングルセル解析

◆ 超高速変異解析

} Premium版 限定機能



各種データベースのダウンロード

リードのインポート、トリミング、メタデータの付加

データに含まれる種の抽出

抽出した種に関するデータベースの作成

GOエンリッチメント解析、パスウェイ解析

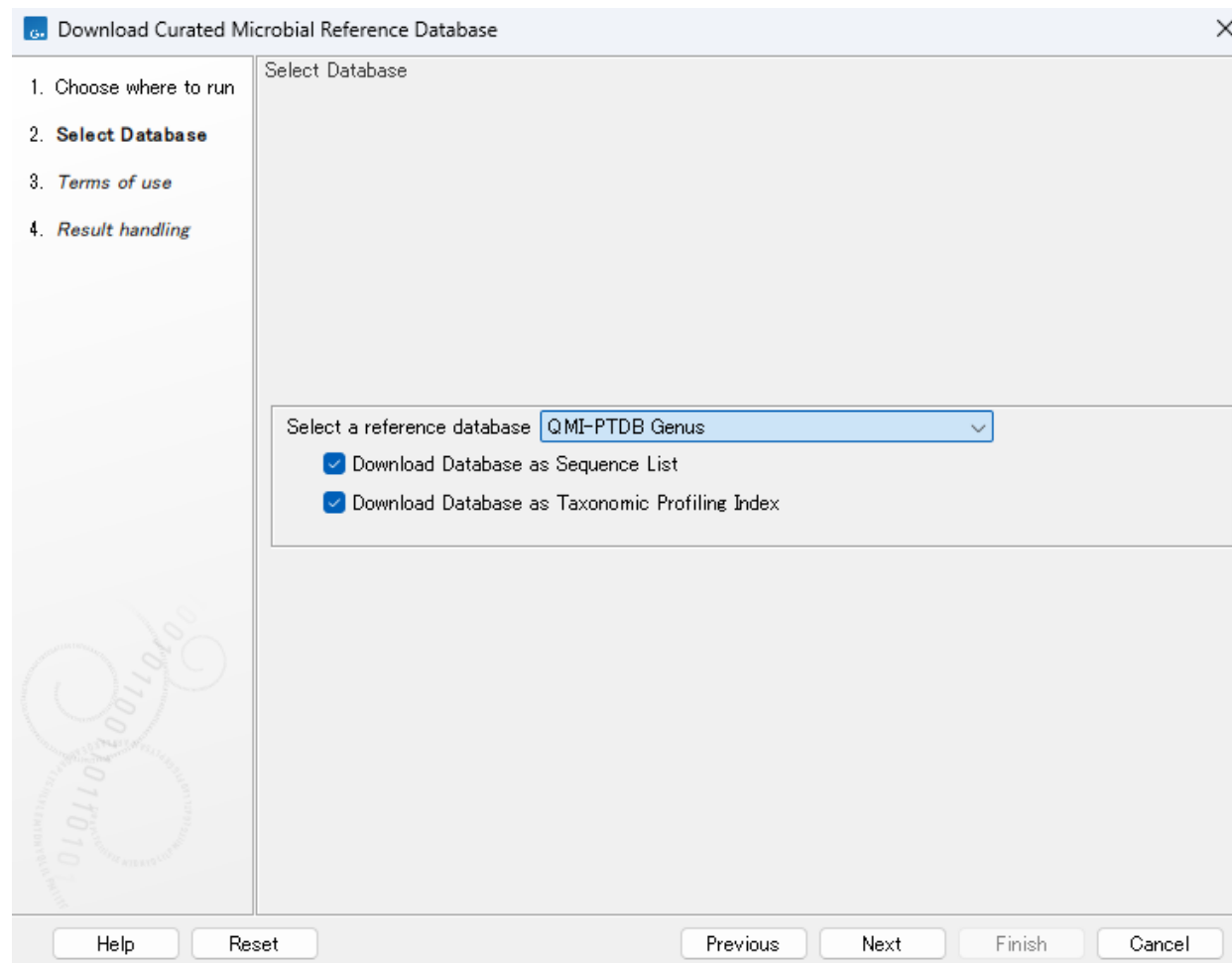
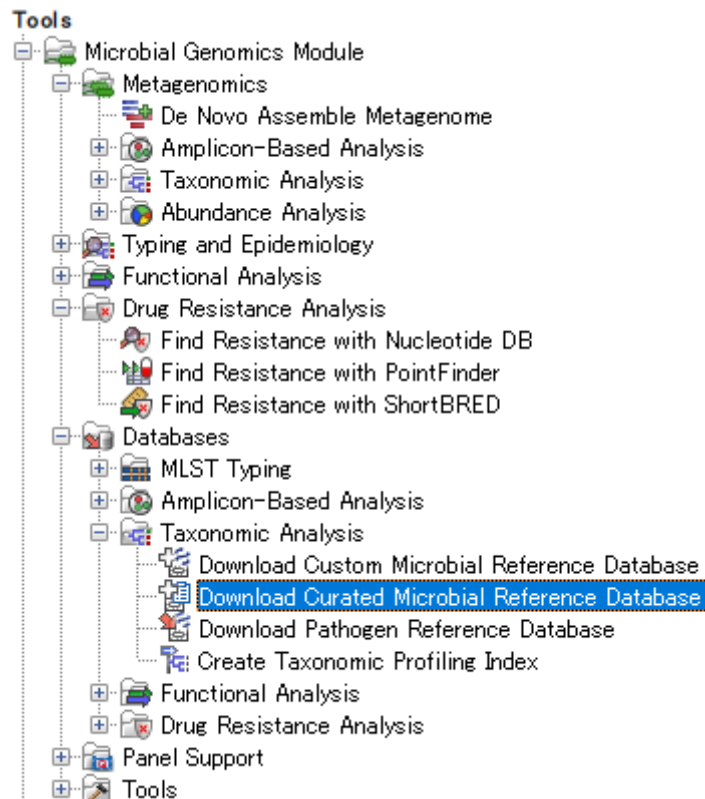
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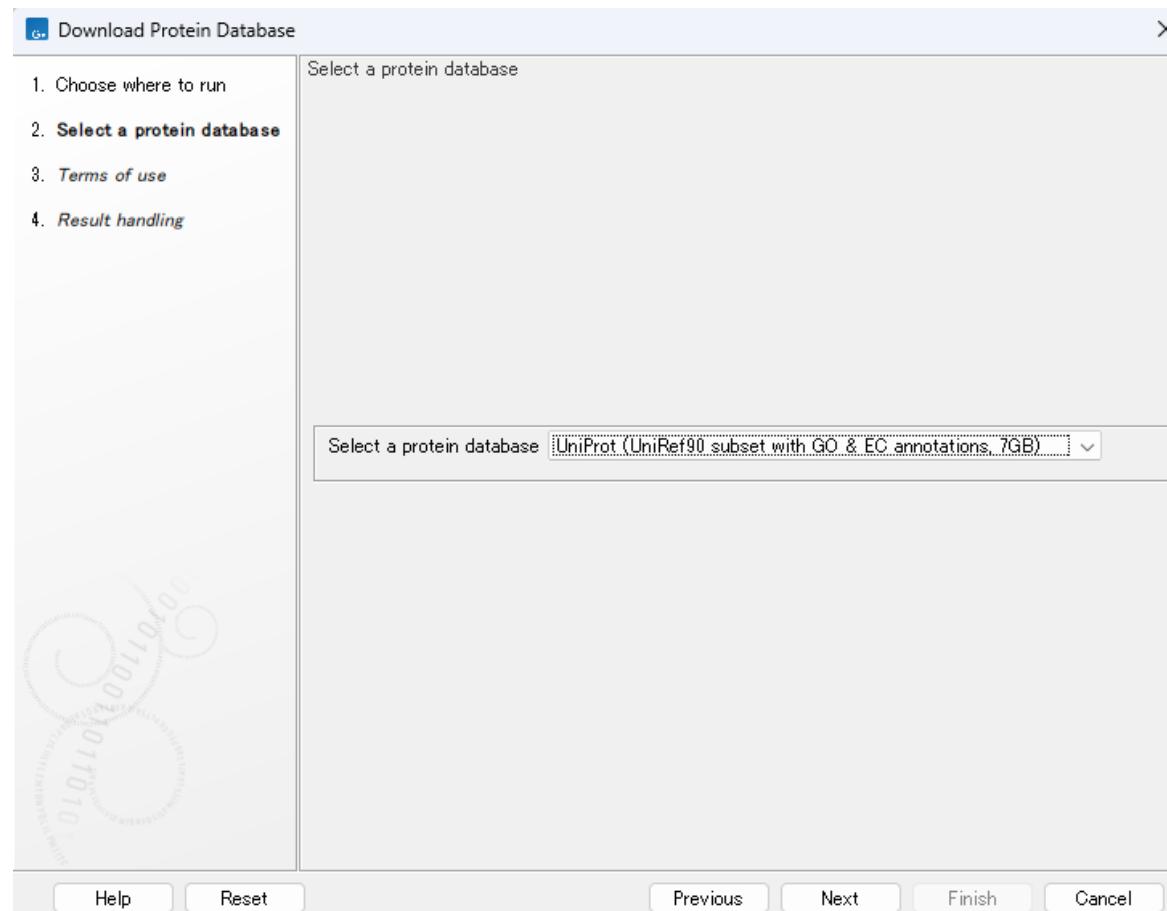
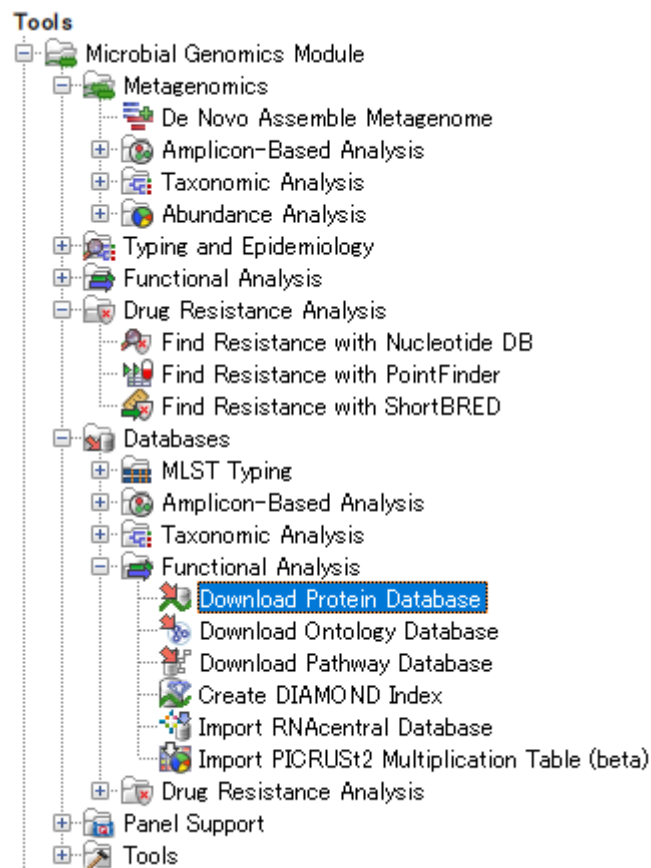
GOエンリッチメント解析、パスウェイ解析



Download Curated Microbial Reference Databaseから、QMI-PTDBをダウンロードします。
※“Download Database as Taxonomic Profiling Index”にチェックをいれます。

The screenshot shows a software interface with a 'Tools' tree on the left and a 'Download Ontology Database' dialog box on the right. The 'Tools' tree includes categories like 'Microbial Genomics Module', 'Metagenomics', 'Typing and Epidemiology', 'Functional Analysis', 'Drug Resistance Analysis', 'Databases', 'Panel Support', and 'Tools'. Under 'Databases', 'Download Ontology Database' is highlighted. The dialog box has a title bar 'Download Ontology Database' and a close button. It contains a list of steps: 1. Choose where to run, 2. **Select ontology database**, 3. Terms of use, and 4. Result handling. The 'Select ontology database' step is active, showing a dropdown menu with the selected option 'Gene Ontology with Pfam2GO mappings (GO)'. At the bottom of the dialog are buttons for 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel'.

Download Ontology Databaseから、Gene Ontology with Pfam2GO mappingsをダウンロードします。



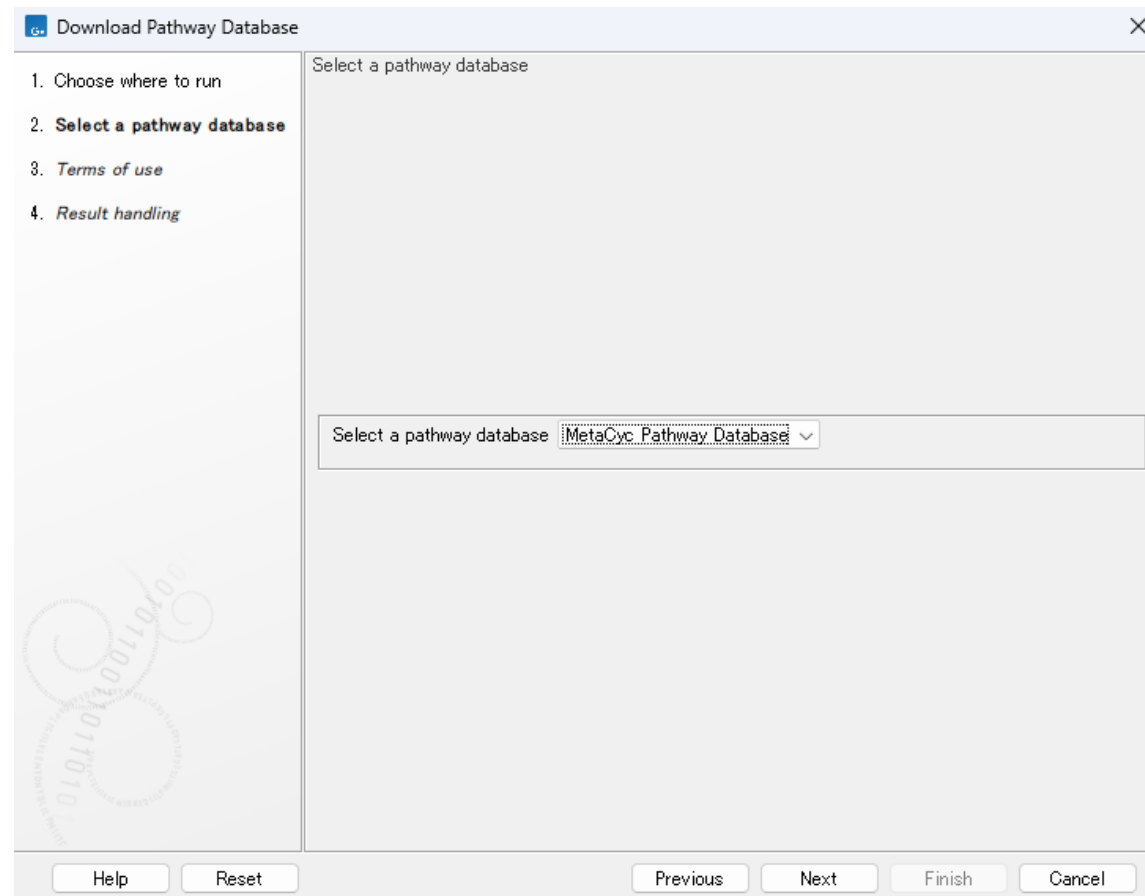
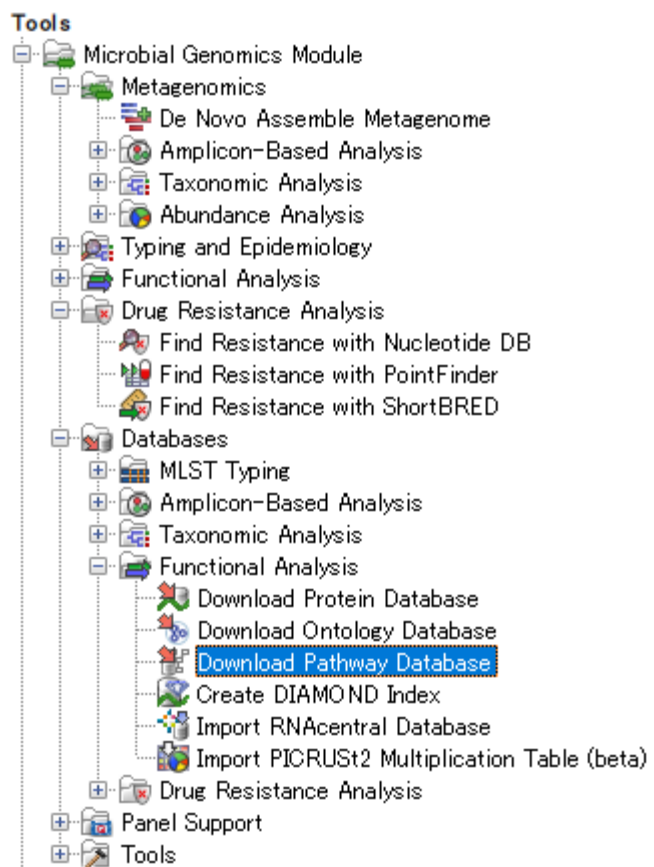
Download Protein Databaseから、UniProt90をダウンロードします。

The screenshot displays the 'Create DIAMOND Index' dialog box in a software application. On the left, a tree view under 'Tools' shows the 'Databases' folder expanded, with 'Create DIAMOND Index' selected. The main area of the dialog is titled 'Select protein sequence database' and contains a 'Navigation Area' with a search bar. The search results list various databases, with 'UniProt (UniRef90 subset with G...)' selected and highlighted in blue. To the right of the search results is a 'Selected elements (1)' list containing the same entry. At the bottom of the dialog, there is a 'Batch' checkbox and several navigation buttons: 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel'.

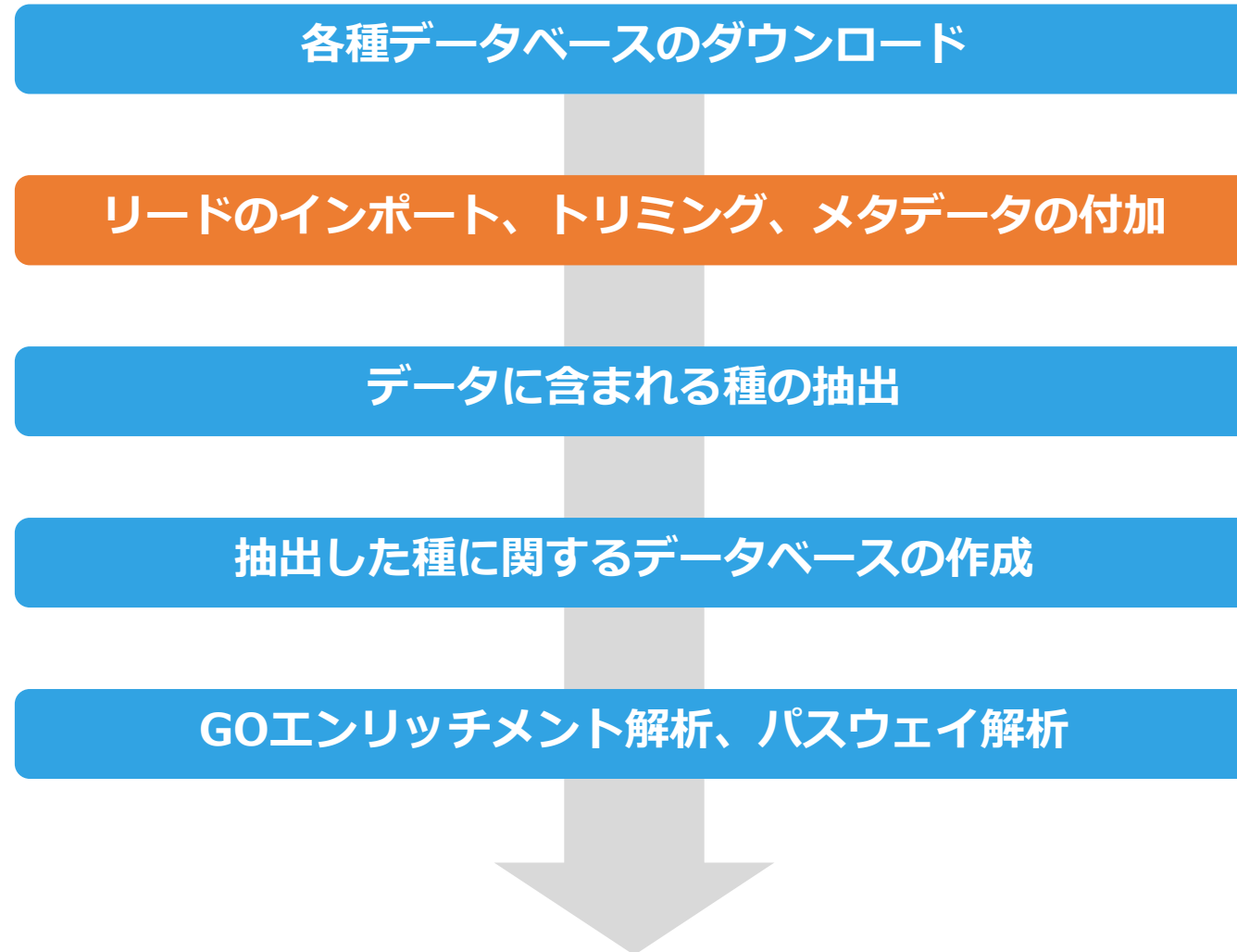
Create DIAMOND Indexで、今ダウンロードしたUniProt90を選択し、DAIMOND Indexを作成します。

The screenshot displays the 'Tools' panel on the left and the 'Download Ontology Database' dialog box on the right. In the 'Tools' panel, the 'Databases' folder is expanded, and 'Download Ontology Database' is highlighted. The dialog box shows a wizard with four steps: 1. Choose where to run, 2. Select ontology database, 3. Terms of use, and 4. Result handling. The 'Select ontology database' step is active, showing a dropdown menu with 'Enzyme Commission Numbers (EC)' selected. The dialog box also has 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel' buttons at the bottom.

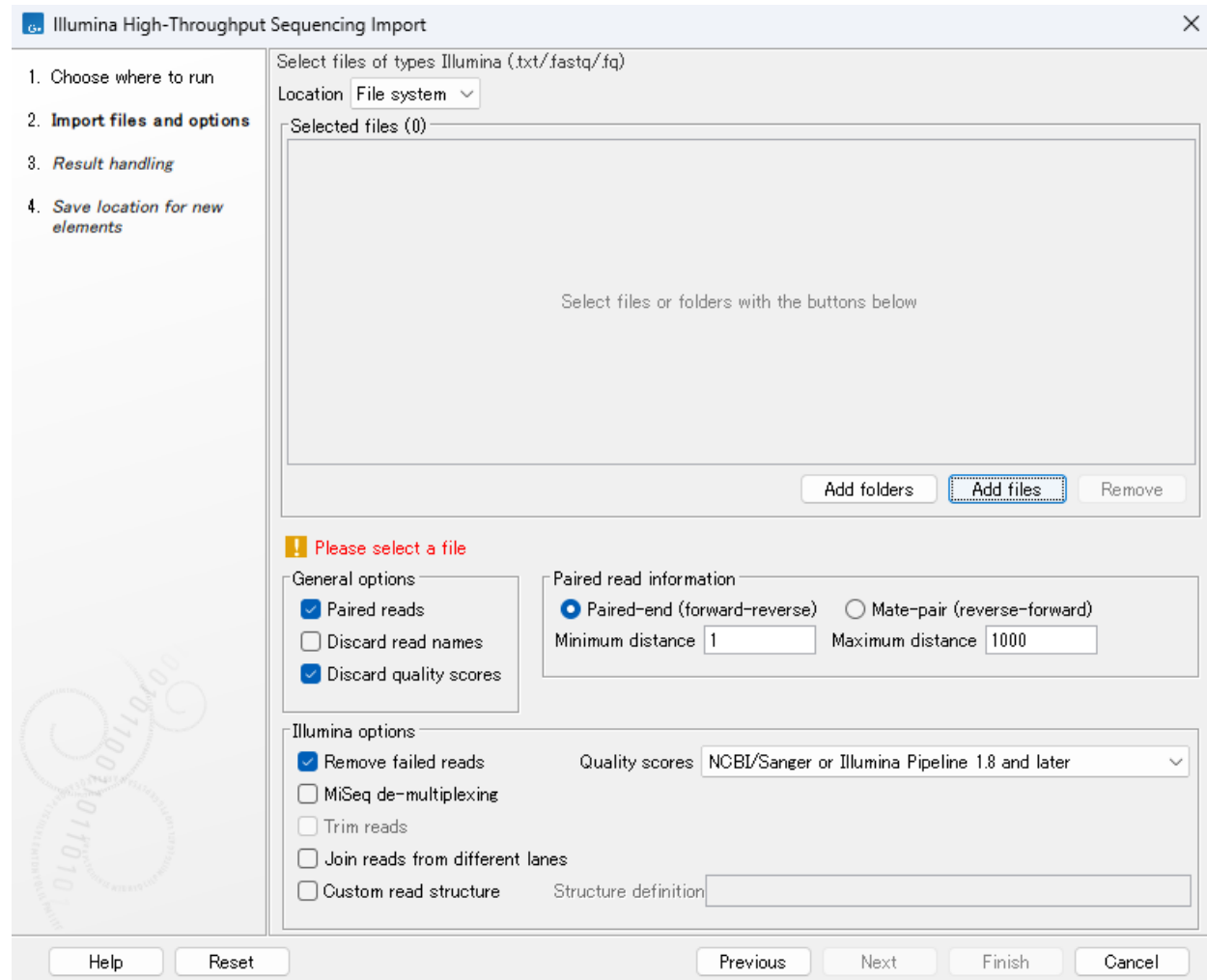
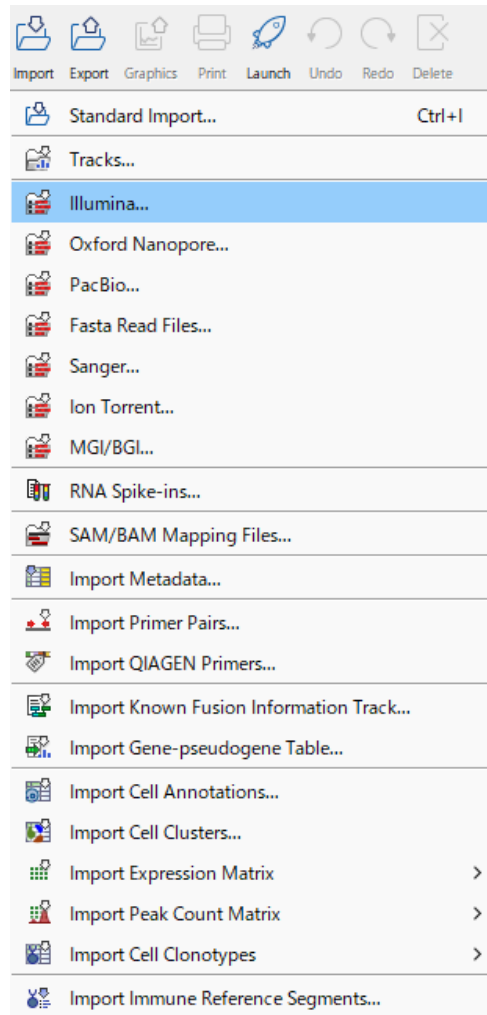
Download Ontology Databaseから、Enzyme Commission Numbersをダウンロードします。



Download Pathway Databaseから、MetaCyc Pathway Databaseをダウンロードします。



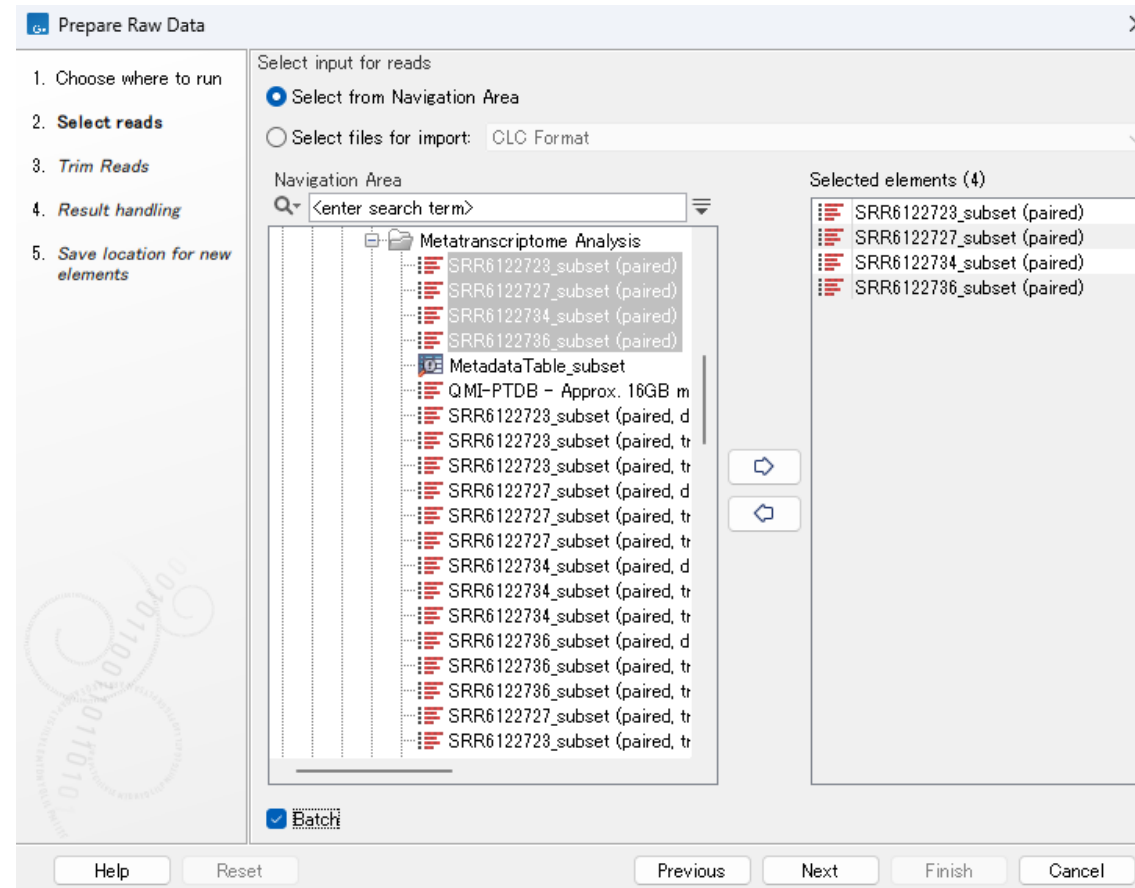
リードのインポート



画面左上のImportメニューからシーケンスプラットフォームを選択し、Fastqファイルを選択します。

Template Workflows

- Preparing Raw Data
 - Import with Metadata
 - Prepare Raw Data**
- Basic Workflow Designs
- Biomedical Workflows
- LightSpeed Workflows
- Genome Finishing Workflows
- Long Read Workflows
- Microbial Workflows
- Single Cell Workflows



Prepare Raw Dataワークフローを利用し、リードの前処理を行います。

The screenshot shows the 'Prepare Raw Data' dialog box with the 'Trim Reads' section selected. The 'Trim adapter list' field is highlighted with a red box. The 'Next' button at the bottom is also highlighted with a red box.

Configurable Parameters	
Trim using quality scores	<input checked="" type="checkbox"/>
Quality limit	0.05
Trim ambiguous nucleotides	<input checked="" type="checkbox"/>
Maximum number of ambiguities	2
Automatic read-through adapter trimming	<input checked="" type="checkbox"/>
Trim adapter list	<input type="text"/>
Remove 5' terminal nucleotides	<input type="checkbox"/>
Number of 5' terminal nucleotides	1
Remove 3' terminal nucleotides	<input type="checkbox"/>
Number of 3' terminal nucleotides	1
Discard short reads	<input type="checkbox"/>
Minimum length	15
Discard long reads	<input type="checkbox"/>
Maximum length	1,000

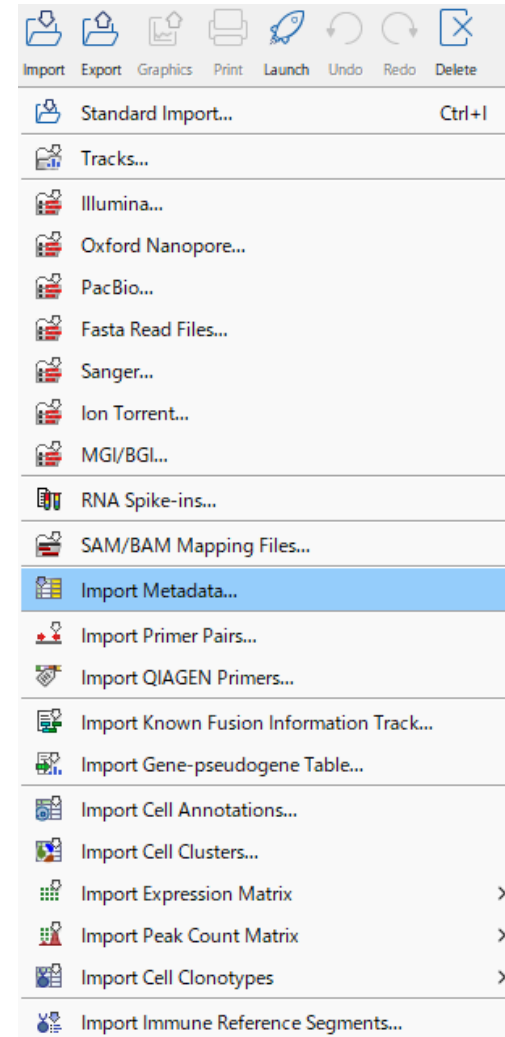
Locked Settings

Buttons: Help, Reset, Previous, Next, Finish, Cancel

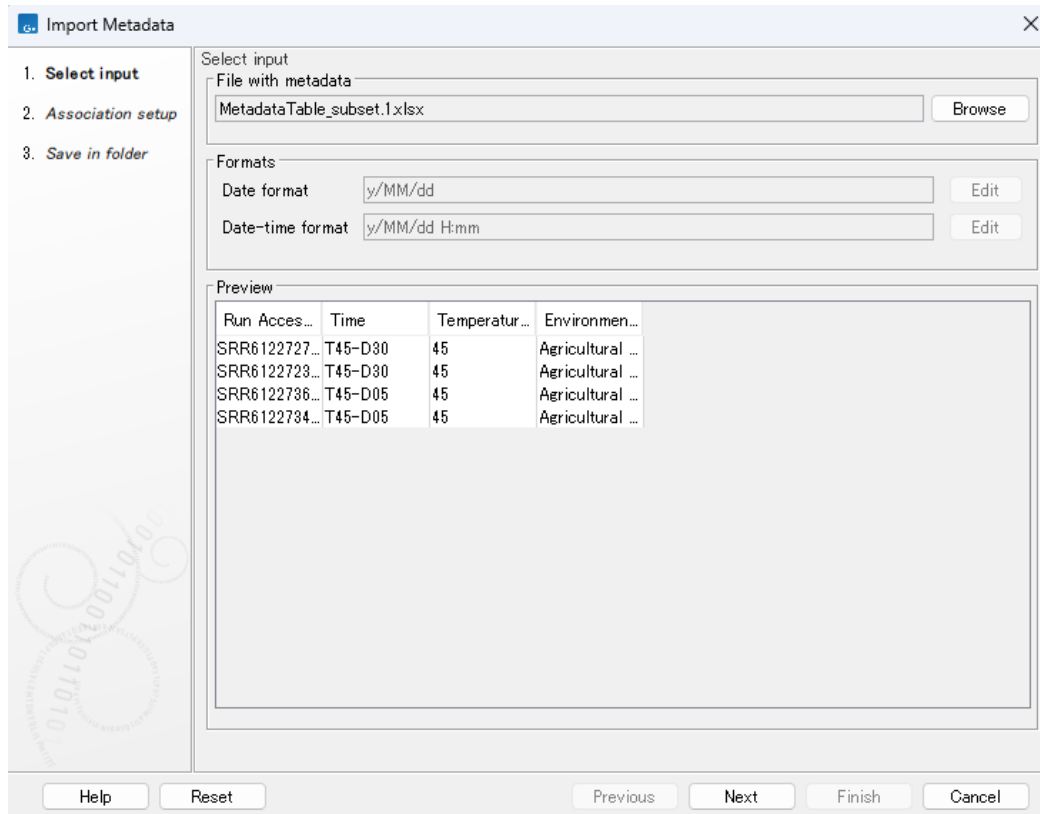
アダプターのトリミングを行う場合、Trim adapter listでアダプターリストを指定します。
アダプターリストは画面左上のNew > Trim Adapter listで別途作成しておく必要があります。

メタデータのインポート

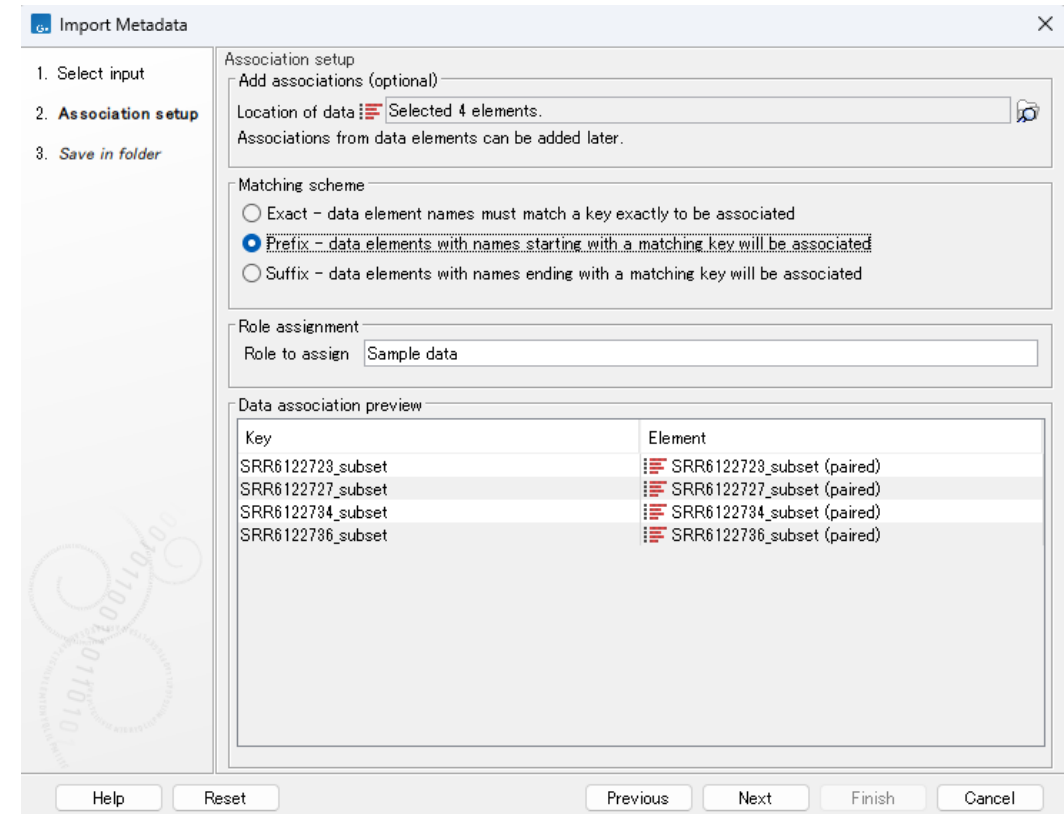
	A	B	C	D	E	F
1	Run Accession	Time	Temperature	Environmental		
2	SRR6122727_subset	T45-D30	45	Agricultural paddy soil		
3	SRR6122723_subset	T45-D30	45	Agricultural paddy soil		
4	SRR6122736_subset	T45-D05	45	Agricultural paddy soil		
5	SRR6122734_subset	T45-D05	45	Agricultural paddy soil		



Excelなどで左のようなメタデータを用意し、ImportメニューのImport Metadataからインポートします。



メタデータのファイルを指定します。



メタデータとリードを名前で紐づけます。
完全一致のほか、前方一致や後方一致で紐づけることが可能です。

各種データベースのダウンロード

リードのインポート、トリミング、メタデータの付加

データに含まれる種の抽出

抽出した種に関するデータベースの作成

GOエンリッチメント解析、パスウェイ解析

Tools

- Microbial Genomics Module
 - Metagenomics
 - De Novo Assemble Metagenome
 - Amplicon-Based Analysis
 - Taxonomic Analysis
 - Bin Pangenomes by Sequence
 - Bin Pangenomes by Taxonomy
 - Taxonomic Profiling**
 - Identify Viral Integration Sites
 - Abundance Analysis

Taxonomic Profiling

- Choose where to run
- Select reads**
- Batch overview
- Parameters
- Result handling

Select reads

Navigation Area

Q- <Enter search term>

- OTU Clustering Step by Step
- OTU Clustering Using Workflows
- Taxonomic Profiling of Whole Shotgun t
- Antibiotic Resistance Analysis
- Working with MLST schemes
- Updating and using attributed sequence
- Metatranscriptome Analysis
 - SRR6122723_subset (paired)
 - SRR6122727_subset (paired)
 - SRR6122734_subset (paired)
 - SRR6122736_subset (paired)
 - MetadataTable_subset
 - QMI-PTDB - Approx. 16GB memory
 - SRR6122723_subset (paired, discarc
 - SRR6122723_subset (paired, trimme
 - SRR6122727_subset (paired, discarc
 - SRR6122727_subset (paired, trimme
 - SRR6122727_subset (paired, trimme
 - SRR6122734_subset (paired, discarc
 - SRR6122734_subset (paired, trimme

Selected elements (4)

- SRR6122723_subset (paired)
- SRR6122727_subset (paired)
- SRR6122734_subset (paired)
- SRR6122736_subset (paired)

Batch

Help Reset Previous Next Finish Cancel

Taxonomic Profilingを起動し、Batchにチェックを入れ、全リードデータを選択します。

Taxonomic Profiling

1. Choose where to run
2. Select reads
3. Batch overview
4. **Parameters**
5. Result handling
6. Save location for new elements

Parameters

Select reference database

Reference index: QMI-PTDB - Approx. 16GB memory required_taxpro_index (January 2022)

Filter host reads

Host genome index: SILVA Tutorial Subset (taxpro index)

Set reads parameters

Auto-detect paired distances

Minimum seed length: 30

Adjust read count abundances

Help Reset Previous Next Finish Cancel

Reference IndexおよびHost genome indexを指定します。

1. Choose where to run
2. Select reads
3. Batch overview
4. Parameters
5. **Result handling**
6. Save location for new elements

Result handling

Output options

Abundance table

Reads matching the reference database

Reads matching host genome

Unclassified reads

Report

Result handling

Open

Save in input folder

Save in specified location

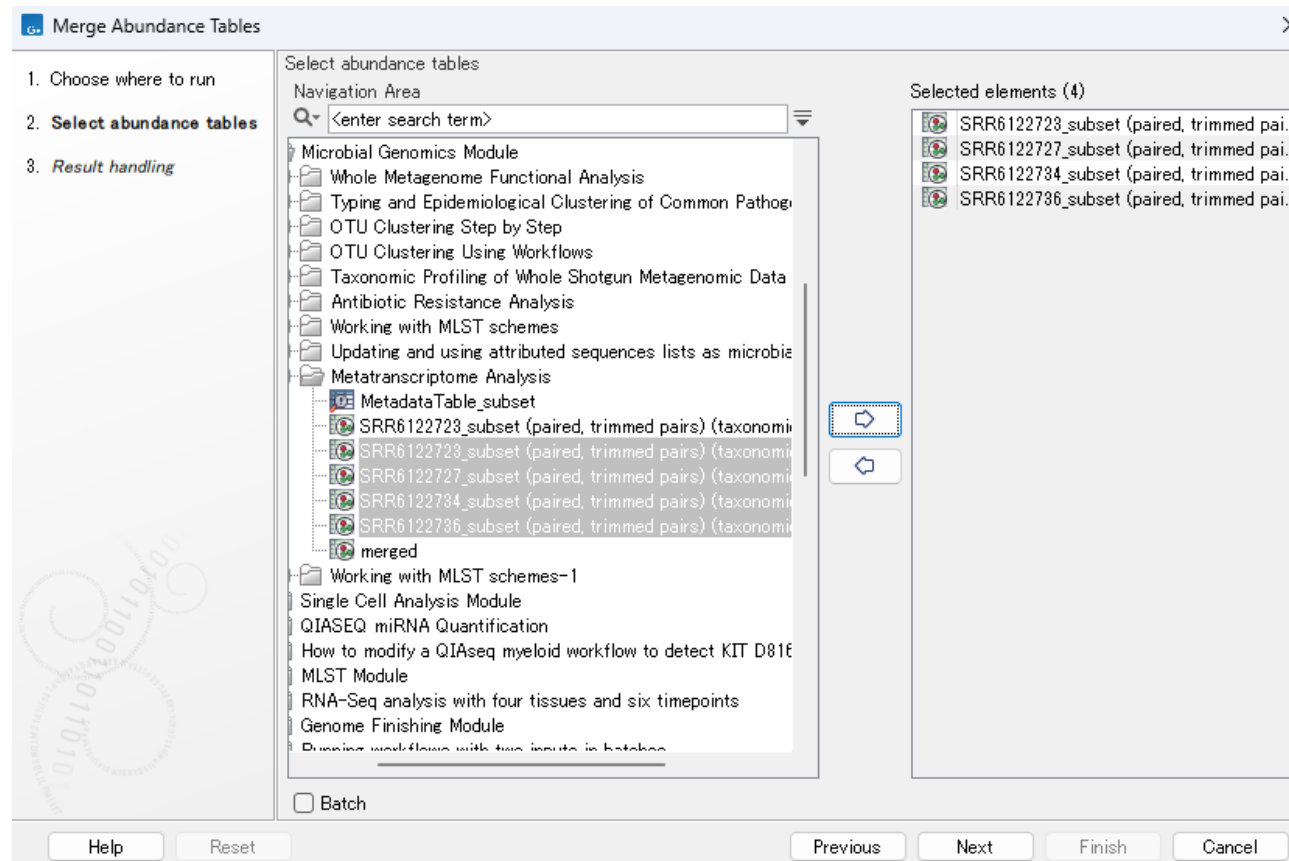
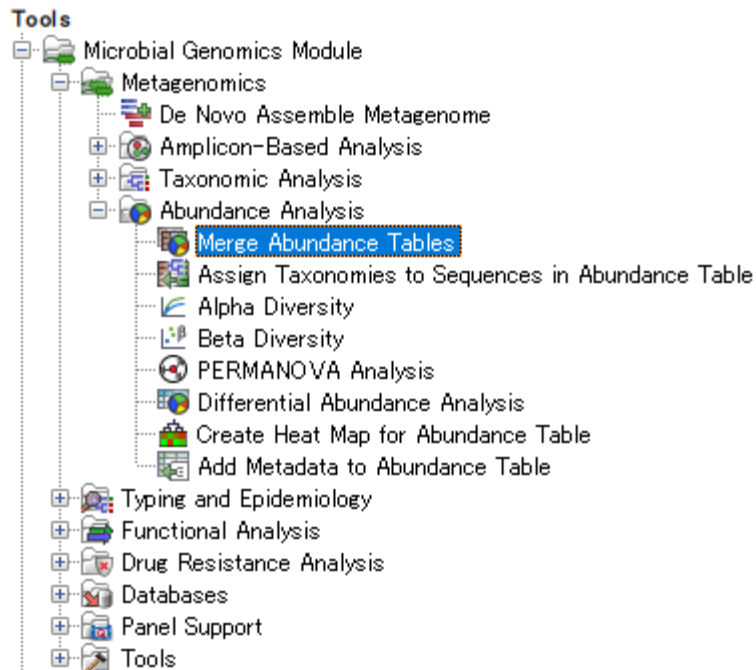
Create subfolders per batch unit

Log handling

Create log

Help Reset Previous Next Finish Cancel

Abundance TableおよびUnclassified Readsを出力します。



作成されたAbundance TableをMerge Abundance Tableで一つにまとめます。

The screenshot shows the 'De Novo Assemble Metagenome' software interface. On the left, a 'Tools' sidebar lists various analysis modules, with 'De Novo Assemble Metagenome' highlighted under the 'Metagenomics' category. The main window is titled 'De Novo Assemble Metagenome' and contains a 'Select metagenome sequencing reads' section. This section includes a 'Navigation Area' with a search bar and a list of reads. The reads are listed with their SRR IDs and statuses, such as 'SRR6122723_subset (paired, discarded)' and 'SRR6122723_subset (paired, trimmed pairs)'. A 'Selected elements (4)' panel on the right shows four unclassified reads selected. The interface also includes a 'Batch' checkbox and navigation buttons like 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel'.

De Novo Assemble Metagenomeを起動し、
Taxonomic profilingツールで作成されたunclassified readsを選択します。

Tools

- Microbial Genomics Module
 - Metagenomics
 - Typing and Epidemiology
 - Functional Analysis
 - Find Prokaryotic Genes
 - Annotate with BLAST
 - Annotate with DIAMOND**
 - Annotate CDS with Best BLAST Hit
 - Annotate CDS with Best DIAMOND Hit
 - Annotate CDS with Pfam Domains
 - Build Functional Profile
 - Infer Functional Profile (beta)
 - Identify Pathways
- Drug Resistance Analysis
- Databases
- Panel Support
- Tools

Annotate with DIAMOND

1. Choose where to run

2. **Select input sequence**

3. Select references and specify search parameters

4. Overlapping hits

5. Output options

6. Result handling

Select input sequence

Navigation Area

Q: <enter search term>

MetadataTable_subset

- QMI-PTDB - Approx. 16GB memory required (January 2022)
- SRR6122723_subset (paired, discarded)
- SRR6122723_subset (paired, trimmed pairs)
- SRR6122723_subset (paired, trimmed orphans)
- SRR6122727_subset (paired, discarded)
- SRR6122727_subset (paired, trimmed pairs)
- SRR6122727_subset (paired, trimmed orphans)
- SRR6122734_subset (paired, discarded)
- SRR6122734_subset (paired, trimmed pairs)
- SRR6122734_subset (paired, trimmed orphans)
- SRR6122736_subset (paired, discarded)
- SRR6122736_subset (paired, trimmed pairs)
- SRR6122736_subset (paired, trimmed orphans)
- SRR6122727_subset (paired, trimmed pairs) (unclassified reads)-1
- SRR6122723_subset (paired, trimmed pairs) (unclassified reads)-2
- SRR6122723_subset (paired, trimmed pairs) (unclassified reads)-1
- SRR6122723_subset (paired, trimmed pairs) (unclassified reads)
- SRR6122727_subset (paired, trimmed pairs) (unclassified reads)
- SRR6122734_subset (paired, trimmed pairs) (unclassified reads)
- SRR6122736_subset (paired, trimmed pairs) (unclassified reads)
- SRR6122727_subset (paired, trimmed pairs) (unclassified reads) contig list
- SRR6122727_subset (paired, trimmed pairs) (unclassified reads) contig list (C
- New sequence list

Selected elements (1)

- SRR6122727_subset (paired, trimmed pairs) (unclassified reads) c...

Batch

Help Reset Previous Next Finish Cancel

De Novo Assemblyで作成したcontig listに対し、DIAMONDによるアノテーションを行います。

Annotate with DIAMOND

1. Choose where to run

2. Select input sequence

3. **Select references and specify search parameters**

4. Overlapping hits

5. Output options

6. Result handling

Select references and specify search parameters

Select reference sequences

Protein Sequence List

DIAMOND Index

CDS Annotations

Protein sequence list

DIAMOND Index: UniProt (UniRef90 subset with GO & EC annotations, 7GB) (2020_11) (DIAMOND index)

CDS annotations from sequence list

Search parameters

Genetic code: 11 Bacterial, Archaeal and Plant Plastid

Sensitivity: More sensitive search

Maximum E-value: 0.00001

Minimum identity (%): 95.0

Minimum reference sequence coverage (%): 0.0

Adjustment

Adjust CDS to open reading frame

Help Reset Previous Next Finish Cancel

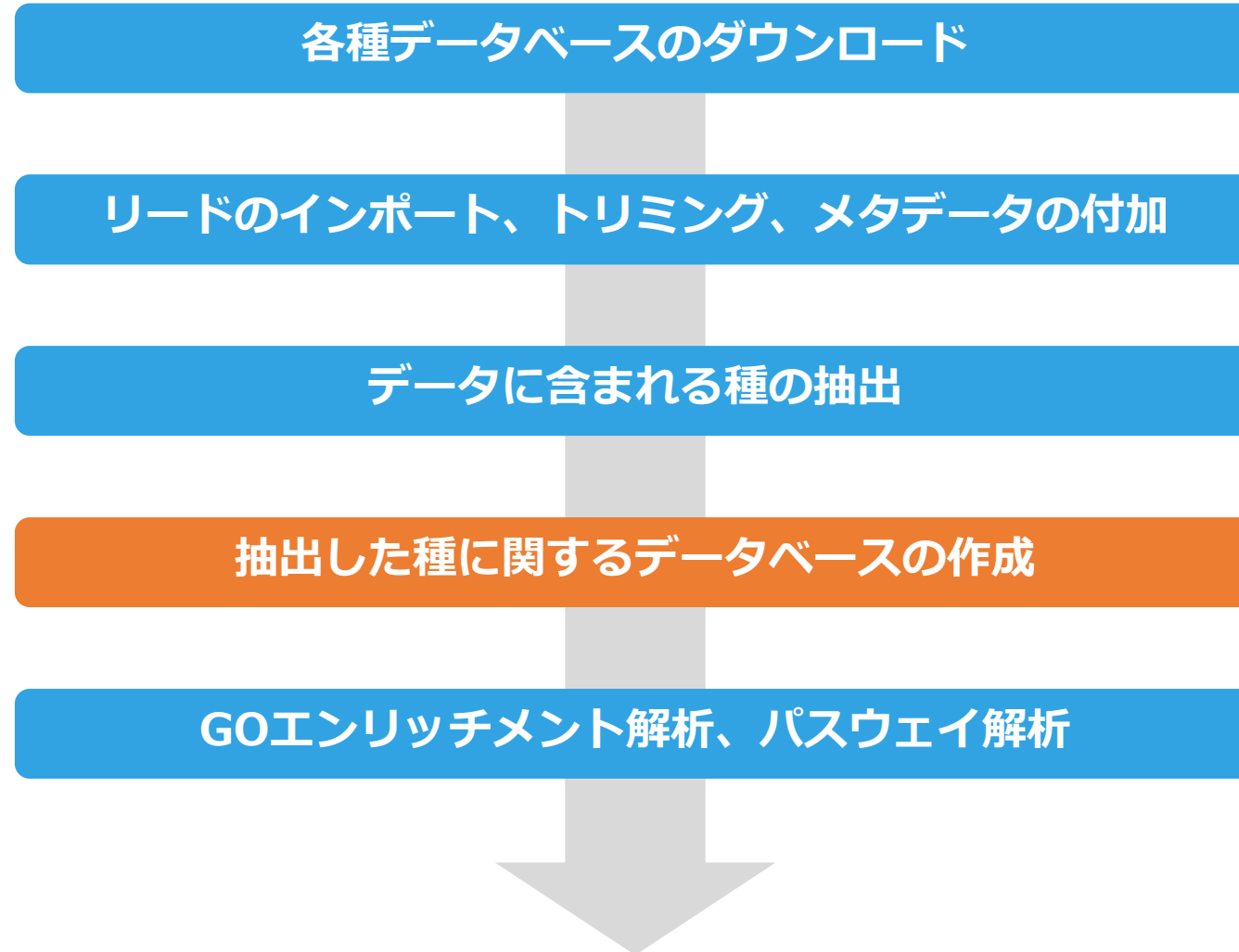
DIAMOND Indexにチェックを入れ、ダウンロードしたUniProtを指定します。

unclassified readのアノテーション

☰ SRR6122727_subset (paired, trimmed pairs) (unclassified reads) contig list (DIAMOND annotations)

Sequence	Name	Type	Region	Qualifiers
SRR6122727_subset_(paired_tri...	UniRef90_Q9C4C0	CDS	complement(228..944)	<pre>/Description=Coenzyme-B sulfoethylthiotransferase (Fragment) n=4 Tax=environmental samples TaxID=68359 RepID=Q9C4C0_9EURY /EC numbers=2.8.4.1 /GO-terms=GO:0015948 /GO-terms=GO:0046872 /GO-terms=GO:0050524 /db_xref=UniProtKB/Swiss-Prot=Q9C4C0 /DIAMOND Hit=UniRef90_Q9C4C0 /E-value=4.35E-157 /Sequence identity (%)=100.0 /Reference sequence coverage (%)=100.0 /Alignment length=239 /Reference sequence length=239</pre>
SRR6122727_subset_(paired_tri...	UniRef90_H814B1	CDS	3442..5112	<pre>/Description=Methyl-coenzyme M reductase subunit alpha n=9 Tax=Archaea TaxID=2157 RepID=H814B1_METCZ /EC numbers=2.8.4.1 /GO-terms=GO:0015948 /GO-terms=GO:0046872 /GO-terms=GO:0050524 /db_xref=UniProtKB/Swiss-Prot=H814B1 /DIAMOND Hit=UniRef90_H814B1 /E-value=0.0 /Sequence identity (%)=96.1 /Reference sequence coverage (%)=100.0 /Alignment length=557 /Reference sequence length=555</pre>

各contigにアノテーションが付与されたデータが作成されます。



データに含まれる種を抽出



The screenshot shows a software interface with a table of data and a settings panel on the right. The table has 65 rows, all of which are selected (highlighted in blue). The first column is labeled 'Assembly ID' and contains various alphanumeric strings. The settings panel on the right is titled 'Table Settings' and has a 'Show column' section with several checkboxes. The 'Assembly ID' checkbox is checked, while all other checkboxes are unchecked. Below the 'Show column' section, there are 'Select All' and 'Deselect All' buttons. At the bottom of the interface, there are three buttons: 'Create Abundance Subtable', 'Create Normalized Abundance Subtable', and 'Extract Reads from Selection'.

mergeしたAbundance Tableを開き、右側のパネルで“Assembly ID”以外のチェックを外します。
Assembly ID列のみの表示になるので、すべての行を選択し、クリップボードにコピーします。

The screenshot displays the 'Split Sequence List' tool interface. On the left, a sidebar contains a tree view of utility tools, with 'Split Sequence List' highlighted. The main window is titled 'Split Sequence List' and features a 'Nucleotide or Protein Sequence List' section. This section includes a 'Navigation Area' with a search bar and a list of sequence lists. The 'QMI-PTDB - Approx. 16GB memory required (January 2022)' item is selected and moved to the 'Selected elements (1)' panel on the right. The interface includes buttons for 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel'.

Split Sequence Listツールを起動し、ダウンロードしたQMI-PTDBを指定します。

Split Sequence List

Settings

1. Choose where to run
2. Nucleotide or Protein Sequence List
3. **Settings**
4. Result handling
5. Save location for new elements

Define splitting

Split into N lists

Number of lists to create: 2

Create lists with N sequences each

Number of sequences per list: 1000

Split based on attribute values

Attribute: Assembly ID

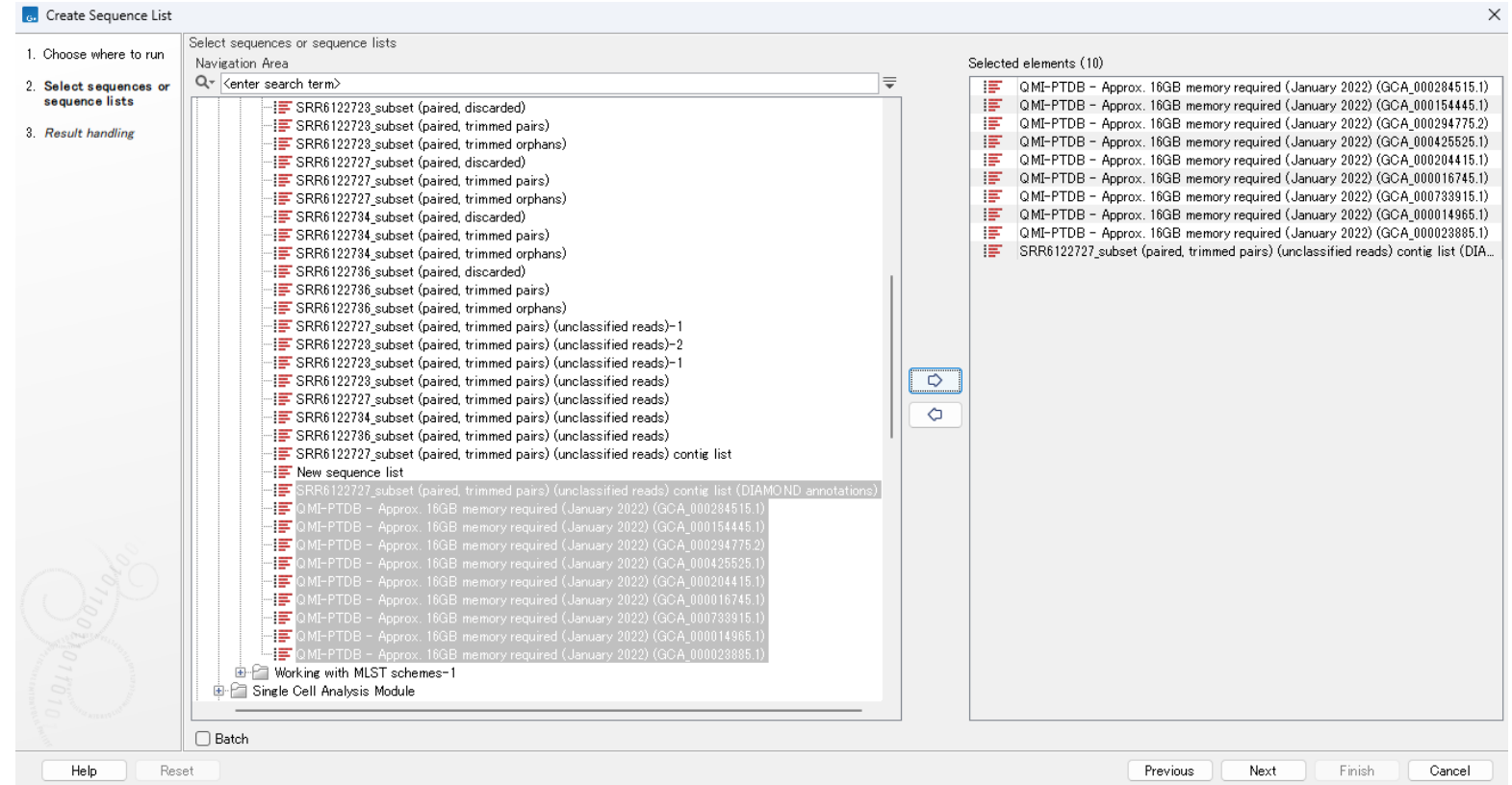
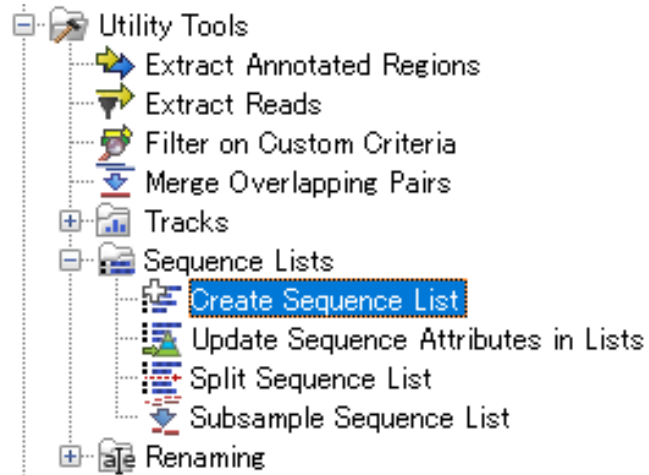
Attribute values:

- GCA_000009825.1
- GCA_000294775.2
- GCA_000785385.1
- GCA_000613125.1
- GCA_000007625.1

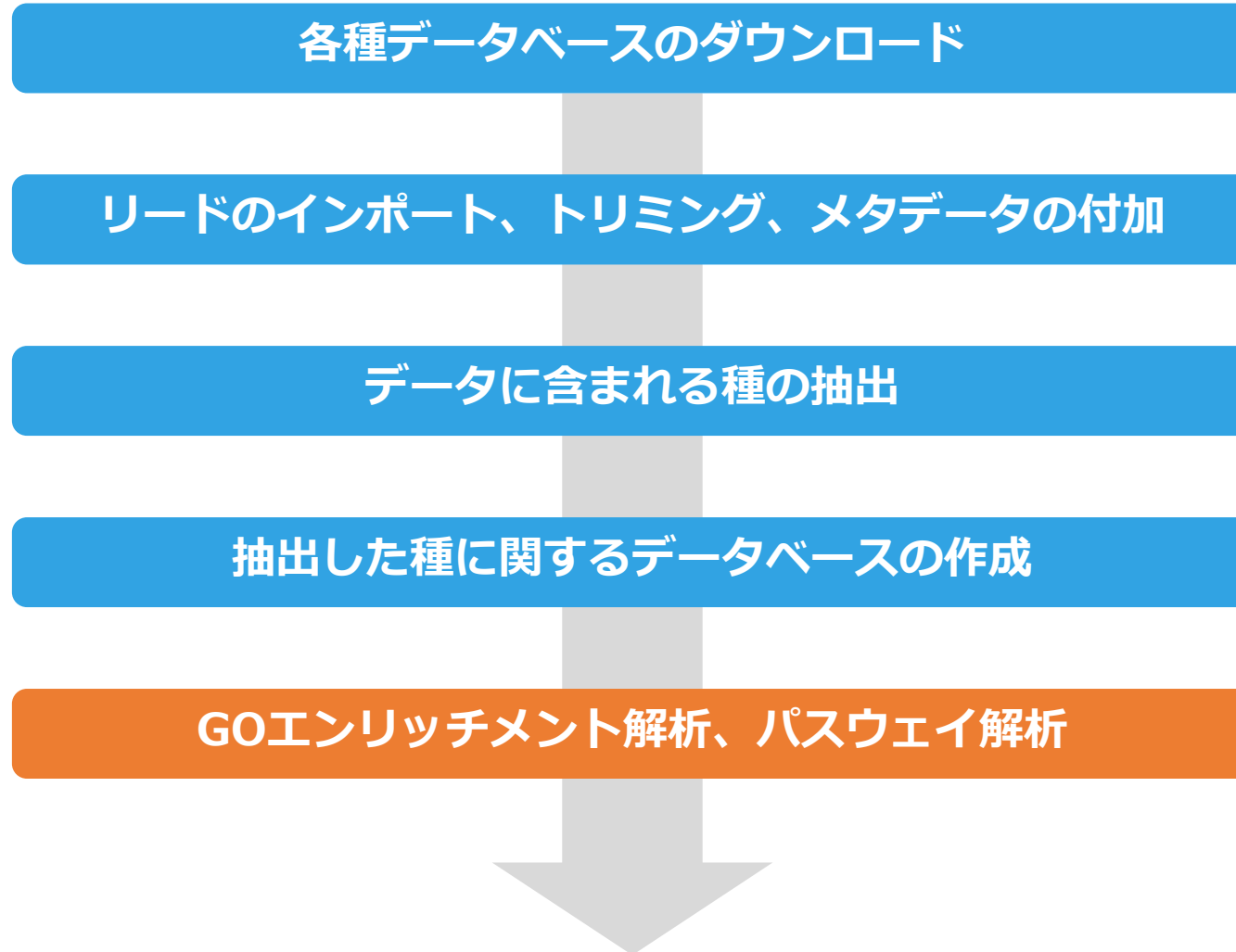
Collect sequences without matches

Help Reset Previous Next Finish Cancel

Split based on attribute valuesにチェックを入れ、AttributeをAssembly IDとし、下の欄にクリップボードの内容をペーストします。



Create Sequence Listツールを起動し、
今抽出した配列リストと、アノテーション付けしたcontigリストを指定します。

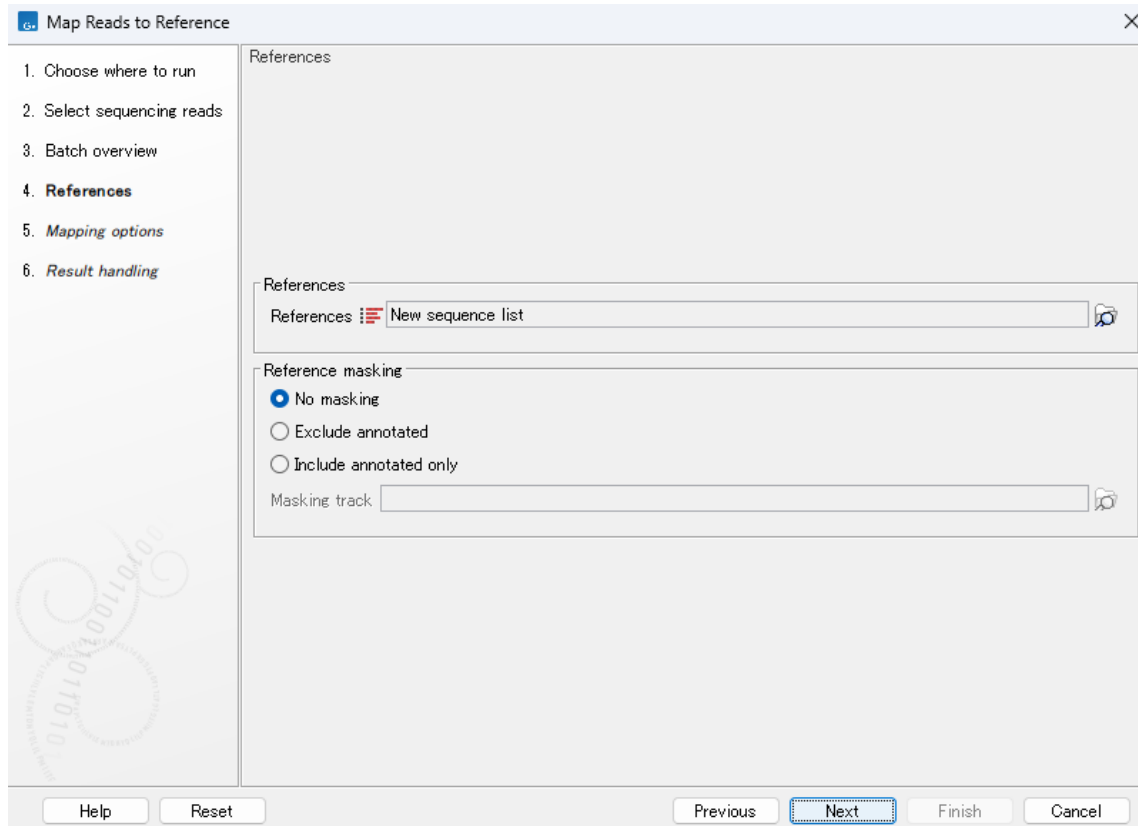


作成したデータベースへリードをマッピング

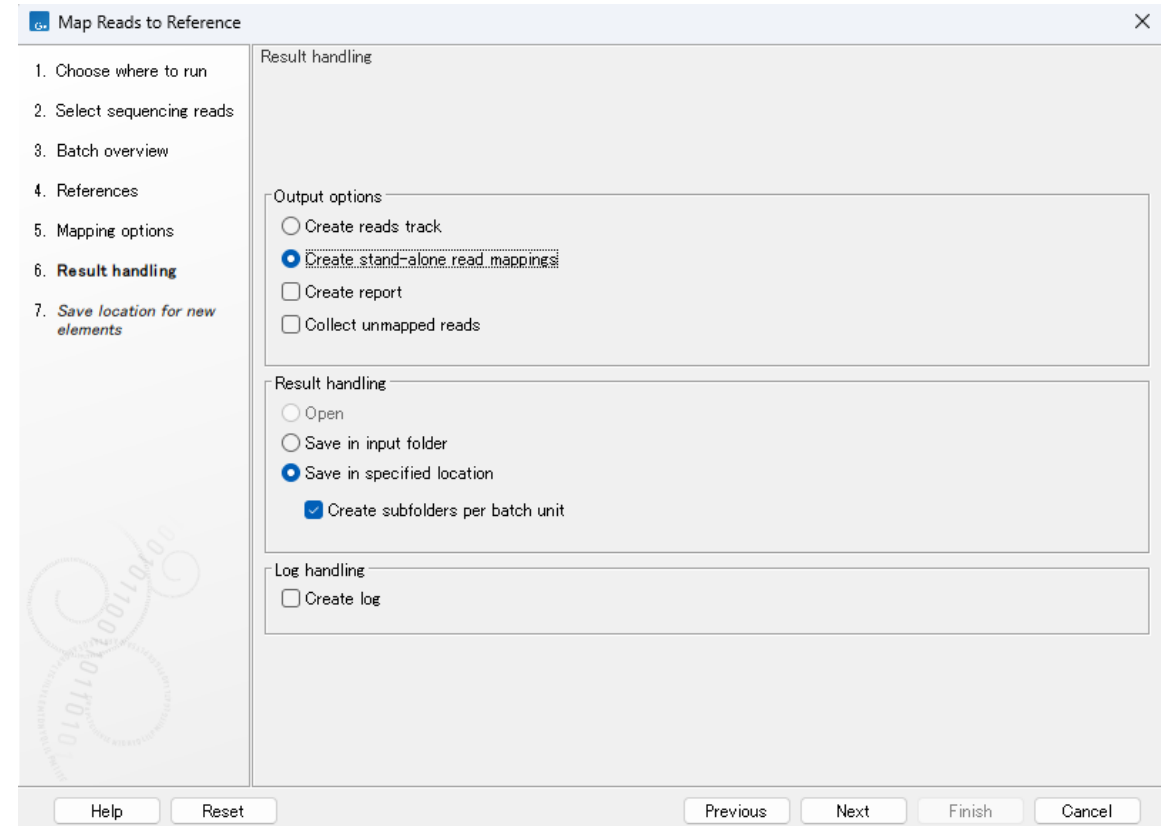
The screenshot displays the 'Map Reads to Reference' software interface. On the left, a tree view shows the analysis workflow, with 'Map Reads to Reference' highlighted. The main window is titled 'Map Reads to Reference' and contains a 'Select sequencing reads' section. This section includes a 'Navigation Area' with a search bar containing '<center search term>'. Below the search bar is a list of sequencing reads, including entries like 'SRR6122723_subset (paired)', 'SRR6122727_subset (paired)', and 'SRR6122734_subset (paired)'. A 'Batch' checkbox is checked at the bottom of the list. On the right side, a 'Selected elements (4)' panel shows four selected read entries. At the bottom of the window, there are buttons for 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel'.

Map Reads to Referenceを起動し、Batchにチェックを入れ、リードデータを選択します。

作成したデータベースヘリッドをマッピング

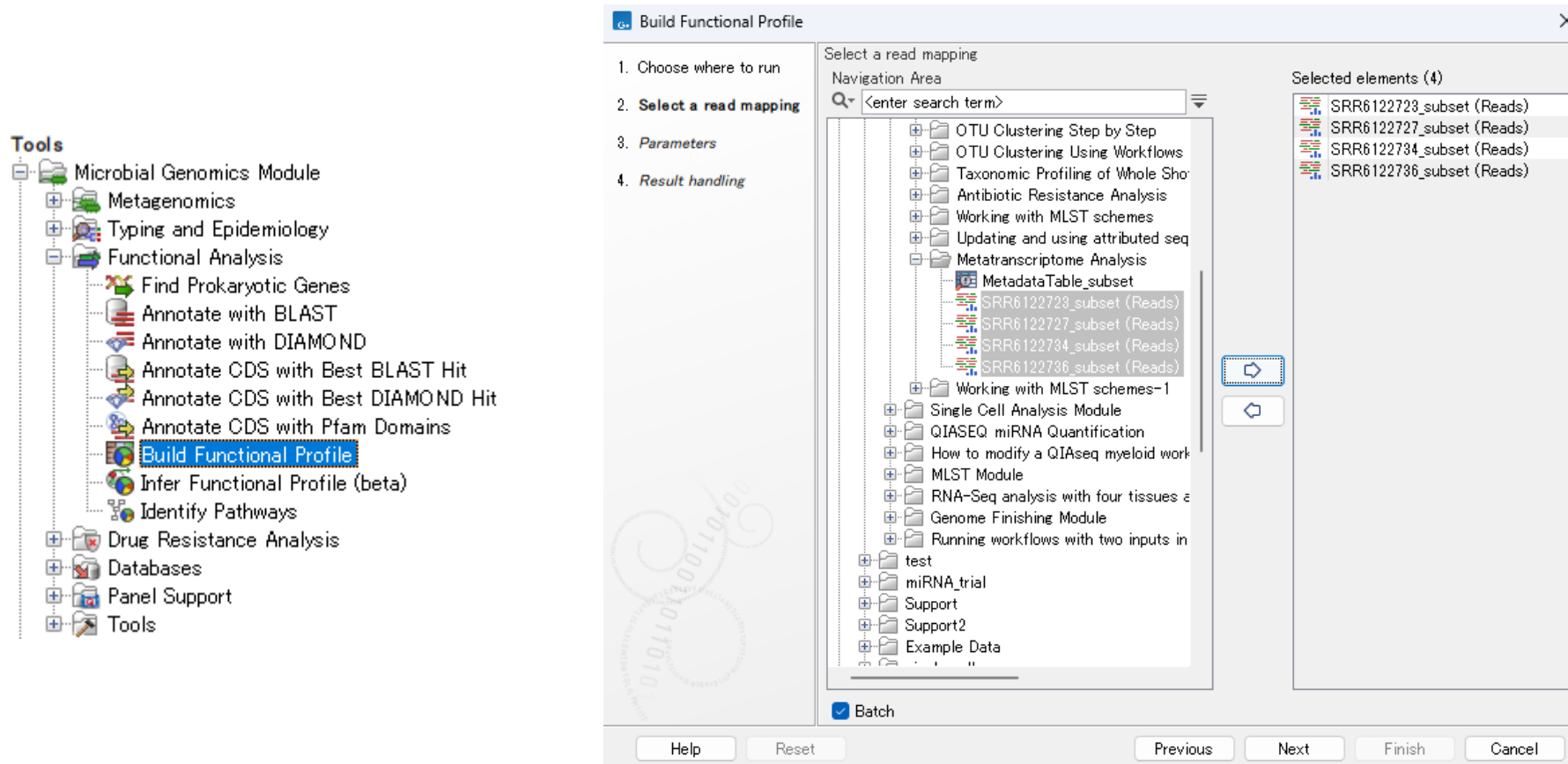


Referenceで先ほど作成したシーケンスリストを指定します。



最後の画面では、Create stand-alone read mapping
にチェックをします。

GO Abundance Tableの作成



Build Functional Profileを起動し、Batchにチェックを入れ、マッピングデータを指定します。

GO Abundance Tableの作成

Build Functional Profile

1. Choose where to run
2. Select a read mapping
3. Batch overview
- 4. Parameters**
5. Result handling

Parameters

Reference

Reference New sequence list

GO parameters

GO database GO database

GO subset Complete GO basic

Propagate GO mapping

EC parameters

EC database EC database

Help Reset Previous Next Finish Cancel

先ほどと同じReferenceデータ、GOデータベース、ECデータベース（オプション）を指定します。

Build Functional Profile

1. Choose where to run
2. Select a read mapping
3. Batch overview
4. Parameters
- 5. Result handling**
6. Save location for new elements

Result handling

Output options

Create Pfam functional profile

Create GO functional profile

Create EC functional profile

Create BLAST hit functional profile

Create DIAMOND hit functional profile

Create report

Result handling

Open

Save in input folder

Save in specified location

Create subfolders per batch unit

Log handling

Create log

Help Reset Previous Next Finish Cancel

Create GO functional profileとCreate EC functional profileにチェックを入れます。

GO Abundance Tableの作成

Tools

- Microbial Genomics Module
 - Metagenomics
 - De Novo Assemble Metagenome
 - Amplicon-Based Analysis
 - Taxonomic Analysis
 - Abundance Analysis
 - Merge Abundance Tables**
 - Assign Taxonomies to Sequences in Abundance Table
 - Alpha Diversity
 - Beta Diversity
 - PERMANOVA Analysis
 - Differential Abundance Analysis
 - Create Heat Map for Abundance Table
 - Add Metadata to Abundance Table
 - Typing and Epidemiology
 - Functional Analysis
 - Drug Resistance Analysis
 - Databases
 - Panel Support
 - Tools

Merge Abundance Tables

1. Choose where to run

2. **Select abundance tables**

3. Result handling

Select abundance tables

Navigation Area

Search: <Enter search term>

Metatranscriptome Analysis

- MetadataTable_subset
 - SRR6122723_subset (paired, trimmed pairs) (GO profile)
 - SRR6122723_subset (paired, trimmed pairs) (EC profile)
 - SRR6122727_subset (paired, trimmed pairs) (GO profile)
 - SRR6122727_subset (paired, trimmed pairs) (EC profile)
 - SRR6122734_subset (paired, trimmed pairs) (GO profile)
 - SRR6122734_subset (paired, trimmed pairs) (EC profile)
 - SRR6122736_subset (paired, trimmed pairs) (GO profile)
 - SRR6122736_subset (paired, trimmed pairs) (EC profile)
 - merged
 - SRR6122723_subset (Reads) (GO profile)
 - SRR6122723_subset (Reads) (EC profile)
 - SRR6122727_subset (Reads) (GO profile)
 - SRR6122727_subset (Reads) (EC profile)
 - SRR6122734_subset (Reads) (GO profile)
 - SRR6122734_subset (Reads) (EC profile)
 - SRR6122736_subset (Reads) (GO profile)
 - SRR6122736_subset (Reads) (EC profile)

- Working with MLST schemes-1
- Single Cell Analysis Module
- QIASEQ miRNA Quantification
- How to modify a QIASEQ myeloid workflow to detect MLST Module
- RNA-Seq analysis with four tissues and six timepoi
- Genome Finishing Module
- Running workflows with two inputs in batches
- test

Selected elements (4)

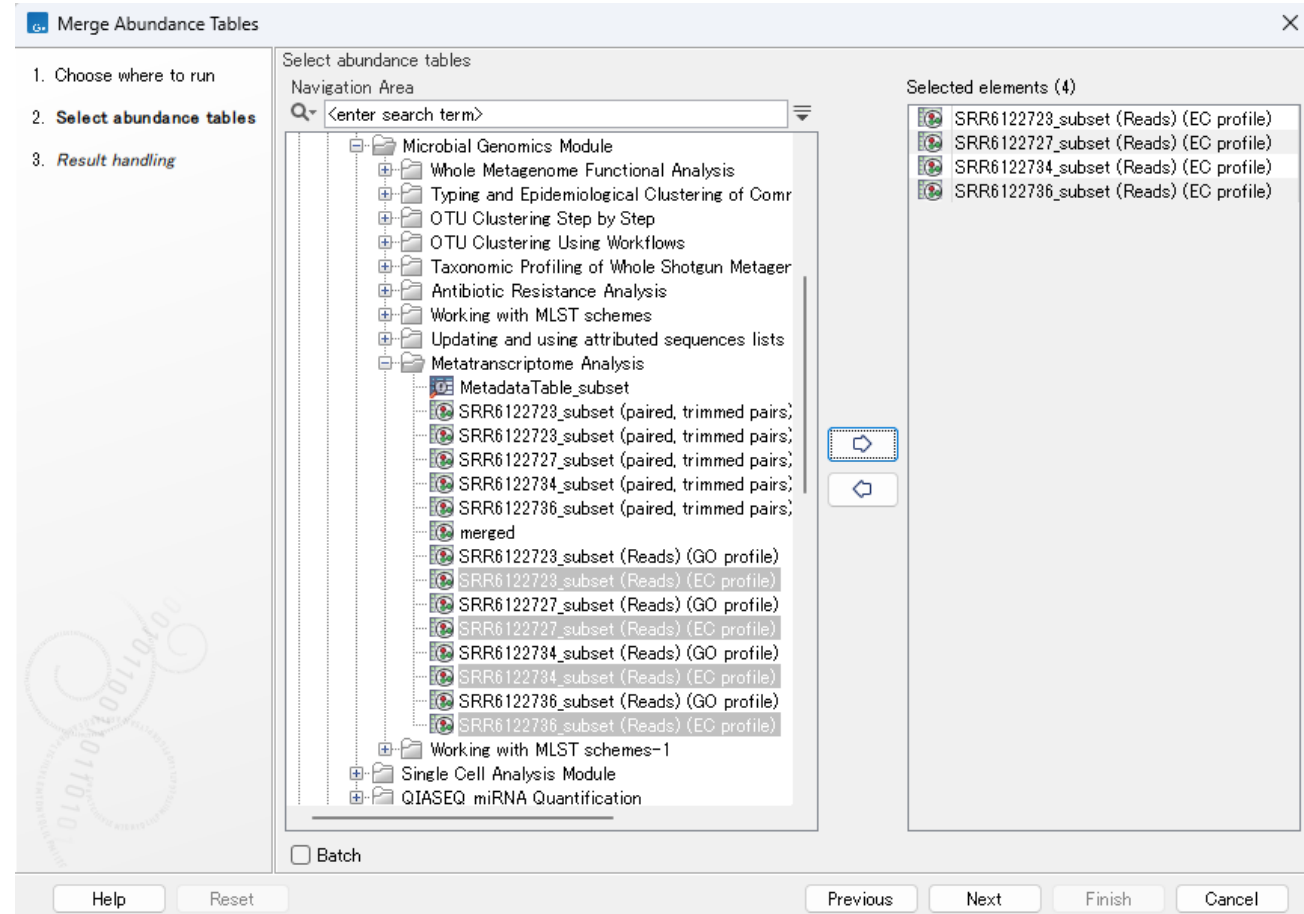
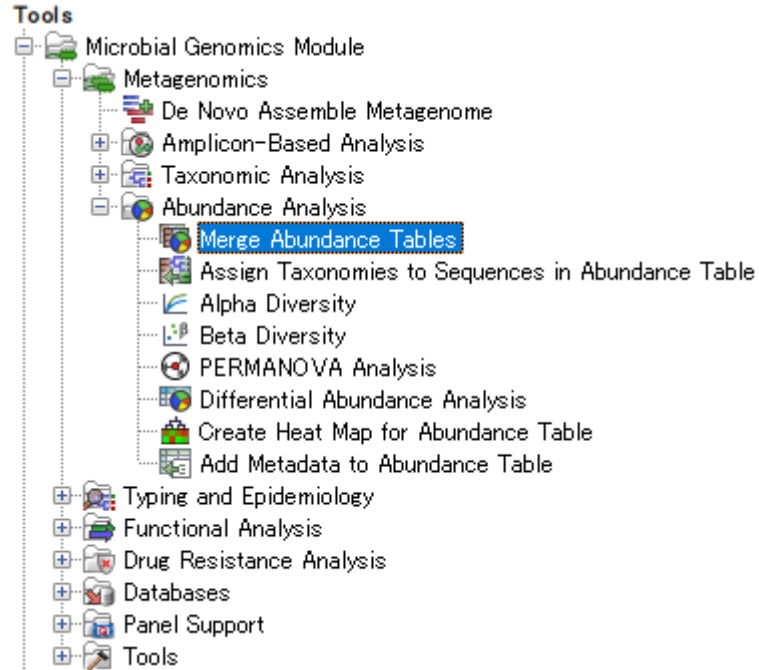
- SRR6122723_subset (Reads) (GO profile)
- SRR6122727_subset (Reads) (GO profile)
- SRR6122734_subset (Reads) (GO profile)
- SRR6122736_subset (Reads) (GO profile)

Batch

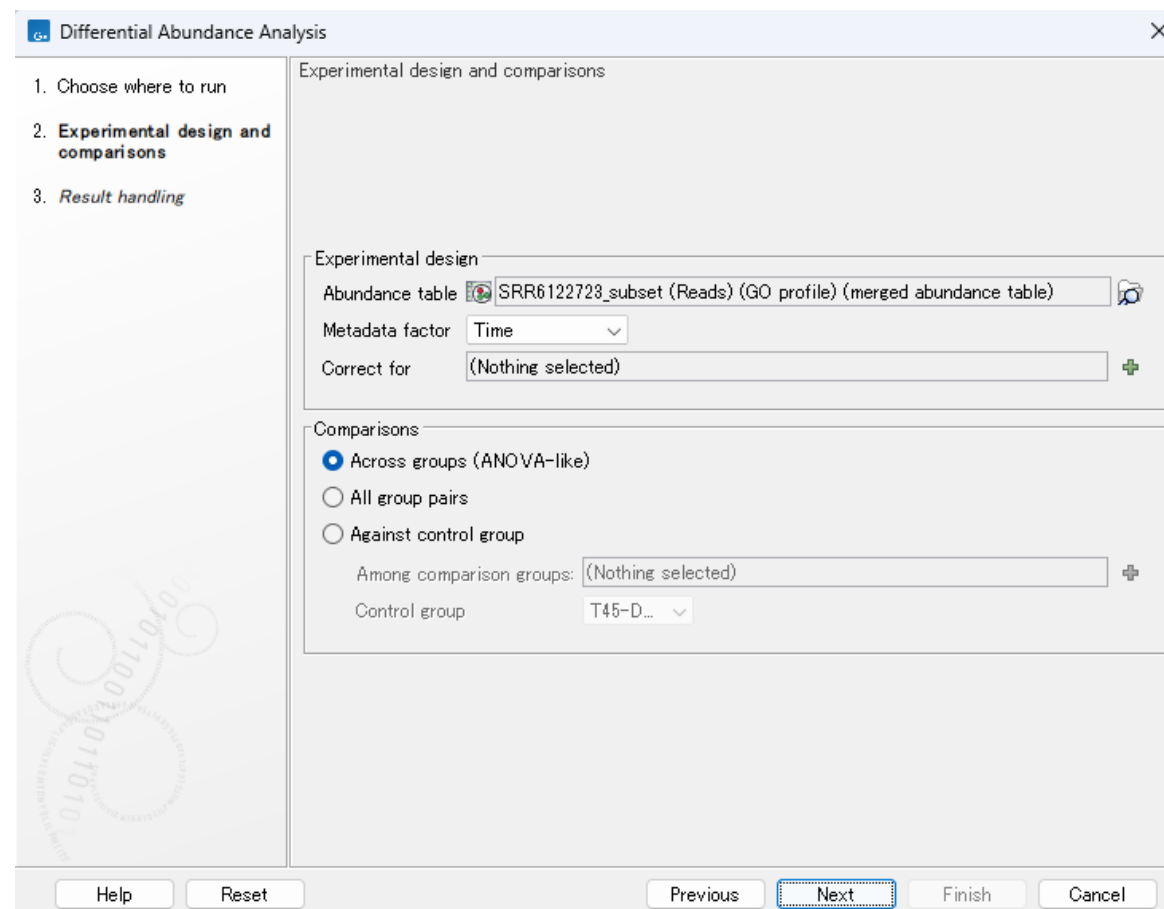
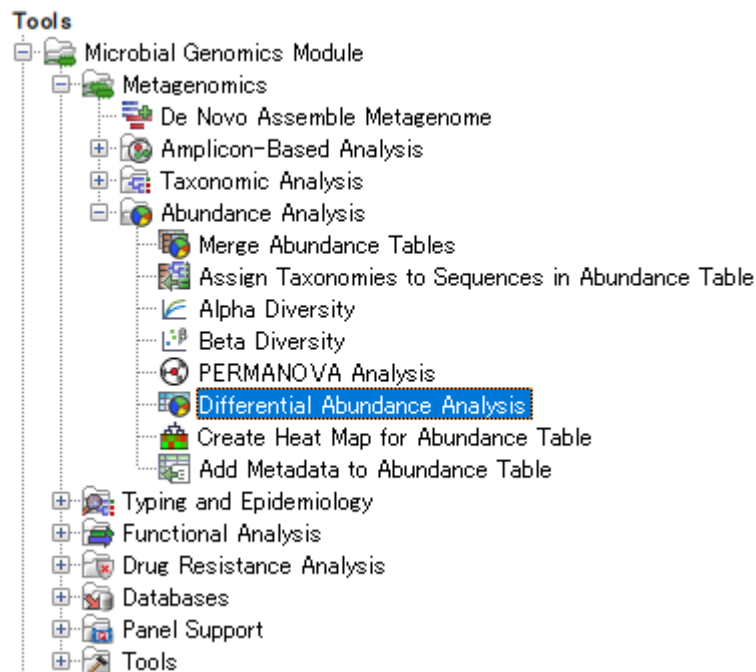
Help Reset Previous Next Finish Cancel

Merge Abundance Tableを起動し、GOに関するAbundance Tableをすべて選択します。

EC Abundance Tableの作成



再びMerge Abundance Tableを利用し、ECに関するAbundance Tableをすべて選択します。



Differential Abundance Analysisを起動し、mergeしたGOに関するAbundance Tableを指定します。
Metadata factorで何の要因について比較を行うかを指定します。

GOエンリッチメント解析

Rows: 168 Venn diagram table Filter to Selection*** Filter

Name	Due to Time					
	Max group m...	Log ₂ fold cha...	Fold change	P-value	FDR p-value	Bonferroni
1902555 // endoribonuclease complex	0.50	-2.65	-6.28	0.45	0.60	1.00
0072521 // purine-containing compound metabolic process	2.50	-4.60	-24.30	0.06	0.16	1.00
0003824 // catalytic activity	40.00	-0.76	-1.69	0.04	0.16	1.00
0045229 // external encapsulating structure organization	10.50	-2.30	-4.93	5.82E-3	0.03	0.98
0003735 // structural constituent of ribosome	326.50	-1.13	-2.19	3.95E-7	1.75E-5	6.63E-5
0003674 // molecular_function	366.50	-1.08	-2.12	1.47E-7	1.75E-5	2.48E-5
0005975 // carbohydrate metabolic process	2.50	-4.60	-24.30	0.07	0.16	1.00
0043038 // amino acid activation	17.00	0.27	1.20	0.52	0.64	1.00
0043039 // tRNA aminoacylation	17.00	0.27	1.20	0.52	0.64	1.00
0055086 // nucleobase-containing small molecule metabolic process	2.50	-4.60	-24.30	0.07	0.16	1.00
0005840 // ribosome	326.50	-1.13	-2.19	9.37E-7	1.75E-5	1.57E-4
0043167 // ion binding	28.50	-0.33	-1.26	0.36	0.60	1.00
0043168 // anion binding	28.50	-0.33	-1.26	0.36	0.60	1.00
0043169 // cation binding	1.00	-3.43	-10.78	0.26	0.48	1.00
0043170 // macromolecule metabolic process	17.50	0.23	1.17	0.59	0.68	1.00
0043228 // non-membrane-bounded organelle	326.50	-1.13	-2.19	9.37E-7	1.75E-5	1.57E-4
0043229 // intracellular organelle	326.50	-1.13	-2.19	9.37E-7	1.75E-5	1.57E-4
0043226 // organelle	326.50	-1.13	-2.19	9.37E-7	1.75E-5	1.57E-4
0043232 // intracellular non-membrane-bounded organelle	326.50	-1.13	-2.19	7.20E-7	1.75E-5	1.21E-4
0005737 // cytoplasm	11.50	-2.43	-5.39	2.85E-3	0.03	0.48
0030680 // dimeric ribonuclease P complex	0.50	-2.65	-6.28	0.45	0.60	1.00
0030677 // ribonuclease P complex	0.50	-2.65	-6.28	0.45	0.60	1.00
0030554 // adenylyl nucleotide binding	18.00	0.19	1.14	0.65	0.72	1.00
0005575 // cellular_component	355.50	-1.05	-2.07	6.46E-7	1.75E-5	1.08E-4
0043436 // oxoacid metabolic process	19.50	0.07	1.05	0.86	0.91	1.00
0005524 // ATP binding	18.00	0.19	1.14	0.65	0.72	1.00
0005515 // protein binding	1.00	-3.43	-10.78	0.26	0.48	1.00

サンプル間で変動のあるGOのリストが作成されます。
ECについても同様のリストを作成することができます。

The screenshot shows the 'Identify Pathways' software interface. On the left, a 'Tools' sidebar lists various analysis modules, with 'Identify Pathways' highlighted. The main window is titled 'Identify Pathways' and contains a 'Select (Differential) Abundance Table' dialog. The dialog has a 'Navigation Area' with a search bar and a tree view of analysis options. The tree view shows a hierarchy of folders and files, with 'SRR6122723_subset (Reads) (EC profile) (merged abundance table)' selected. The 'Selected elements (1)' pane on the right shows the selected item. The dialog also includes a 'Batch' checkbox and buttons for 'Help', 'Reset', 'Previous', 'Next', 'Finish', and 'Cancel'.

Identify Pathwaysを起動し、ECのAbundance Tableを選択します。

Rows: 19		Filter to Selection**	SRR6122723_subs		
Name	MetaCyc ID	Min. Solution	Confidence	Coverage	Filter
tRNA charging	TRNA-CHARGING-PWY	<input checked="" type="checkbox"/>	1.00	0.05	
tRNA processing	PWY0-1479	<input checked="" type="checkbox"/>	1.00	0.20	
UDP- <i>N</i> -acetylmuramoyl-pentapeptide biosynthesis III (<i>meso</i> -diaminopimelate containing)	PWY-7953	<input checked="" type="checkbox"/>	0.26	0.12	
UDP- <i>N</i> -acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing)	PWY-6386	<input checked="" type="checkbox"/>	0.25	0.12	
anhydromuropeptides recycling I	PWY0-1261	<input checked="" type="checkbox"/>	0.25	0.08	
UDP- <i>N</i> -acetylmuramoyl-pentapeptide biosynthesis I (<i>meso</i> -diaminopimelate containing)	PWY-6387	<input checked="" type="checkbox"/>	0.24	0.12	
gluconeogenesis I	GLUCONEO-PWY	<input checked="" type="checkbox"/>	0.09	0.08	
Calvin-Benson-Bassham cycle	CALVIN-PWY	<input checked="" type="checkbox"/>	0.09	0.15	
glycolysis I (from glucose 6-phosphate)	GLYCOLYSIS	<input checked="" type="checkbox"/>	0.09	0.08	
glycolysis V (Pyrococcus)	P341-PWY	<input checked="" type="checkbox"/>	0.09	0.10	
sucrose degradation V (sucrose α -glucosidase)	PWY66-373	<input checked="" type="checkbox"/>	0.08	0.20	
sedoheptulose biphosphate bypass	PWY0-1517	<input checked="" type="checkbox"/>	0.08	0.50	
formaldehyde assimilation II (assimilatory RuMP Cycle)	PWY-1861	<input checked="" type="checkbox"/>	0.08	0.11	
gluconeogenesis III	PWY66-399	<input checked="" type="checkbox"/>	0.07	0.08	
formaldehyde assimilation III (dihydroxyacetone cycle)	P185-PWY	<input checked="" type="checkbox"/>	0.07	0.08	
glycolysis II (from fructose 6-phosphate)	PWY-5484	<input checked="" type="checkbox"/>	0.07	0.09	
glycolysis III (from glucose)	ANAGLYCOLYSIS-PWY	<input checked="" type="checkbox"/>	0.07	0.09	
glycolysis IV (plant cytosol)	PWY-1042	<input checked="" type="checkbox"/>	0.06	0.10	
1,3-propanediol biosynthesis (engineered)	PWY-7385	<input checked="" type="checkbox"/>	0.06	0.12	

関連するパスウェイのリストが表示されます。

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