0.1 Activate Conda environment
Conda envionemnt: "magsearcher" was loaded successfully

0.2 Operation mode
MAGsearcher is operated in "Proteoms" mode.

0.3 Location of metagenomic data analysed
Directory to metagenomic raw data:
/home/ah830/NSF_metagenomics/NGS_data/metagenomics/raw
Directory containing binned metagenomes:
/home/ah830/NSF_metagenomics/NGS_data/metagenomics/mags_raw

0.4 Load additional proteome data
Top directory conatining proteomes derived from WGAs:
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/SOKS/B1_Thiamine/B
1_Thiamine_SOKS/ncbi_dataset/data/

Within the top directory:
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/SOKS/B1_Thiamine/B
1_Thiamine_SOKS/ncbi_dataset/data/ files with the extension: */*.faa are
analysed

0.5 Location of templates
template information will be stored under: ../common_data/templates

0.6 Load queries
Queries used: ../example_data/queries/

0.7 Load thresholds
Tresholds used: ../example_data/thresholds.csv

0.8 Specify output directory
Output directory:
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1

1. Prepare template files
1.3 Organise into one directory
Processed fasta files can be found in: ../common_data/templates

1.4 Make all template files headers unique
── Attaching packages ──────────────────────────────────── tidyverse
1.3.0 ──
✔ ggplot2 3.3.6   ✔ purrr   0.3.4
✔ tibble 3.1.8   ✔ dplyr   1.0.10
✔ tidyr   1.2.1   ✔ stringr 1.4.1
✔ readr   2.1.2   ✔ forcats 0.5.2
── Conflicts ──
tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()   masks stats::lag()
Warning messages:
1: package 'ggplot2' was built under R version 4.0.5
2: package 'tibble' was built under R version 4.0.5
3: package 'tidyr' was built under R version 4.0.5
4: package 'readr' was built under R version 4.0.5
5: package 'dplyr' was built under R version 4.0.5

```
6: package 'stringr' was built under R version 4.0.5
7: package 'forcats' was built under R version 4.0.5
[1] "Importing:1/26 : GCA_905232135.1_protein.faa"
[1] "Importing:2/26 : GCF_000005845.2_protein.faa"
[1] "Importing:3/26 : GCF_000006945.2_protein.faa"
[1] "Importing:4/26 : GCF_000006965.1_protein.faa"
[1] "Importing:5/26 : GCF_000009045.1_protein.faa"
[1] "Importing:6/26 : GCF_000009265.1_protein.faa"
[1] "Importing:7/26 : GCF_000009625.1_protein.faa"
[1] "Importing:8/26 : GCF_000014045.1_protein.faa"
[1] "Importing:9/26 : GCF_000018145.1_protein.faa"
[1] "Importing:10/26 : GCF_000018865.1_protein.faa"
[1] "Importing:11/26 : GCF_000021945.1_protein.faa"
[1] "Importing:12/26 : GCF_000092045.1_protein.faa"
[1] "Importing:13/26 : GCF_000092065.1_protein.faa"
[1] "Importing:14/26 : GCF_000146045.2_protein.faa"
[1] "Importing:15/26 : GCF_000151265.2_protein.faa"
[1] "Importing:16/26 : GCF_000154785.2_protein.faa"
[1] "Importing:17/26 : GCF_000330885.1_protein.faa"
[1] "Importing:18/26 : GCF_000372725.1_protein.faa"
[1] "Importing:19/26 : GCF_000373425.1_protein.faa"
[1] "Importing:20/26 : GCF_000427765.1_protein.faa"
[1] "Importing:21/26 : GCF_001664385.1_protein.faa"
[1] "Importing:22/26 : GCF_002417665.1_protein.faa"
[1] "Importing:23/26 : GCF_007827425.1_protein.faa"
[1] "Importing:24/26 : GCF_010365265.1_protein.faa"
[1] "Importing:25/26 : GCF_013752735.1_protein.faa"
[1] "Importing:26/26 : GCF_014194605.1_protein.faa"
[1] "Duplicated headers found in original fastas: TRUE"
[1] "Duplicated headers found in reformatted fastas: FALSE"


2. Run BUSCO on templates (this step will take a while)
2.1 Download Busco reference if absent
Processing: 1/26 GCA_905232135.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:38:27 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCA_90523
2135.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:38:27
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
```

```
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:29.8%[S:29.0%,D:0.8%],F:12.9%,M:57.3%,n:124

INFO:


        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:29.8%[S:29.0%,D:0.8%],F:12.9%,M:57.3%,n:124    |
        |37   Complete BUSCOs (C)                         |
        |36   Complete and single-copy BUSCOs (S)         |
        |1    Complete and duplicated BUSCOs (D)          |
        |16   Fragmented BUSCOs (F)                       |
        |71   Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 10 seconds
INFO: Results written in ../common_data/busco/GCA_905232135.1_protein


Processing: 2/26 GCF_000005845.2_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:38:37 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00000
5845.2_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:38:37
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124

INFO:


        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124    |
        |124  Complete BUSCOs (C)                         |
        |124  Complete and single-copy BUSCOs (S)         |
        |0    Complete and duplicated BUSCOs (D)          |
        |0    Fragmented BUSCOs (F)                        |
        |0    Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
```

```
          --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 4 seconds
INFO: Results written in ../common_data/busco/GCF_000005845.2_protein


Processing: 3/26 GCF_000006945.2_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:38:42 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00000
6945.2_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:38:43
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124

INFO:

          --------------------------------------------------
          |Results from dataset bacteria_odb10              |
          --------------------------------------------------
          |C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124    |
          |124  Complete BUSCOs (C)                         |
          |124  Complete and single-copy BUSCOs (S)         |
          |0    Complete and duplicated BUSCOs (D)          |
          |0    Fragmented BUSCOs (F)                        |
          |0    Missing BUSCOs (M)                          |
          |124  Total BUSCO groups searched                 |
          --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000006945.2_protein


Processing: 4/26 GCF_000006965.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:38:48 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00000
6965.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
```

```
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:38:50
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:99.2%,D:0.8%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10               |
        ---------------------------------------------------
        |C:100.0%[S:99.2%,D:0.8%],F:0.0%,M:0.0%,n:124      |
        |124  Complete BUSCOs (C)                          |
        |123  Complete and single-copy BUSCOs (S)          |
        |1    Complete and duplicated BUSCOs (D)           |
        |0    Fragmented BUSCOs (F)                         |
        |0    Missing BUSCOs (M)                           |
        |124  Total BUSCO groups searched                  |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000006965.1_protein


Processing: 5/26 GCF_000009045.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:38:54 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00000
9045.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:38:56
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124
```

```
INFO:

      --------------------------------------------------
      |Results from dataset bacteria_odb10              |
      --------------------------------------------------
      |C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124    |
      |124  Complete BUSCOs (C)                         |
      |124  Complete and single-copy BUSCOs (S)         |
      |0    Complete and duplicated BUSCOs (D)          |
      |0    Fragmented BUSCOs (F)                        |
      |0    Missing BUSCOs (M)                          |
      |124  Total BUSCO groups searched                 |
      --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 5 seconds
INFO: Results written in ../common_data/busco/GCF_000009045.1_protein


Processing: 6/26 GCF_000009265.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:00 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00000
9265.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:02
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:96.8%,D:3.2%],F:0.0%,M:0.0%,n:124

INFO:

      --------------------------------------------------
      |Results from dataset bacteria_odb10              |
      --------------------------------------------------
      |C:100.0%[S:96.8%,D:3.2%],F:0.0%,M:0.0%,n:124     |
      |124  Complete BUSCOs (C)                         |
      |120  Complete and single-copy BUSCOs (S)         |
      |4    Complete and duplicated BUSCOs (D)          |
      |0    Fragmented BUSCOs (F)                        |
      |0    Missing BUSCOs (M)                          |
      |124  Total BUSCO groups searched                 |
      --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 7 seconds
```

INFO: Results written in ../common_data/busco/GCF_000009265.1_protein

Processing: 7/26 GCF_000009625.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:07 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00000
9625.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:08
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results: C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124

INFO:

        |Results from dataset bacteria_odb10 |

        |C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124 |
        |124 Complete BUSCOs (C) |
        |122 Complete and single-copy BUSCOs (S) |
        |2   Complete and duplicated BUSCOs (D) |
        |0   Fragmented BUSCOs (F) |
        |0   Missing BUSCOs (M) |
        |124 Total BUSCO groups searched |

INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000009625.1_protein

Processing: 8/26 GCF_000014045.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:13 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00001
4045.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)

```
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:14
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:98.4%[S:96.8%,D:1.6%],F:0.0%,M:1.6%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:98.4%[S:96.8%,D:1.6%],F:0.0%,M:1.6%,n:124      |
        |122  Complete BUSCOs (C)                         |
        |120  Complete and single-copy BUSCOs (S)         |
        |2    Complete and duplicated BUSCOs (D)          |
        |0    Fragmented BUSCOs (F)                        |
        |2    Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 4 seconds
INFO: Results written in ../common_data/busco/GCF_000014045.1_protein


Processing: 9/26 GCF_000018145.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:18 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00001
8145.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:20
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124

INFO:
```

```
        --------------------------------------------------
        |Results from dataset bacteria_odb10              |
        --------------------------------------------------
        |C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124     |
        |124  Complete BUSCOs (C)                         |
        |122  Complete and single-copy BUSCOs (S)         |
        |2    Complete and duplicated BUSCOs (D)          |
        |0    Fragmented BUSCOs (F)                        |
        |0    Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000018145.1_protein


Processing: 10/26 GCF_000018865.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:24 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00001
8865.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:26
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:   C:95.2%[S:94.4%,D:0.8%],F:2.4%,M:2.4%,n:124

INFO:

        --------------------------------------------------
        |Results from dataset bacteria_odb10              |
        --------------------------------------------------
        |C:95.2%[S:94.4%,D:0.8%],F:2.4%,M:2.4%,n:124      |
        |118  Complete BUSCOs (C)                         |
        |117  Complete and single-copy BUSCOs (S)         |
        |1    Complete and duplicated BUSCOs (D)          |
        |3    Fragmented BUSCOs (F)                        |
        |3    Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000018865.1_protein
```

```
Processing: 11/26 GCF_000021945.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:30 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00002
1945.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:32
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:95.1%[S:93.5%,D:1.6%],F:1.6%,M:3.3%,n:124

INFO:

        --------------------------------------------------
        |Results from dataset bacteria_odb10             |
        --------------------------------------------------
        |C:95.1%[S:93.5%,D:1.6%],F:1.6%,M:3.3%,n:124     |
        |118  Complete BUSCOs (C)                        |
        |116  Complete and single-copy BUSCOs (S)        |
        |2    Complete and duplicated BUSCOs (D)         |
        |2    Fragmented BUSCOs (F)                      |
        |4    Missing BUSCOs (M)                         |
        |124  Total BUSCO groups searched                |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000021945.1_protein


Processing: 12/26 GCF_000092045.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:36 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00009
2045.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
```

```
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:38
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------
        |Results from dataset bacteria_odb10         |
        ---------------------------------------------
        |C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124    |
        |124  Complete BUSCOs (C)                    |
        |122  Complete and single-copy BUSCOs (S)    |
        |2    Complete and duplicated BUSCOs (D)     |
        |0    Fragmented BUSCOs (F)                  |
        |0    Missing BUSCOs (M)                     |
        |124  Total BUSCO groups searched            |
        ---------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000092045.1_protein


Processing: 13/26 GCF_000092065.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:43 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00009
2065.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:44
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:64.5%[S:52.4%,D:12.1%],F:11.3%,M:24.2%,n:124

INFO:
```

```
        --------------------------------------------------
        |Results from dataset bacteria_odb10              |
        --------------------------------------------------
        |C:64.5%[S:52.4%,D:12.1%],F:11.3%,M:24.2%,n:124   |
        |80   Complete BUSCOs (C)                         |
        |65   Complete and single-copy BUSCOs (S)         |
        |15   Complete and duplicated BUSCOs (D)          |
        |14   Fragmented BUSCOs (F)                       |
        |30   Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 8 seconds
INFO: Results written in ../common_data/busco/GCF_000092065.1_protein


Processing: 14/26 GCF_000146045.2_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:51 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00014
6045.2_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:51
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:35.4%[S:29.8%,D:5.6%],F:12.9%,M:51.7%,n:124

INFO:

        --------------------------------------------------
        |Results from dataset bacteria_odb10              |
        --------------------------------------------------
        |C:35.4%[S:29.8%,D:5.6%],F:12.9%,M:51.7%,n:124    |
        |44   Complete BUSCOs (C)                         |
        |37   Complete and single-copy BUSCOs (S)         |
        |7    Complete and duplicated BUSCOs (D)          |
        |16   Fragmented BUSCOs (F)                       |
        |64   Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 7 seconds
INFO: Results written in ../common_data/busco/GCF_000146045.2_protein
```

```
Processing: 15/26 GCF_000151265.2_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:39:58 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00015
1265.2_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:39:59
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:   C:60.5%[S:54.0%,D:6.5%],F:16.9%,M:22.6%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:60.5%[S:54.0%,D:6.5%],F:16.9%,M:22.6%,n:124    |
        |75   Complete BUSCOs (C)                         |
        |67   Complete and single-copy BUSCOs (S)         |
        |8    Complete and duplicated BUSCOs (D)          |
        |21   Fragmented BUSCOs (F)                       |
        |28   Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 10 seconds
INFO: Results written in ../common_data/busco/GCF_000151265.2_protein


Processing: 16/26 GCF_000154785.2_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:40:08 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00015
4785.2_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:40:09
```

```
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124     |
        |124   Complete BUSCOs (C)                        |
        |122   Complete and single-copy BUSCOs (S)        |
        |2     Complete and duplicated BUSCOs (D)         |
        |0     Fragmented BUSCOs (F)                      |
        |0     Missing BUSCOs (M)                         |
        |124   Total BUSCO groups searched                |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 5 seconds
INFO: Results written in ../common_data/busco/GCF_000154785.2_protein


Processing: 17/26 GCF_000330885.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:40:13 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00033
0885.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:40:15
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
```

```
        --------------------------------------------------
        |C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124      |
        |124  Complete BUSCOs (C)                          |
        |122  Complete and single-copy BUSCOs (S)          |
        |2    Complete and duplicated BUSCOs (D)           |
        |0    Fragmented BUSCOs (F)                         |
        |0    Missing BUSCOs (M)                            |
        |124  Total BUSCO groups searched                  |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000330885.1_protein


Processing: 18/26 GCF_000372725.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:40:20 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00037
2725.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:40:21
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:   C:42.8%[S:21.8%,D:21.0%],F:17.7%,M:39.5%,n:124

INFO:

        --------------------------------------------------
        |Results from dataset bacteria_odb10               |
        --------------------------------------------------
        |C:42.8%[S:21.8%,D:21.0%],F:17.7%,M:39.5%,n:124    |
        |53   Complete BUSCOs (C)                           |
        |27   Complete and single-copy BUSCOs (S)           |
        |26   Complete and duplicated BUSCOs (D)            |
        |22   Fragmented BUSCOs (F)                          |
        |49   Missing BUSCOs (M)                             |
        |124  Total BUSCO groups searched                   |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 25 seconds
INFO: Results written in ../common_data/busco/GCF_000372725.1_protein


Processing: 19/26 GCF_000373425.1_protein.faa
```

```
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:40:45 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00037
3425.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:40:45
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:97.6%,D:2.4%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:100.0%[S:97.6%,D:2.4%],F:0.0%,M:0.0%,n:124     |
        |124  Complete BUSCOs (C)                         |
        |121  Complete and single-copy BUSCOs (S)         |
        |3    Complete and duplicated BUSCOs (D)          |
        |0    Fragmented BUSCOs (F)                       |
        |0    Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000373425.1_protein


Processing: 20/26 GCF_000427765.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:40:51 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00042
7765.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:40:51
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
```

```
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:96.8%,D:3.2%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------
        |Results from dataset bacteria_odb10           |
        ---------------------------------------------
        |C:100.0%[S:96.8%,D:3.2%],F:0.0%,M:0.0%,n:124    |
        |124   Complete BUSCOs (C)                        |
        |120   Complete and single-copy BUSCOs (S)        |
        |4     Complete and duplicated BUSCOs (D)         |
        |0     Fragmented BUSCOs (F)                      |
        |0     Missing BUSCOs (M)                         |
        |124   Total BUSCO groups searched                |
        ---------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_000427765.1_protein


Processing: 21/26 GCF_001664385.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:40:57 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00166
4385.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:40:57
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:99.2%,D:0.8%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------
        |Results from dataset bacteria_odb10           |
        ---------------------------------------------
        |C:100.0%[S:99.2%,D:0.8%],F:0.0%,M:0.0%,n:124    |
```

```
            |124  Complete BUSCOs (C)                       |
            |123  Complete and single-copy BUSCOs (S)       |
            |1    Complete and duplicated BUSCOs (D)         |
            |0    Fragmented BUSCOs (F)                      |
            |0    Missing BUSCOs (M)                         |
            |124  Total BUSCO groups searched               |
            -------------------------------------------------
INFO: BUSCO analysis done. Total running time: 5 seconds
INFO: Results written in ../common_data/busco/GCF_001664385.1_protein


Processing: 22/26 GCF_002417665.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:41:03 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00241
7665.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:41:03
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124

INFO:

            -------------------------------------------------
            |Results from dataset bacteria_odb10            |
            -------------------------------------------------
            |C:100.0%[S:100.0%,D:0.0%],F:0.0%,M:0.0%,n:124  |
            |124  Complete BUSCOs (C)                       |
            |124  Complete and single-copy BUSCOs (S)       |
            |0    Complete and duplicated BUSCOs (D)         |
            |0    Fragmented BUSCOs (F)                      |
            |0    Missing BUSCOs (M)                         |
            |124  Total BUSCO groups searched               |
            -------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_002417665.1_protein


Processing: 23/26 GCF_007827425.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:41:09 *****
```

```
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_00782
7425.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:41:09
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:96.0%,D:4.0%],F:0.0%,M:0.0%,n:124

INFO:

        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:100.0%[S:96.0%,D:4.0%],F:0.0%,M:0.0%,n:124     |
        |124  Complete BUSCOs (C)                         |
        |119  Complete and single-copy BUSCOs (S)         |
        |5    Complete and duplicated BUSCOs (D)          |
        |0    Fragmented BUSCOs (F)                        |
        |0    Missing BUSCOs (M)                           |
        |124  Total BUSCO groups searched                 |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 6 seconds
INFO: Results written in ../common_data/busco/GCF_007827425.1_protein


Processing: 24/26 GCF_010365265.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:41:15 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_01036
5265.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:41:15
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
```

```
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124

INFO:


        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:100.0%[S:98.4%,D:1.6%],F:0.0%,M:0.0%,n:124     |
        |124  Complete BUSCOs (C)                         |
        |122  Complete and single-copy BUSCOs (S)         |
        |2    Complete and duplicated BUSCOs (D)          |
        |0    Fragmented BUSCOs (F)                       |
        |0    Missing BUSCOs (M)                          |
        |124  Total BUSCO groups searched                 |
        ---------------------------------------------------
INFO: BUSCO analysis done. Total running time: 5 seconds
INFO: Results written in ../common_data/busco/GCF_010365265.1_protein


Processing: 25/26 GCF_013752735.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:41:21 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_01375
2735.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:41:21
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:    C:99.2%[S:97.6%,D:1.6%],F:0.8%,M:0.0%,n:124

INFO:


        ---------------------------------------------------
        |Results from dataset bacteria_odb10              |
        ---------------------------------------------------
        |C:99.2%[S:97.6%,D:1.6%],F:0.8%,M:0.0%,n:124      |
        |123  Complete BUSCOs (C)                         |
```

```
            |121  Complete and single-copy BUSCOs (S)       |
            |2    Complete and duplicated BUSCOs (D)         |
            |1    Fragmented BUSCOs (F)                      |
            |0    Missing BUSCOs (M)                         |
            |124  Total BUSCO groups searched               |
            --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 7 seconds
INFO: Results written in ../common_data/busco/GCF_013752735.1_protein


Processing: 26/26 GCF_014194605.1_protein.faa
INFO: ***** Start a BUSCO v4.1.4 analysis, current time: 01/31/2023
09:41:28 *****
INFO: Configuring BUSCO with
/Users/ah830/miniconda3/envs/magsearcher/share/busco/config.ini
INFO: Mode is proteins
INFO: Input file is
/Users/ah830/Documents/GitHub/MAGsearcher/common_data/templates/GCF_01419
4605.1_protein.faa
INFO: Downloading information on latest versions of BUSCO data...
INFO: Running BUSCO using lineage dataset bacteria_odb10 (prokaryota,
2020-03-06)
INFO: ***** Run HMMER on gene sequences *****
INFO: Running 124 job(s) on hmmsearch, starting at 01/31/2023 09:41:28
INFO: [hmmsearch] 13 of 124 task(s) completed
INFO: [hmmsearch] 25 of 124 task(s) completed
INFO: [hmmsearch] 38 of 124 task(s) completed
INFO: [hmmsearch] 50 of 124 task(s) completed
INFO: [hmmsearch] 63 of 124 task(s) completed
INFO: [hmmsearch] 75 of 124 task(s) completed
INFO: [hmmsearch] 87 of 124 task(s) completed
INFO: [hmmsearch] 100 of 124 task(s) completed
INFO: [hmmsearch] 112 of 124 task(s) completed
INFO: [hmmsearch] 124 of 124 task(s) completed
INFO: Results:   C:97.6%[S:96.0%,D:1.6%],F:1.6%,M:0.8%,n:124

INFO:

        --------------------------------------------------
        |Results from dataset bacteria_odb10             |
        --------------------------------------------------
        |C:97.6%[S:96.0%,D:1.6%],F:1.6%,M:0.8%,n:124     |
        |121  Complete BUSCOs (C)                        |
        |119  Complete and single-copy BUSCOs (S)        |
        |2    Complete and duplicated BUSCOs (D)         |
        |2    Fragmented BUSCOs (F)                       |
        |1    Missing BUSCOs (M)                         |
        |124  Total BUSCO groups searched               |
        --------------------------------------------------
INFO: BUSCO analysis done. Total running time: 7 seconds
INFO: Results written in ../common_data/busco/GCF_014194605.1_protein


2.2 Parse busco output to csv file

platform       x86_64-apple-darwin13.4.0
arch           x86_64
```

```
os              darwin13.4.0
system          x86_64, darwin13.4.0
status
major           4
minor           0.3
year            2020
month           10
day             10
svn rev         79318
language        R
version.string R version 4.0.3 (2020-10-10)
nickname        Bunny-Wunnies Freak Out
[1] "Working directory: /Users/ah830/Documents/GitHub/MAGsearcher/src"
[1] "Saving BUSCO files from: ../common_data/busco to:
../common_data/busco_summary.csv"
── Attaching packages ──────────────────────────────────── tidyverse
1.3.0 ──
✔ ggplot2 3.3.6      ✔ purrr   0.3.4
✔ tibble  3.1.8      ✔ dplyr   1.0.10
✔ tidyr   1.2.1      ✔ stringr 1.4.1
✔ readr   2.1.2      ✔ forcats 0.5.2
── Conflicts ───────────────────────────────────────
tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()    masks stats::lag()
[1] "Processing file: 1 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCA_905232135.1_protein/short_summary.specific.bact
eria_odb10.GCA_905232135.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCA_905232135.1_protein/short_summary.specific.bact
eria_odb10.GCA_905232135.1_protein.txt'

[1] "Processing file: 2 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000005845.2_protein/short_summary.specific.bact
eria_odb10.GCF_000005845.2_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000005845.2_protein/short_summary.specific.bact
eria_odb10.GCF_000005845.2_protein.txt'

[1] "Processing file: 3 / 26"
Warning: 2 parsing failures.
row col  expected
actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000006945.2_protein/short_summary.specific.bact
eria_odb10.GCF_000006945.2_protein.txt'
```

```
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000006945.2_protein/short_summary.specific.bact
eria_odb10.GCF_000006945.2_protein.txt'

[1] "Processing file: 4 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000006965.1_protein/short_summary.specific.bact
eria_odb10.GCF_000006965.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000006965.1_protein/short_summary.specific.bact
eria_odb10.GCF_000006965.1_protein.txt'

[1] "Processing file: 5 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000009045.1_protein/short_summary.specific.bact
eria_odb10.GCF_000009045.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000009045.1_protein/short_summary.specific.bact
eria_odb10.GCF_000009045.1_protein.txt'

[1] "Processing file: 6 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000009265.1_protein/short_summary.specific.bact
eria_odb10.GCF_000009265.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000009265.1_protein/short_summary.specific.bact
eria_odb10.GCF_000009265.1_protein.txt'

[1] "Processing file: 7 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000009625.1_protein/short_summary.specific.bact
eria_odb10.GCF_000009625.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000009625.1_protein/short_summary.specific.bact
eria_odb10.GCF_000009625.1_protein.txt'

[1] "Processing file: 8 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000014045.1_protein/short_summary.specific.bact
eria_odb10.GCF_000014045.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000014045.1_protein/short_summary.specific.bact
eria_odb10.GCF_000014045.1_protein.txt'
```

```
[1] "Processing file: 9 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000018145.1_protein/short_summary.specific.bact
eria_odb10.GCF_000018145.1_protein.txt'
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000018145.1_protein/short_summary.specific.bact
eria_odb10.GCF_000018145.1_protein.txt'

[1] "Processing file: 10 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000018865.1_protein/short_summary.specific.bact
eria_odb10.GCF_000018865.1_protein.txt'
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000018865.1_protein/short_summary.specific.bact
eria_odb10.GCF_000018865.1_protein.txt'

[1] "Processing file: 11 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000021945.1_protein/short_summary.specific.bact
eria_odb10.GCF_000021945.1_protein.txt'
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000021945.1_protein/short_summary.specific.bact
eria_odb10.GCF_000021945.1_protein.txt'

[1] "Processing file: 12 / 26"
Warning: 2 parsing failures.
row col  expected
actual
file
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000092045.1_protein/short_summary.specific.bact
eria_odb10.GCF_000092045.1_protein.txt'
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000092045.1_protein/short_summary.specific.bact
eria_odb10.GCF_000092045.1_protein.txt'

[1] "Processing file: 13 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000092065.1_protein/short_summary.specific.bact
eria_odb10.GCF_000092065.1_protein.txt'
  1 -- 1 columns 2 columns
'../common_data/busco/GCF_000092065.1_protein/short_summary.specific.bact
eria_odb10.GCF_000092065.1_protein.txt'

[1] "Processing file: 14 / 26"
```

```
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000146045.2_protein/short_summary.specific.bact
eria_odb10.GCF_000146045.2_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000146045.2_protein/short_summary.specific.bact
eria_odb10.GCF_000146045.2_protein.txt'

[1] "Processing file: 15 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000151265.2_protein/short_summary.specific.bact
eria_odb10.GCF_000151265.2_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000151265.2_protein/short_summary.specific.bact
eria_odb10.GCF_000151265.2_protein.txt'

[1] "Processing file: 16 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000154785.2_protein/short_summary.specific.bact
eria_odb10.GCF_000154785.2_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000154785.2_protein/short_summary.specific.bact
eria_odb10.GCF_000154785.2_protein.txt'

[1] "Processing file: 17 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000330885.1_protein/short_summary.specific.bact
eria_odb10.GCF_000330885.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000330885.1_protein/short_summary.specific.bact
eria_odb10.GCF_000330885.1_protein.txt'

[1] "Processing file: 18 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000372725.1_protein/short_summary.specific.bact
eria_odb10.GCF_000372725.1_protein.txt'
  1  -- 1 columns 2 columns
'../common_data/busco/GCF_000372725.1_protein/short_summary.specific.bact
eria_odb10.GCF_000372725.1_protein.txt'

[1] "Processing file: 19 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
```

```
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_000373425.1_protein/short_summary.specific.bact
eria_odb10.GCF_000373425.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_000373425.1_protein/short_summary.specific.bact
eria_odb10.GCF_000373425.1_protein.txt'

[1] "Processing file: 20 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_000427765.1_protein/short_summary.specific.bact
eria_odb10.GCF_000427765.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_000427765.1_protein/short_summary.specific.bact
eria_odb10.GCF_000427765.1_protein.txt'

[1] "Processing file: 21 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_001664385.1_protein/short_summary.specific.bact
eria_odb10.GCF_001664385.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_001664385.1_protein/short_summary.specific.bact
eria_odb10.GCF_001664385.1_protein.txt'

[1] "Processing file: 22 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_002417665.1_protein/short_summary.specific.bact
eria_odb10.GCF_002417665.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_002417665.1_protein/short_summary.specific.bact
eria_odb10.GCF_002417665.1_protein.txt'

[1] "Processing file: 23 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_007827425.1_protein/short_summary.specific.bact
eria_odb10.GCF_007827425.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_007827425.1_protein/short_summary.specific.bact
eria_odb10.GCF_007827425.1_protein.txt'

[1] "Processing file: 24 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_010365265.1_protein/short_summary.specific.bact
eria_odb10.GCF_010365265.1_protein.txt'
```

```
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_010365265.1_protein/short_summary.specific.bact
eria_odb10.GCF_010365265.1_protein.txt'

[1] "Processing file: 25 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_013752735.1_protein/short_summary.specific.bact
eria_odb10.GCF_013752735.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_013752735.1_protein/short_summary.specific.bact
eria_odb10.GCF_013752735.1_protein.txt'

[1] "Processing file: 26 / 26"
Warning: 2 parsing failures.
row col  expected    actual
file
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_014194605.1_protein/short_summary.specific.bact
eria_odb10.GCF_014194605.1_protein.txt'
    1  -- 1 columns 2 columns
'../common_data/busco/GCF_014194605.1_protein/short_summary.specific.bact
eria_odb10.GCF_014194605.1_protein.txt'

There were 33 warnings (use warnings() to see them)

3. Prepare queries
3.1 Download KEGG data if not present already
ko_list file found at: ../common_data/dbs/keggorthologue/ko_list
profiles directory found at: ../common_data/dbs/keggorthologue/profiles

3.2 Copy all kos from thresholds
All Kegg orthologues copied successfully
All queries in thresholds spreadsheet are found in:
../example_data/queries/

4. Run queries against templates (this step will take a while)
4.1 05_query_vs_proteomes_helper.py

GCF_000014045.1_protein
ssi index absent
Creating SSI index for
../common_data/templates/GCF_000014045.1_protein.faa...    done.
Indexed 3970 sequences (3970 names).
SSI index written to file
../common_data/templates/GCF_000014045.1_protein.faa.ssi
Searching K00059.hmm against GCF_000014045.1_protein
Searching K00208.hmm against GCF_000014045.1_protein
Searching K00278.hmm against GCF_000014045.1_protein
Searching K00322.hmm against GCF_000014045.1_protein
Searching K00323.hmm against GCF_000014045.1_protein
Searching K00324.hmm against GCF_000014045.1_protein
Searching K00325.hmm against GCF_000014045.1_protein
Searching K00486.hmm against GCF_000014045.1_protein
Searching K00548.hmm against GCF_000014045.1_protein
Searching K00549.hmm against GCF_000014045.1_protein
```

```
Searching K00589.hmm against GCF_000014045.1_protein
Searching K00595.hmm against GCF_000014045.1_protein
Searching K00643.hmm against GCF_000014045.1_protein
Searching K00647.hmm against GCF_000014045.1_protein
Searching K00652.hmm against GCF_000014045.1_protein
Searching K00767.hmm against GCF_000014045.1_protein
Searching K00768.hmm against GCF_000014045.1_protein
Searching K00788.hmm against GCF_000014045.1_protein
Searching K00793.hmm against GCF_000014045.1_protein
Searching K00798.hmm against GCF_000014045.1_protein
Searching K00833.hmm against GCF_000014045.1_protein
Searching K00858.hmm against GCF_000014045.1_protein
Searching K00877.hmm against GCF_000014045.1_protein
Searching K00878.hmm against GCF_000014045.1_protein
Searching K00941.hmm against GCF_000014045.1_protein
Searching K00946.hmm against GCF_000014045.1_protein
Searching K00949.hmm against GCF_000014045.1_protein
Searching K00952.hmm against GCF_000014045.1_protein
Searching K00969.hmm against GCF_000014045.1_protein
Searching K01012.hmm against GCF_000014045.1_protein
Searching K01077.hmm against GCF_000014045.1_protein
Searching K01078.hmm against GCF_000014045.1_protein
Searching K01435.hmm against GCF_000014045.1_protein
Searching K01513.hmm against GCF_000014045.1_protein
Searching K01556.hmm against GCF_000014045.1_protein
Searching K01662.hmm against GCF_000014045.1_protein
Searching K01698.hmm against GCF_000014045.1_protein
Searching K01719.hmm against GCF_000014045.1_protein
Searching K01749.hmm against GCF_000014045.1_protein
Searching K01845.hmm against GCF_000014045.1_protein
Searching K01885.hmm against GCF_000014045.1_protein
Searching K01906.hmm against GCF_000014045.1_protein
Searching K01916.hmm against GCF_000014045.1_protein
Searching K01935.hmm against GCF_000014045.1_protein
Searching K01950.hmm against GCF_000014045.1_protein
Searching K02169.hmm against GCF_000014045.1_protein
Searching K02170.hmm against GCF_000014045.1_protein
Searching K02188.hmm against GCF_000014045.1_protein
Searching K02189.hmm against GCF_000014045.1_protein
Searching K02190.hmm against GCF_000014045.1_protein
Searching K02191.hmm against GCF_000014045.1_protein
Searching K02224.hmm against GCF_000014045.1_protein
Searching K02225.hmm against GCF_000014045.1_protein
Searching K02226.hmm against GCF_000014045.1_protein
Searching K02227.hmm against GCF_000014045.1_protein
Searching K02228.hmm against GCF_000014045.1_protein
Searching K02229.hmm against GCF_000014045.1_protein
Searching K02230.hmm against GCF_000014045.1_protein
Searching K02231.hmm against GCF_000014045.1_protein
Searching K02232.hmm against GCF_000014045.1_protein
Searching K02233.hmm against GCF_000014045.1_protein
Searching K02302.hmm against GCF_000014045.1_protein
Searching K02303.hmm against GCF_000014045.1_protein
Searching K02304.hmm against GCF_000014045.1_protein
Searching K02372.hmm against GCF_000014045.1_protein
Searching K02492.hmm against GCF_000014045.1_protein
Searching K02496.hmm against GCF_000014045.1_protein
Searching K03146.hmm against GCF_000014045.1_protein
```

```
Searching K03147.hmm against GCF_000014045.1_protein
Searching K03148.hmm against GCF_000014045.1_protein
Searching K03149.hmm against GCF_000014045.1_protein
Searching K03150.hmm against GCF_000014045.1_protein
Searching K03151.hmm against GCF_000014045.1_protein
Searching K03153.hmm against GCF_000014045.1_protein
Searching K03154.hmm against GCF_000014045.1_protein
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Searching PF02574_S-methyl_trans.hmm.txt against GCF_000373425.1_protein
Searching PF02965_Met_synt_B12.hmm.txt against GCF_000373425.1_protein
Searching PF08267_Meth_synt_1.hmm.txt against GCF_000373425.1_protein
--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000373425.1_protein
Searching METH_Cre06.g250902.fa against GCF_000373425.1_protein
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-->Performing accession stats and obtaining protein fasta files

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--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000009265.1_protein
Searching METH_Cre06.g250902.fa against GCF_000009265.1_protein
-->Performing accession stats and obtaining protein fasta files

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--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000092065.1_protein
Searching METH_Cre06.g250902.fa against GCF_000092065.1_protein
-->Performing accession stats and obtaining protein fasta files

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Searching METE_Cre03.g180750.fa against GCF_000005845.2_protein
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Searching METE_Cre03.g180750.fa against GCF_000021945.1_protein
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Searching PF02574_S-methyl_trans.hmm.txt against GCF_002417665.1_protein
Searching PF02965_Met_synt_B12.hmm.txt against GCF_002417665.1_protein
Searching PF08267_Meth_synt_1.hmm.txt against GCF_002417665.1_protein
--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_002417665.1_protein
Searching METH_Cre06.g250902.fa against GCF_002417665.1_protein
-->Performing accession stats and obtaining protein fasta files

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Indexed 6079 sequences (6079 names).
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Searching K00322.hmm against GCF_000330885.1_protein
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-->Performing accession stats and obtaining protein fasta files

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Indexed 8240 sequences (8240 names).
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-->Performing accession stats and obtaining protein fasta files

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Indexed 7171 sequences (7171 names).
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Searching METE_Cre03.g180750.fa against GCF_000092045.1_protein
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Searching PF01497_Peripla_BP_2.hmm against GCF_013752735.1_protein
Searching PF07715_Plug.hmm against GCF_013752735.1_protein
Searching PF00809_Pterin_bind.hmm.txt against GCF_013752735.1_protein
Searching PF01717_Meth_synt_2.hmm.txt against GCF_013752735.1_protein
Searching PF02310_B12-binding.hmm.txt against GCF_013752735.1_protein
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Searching PF08267_Meth_synt_1.hmm.txt against GCF_013752735.1_protein
--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_013752735.1_protein
Searching METH_Cre06.g250902.fa against GCF_013752735.1_protein
-->Performing accession stats and obtaining protein fasta files

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Searching K00322.hmm against GCF_007827425.1_protein
Searching K00323.hmm against GCF_007827425.1_protein
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--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_007827425.1_protein
Searching METH_Cre06.g250902.fa against GCF_007827425.1_protein
-->Performing accession stats and obtaining protein fasta files

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--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000006945.2_protein
Searching METH_Cre06.g250902.fa against GCF_000006945.2_protein
-->Performing accession stats and obtaining protein fasta files

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Searching METE_Cre03.g180750.fa against GCF_000009045.1_protein
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-->Performing accession stats and obtaining protein fasta files

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--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000018145.1_protein
Searching METH_Cre06.g250902.fa against GCF_000018145.1_protein
-->Performing accession stats and obtaining protein fasta files

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Searching PF08267_Meth_synt_1.hmm.txt against GCF_000006965.1_protein
--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000006965.1_protein
Searching METH_Cre06.g250902.fa against GCF_000006965.1_protein
-->Performing accession stats and obtaining protein fasta files

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--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000018865.1_protein
Searching METH_Cre06.g250902.fa against GCF_000018865.1_protein
-->Performing accession stats and obtaining protein fasta files

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Searching METE_Cre03.g180750.fa against GCF_010365265.1_protein
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Searching PF00677_Lum_binding.hmm against GCF_001664385.1_protein
Searching PF01032_FecCD.hmm against GCF_001664385.1_protein
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Searching PF07715_Plug.hmm against GCF_001664385.1_protein
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Searching PF08267_Meth_synt_1.hmm.txt against GCF_001664385.1_protein
--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_001664385.1_protein
Searching METH_Cre06.g250902.fa against GCF_001664385.1_protein
-->Performing accession stats and obtaining protein fasta files

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Searching PF08267_Meth_synt_1.hmm.txt against GCF_000009625.1_protein
--> Performing fasta search
Searching METE_Cre03.g180750.fa against GCF_000009625.1_protein
Searching METH_Cre06.g250902.fa against GCF_000009625.1_protein
-->Performing accession stats and obtaining protein fasta files

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Searching METE_Cre03.g180750.fa against GCA_905232135.1_protein
Searching METH_Cre06.g250902.fa against GCA_905232135.1_protein
-->Performing accession stats and obtaining protein fasta files

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-->Performing accession stats and obtaining protein fasta files

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./search_output/GCF_000154785.2_protein/queries_dtbl/K00647.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03147.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03146.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K05936.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K18278.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF02965_Met_synt_B12
.hmm.txt.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03426.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00486.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K21479.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00969.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01556.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K04765.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02170.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02189.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02188.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00548.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00549.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K14154.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01435.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00767.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF00005_ABC_tran.hmm
.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/METE_Cre03.g180750.f
a.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03150.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03151.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K09789.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01935.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K19561.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K19560.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/METH_Cre06.g250902.f
a.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00941.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01719.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K14394.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF02574_S-
methyl_trans.hmm.txt.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K06858.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00877.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00788.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02190.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02191.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00952.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF01497_Peripla_BP_2
.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02225.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00322.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00323.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02224.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01950.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03149.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03148.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF00809_Pterin_bind.
hmm.txt.dtbl
```

```
./search_output/GCF_000154785.2_protein/queries_dtbl/K09458.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01749.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K13540.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K13541.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K08260.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00643.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K06949.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02232.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02233.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03394.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00768.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K21219.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K06074.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02372.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02304.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K19221.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01662.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K22911.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K16901.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00878.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K22316.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01845.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02169.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00208.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K22699.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03154.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K19562.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K19563.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF08267_Meth_synt_1.
hmm.txt.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K06073.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02303.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02302.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K14163.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K06989.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K21220.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00949.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00278.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02496.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03399.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K04487.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K03153.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00652.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K19712.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00325.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K00324.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF07715_Plug.hmm.dtb
l
./search_output/GCF_000154785.2_protein/queries_dtbl/K01077.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/PF02310_B12-
binding.hmm.txt.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K13786.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K01885.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02228.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K02229.hmm.dtbl
./search_output/GCF_000154785.2_protein/queries_dtbl/K05934.hmm.dtbl

Done
```

4.2 06_read_hmmer_output_common_format.py

4.3 07_protein_domain_annotation_for_each_target.R
Warning message:
package 'optparse' was built under R version 4.0.5
── Attaching packages ────────────────────────────────── tidyverse
1.3.0 ──
✔ ggplot2 3.3.6   ✔ purrr   0.3.4
✔ tibble 3.1.8   ✔ dplyr   1.0.10
✔ tidyr   1.2.1   ✔ stringr 1.4.1
✔ readr   2.1.2   ✔ forcats 0.5.2
── Conflicts ─────────────────────────────────────
tidyverse_conflicts() ──
✖ dplyr::filter() masks stats::filter()
✖ dplyr::lag()   masks stats::lag()
Warning messages:
1: package 'ggplot2' was built under R version 4.0.5
2: package 'tibble' was built under R version 4.0.5
3: package 'tidyr' was built under R version 4.0.5
4: package 'readr' was built under R version 4.0.5
5: package 'dplyr' was built under R version 4.0.5
6: package 'stringr' was built under R version 4.0.5
7: package 'forcats' was built under R version 4.0.5
Joining, by = c("organism", "target_name", "Pathway")
[1] "Replacing: BIO3-BIO1_bio3-bio1 NA values with FALSE"
[1] "Replacing: BIOB_bioB NA values with FALSE"
[1] "Replacing: BtuD NA values with FALSE"
[1] "Replacing: EARS, GltX_EARS, gltX NA values with FALSE"
[1] "Replacing: FABG_fabG NA values with FALSE"
[1] "Replacing: HemA_hemA_v2 NA values with FALSE"
[1] "Replacing: HemB, ALAD_hemB, ALAD NA values with FALSE"
[1] "Replacing: HemC, HMBS_hemC, HMBS NA values with FALSE"
[1] "Replacing: HemD, UROS_hemD, UROS NA values with FALSE"
[1] "Replacing: HETK_THI6 NA values with FALSE"
[1] "Replacing: HETK_thiM NA values with FALSE"
[1] "Replacing: HMP(P)K / TMP-Ppse_THI6 NA values with FALSE"
[1] "Replacing: HMP(P)K / TMP-Ppse_thiE NA values with FALSE"
[1] "Replacing: KMO_KMO NA values with FALSE"
[1] "Replacing: KYNU_kynu NA values with FALSE"
[1] "Replacing: MET1_met1 NA values with FALSE"
[1] "Replacing: MET8_met8 NA values with FALSE"
[1] "Replacing: mete NA values with FALSE"
[1] "Replacing: meth NA values with FALSE"
[1] "Replacing: NADK_ppnK NA values with FALSE"
[1] "Replacing: NADS_NADSYN1 NA values with FALSE"
[1] "Replacing: NifS_icsS NA values with FALSE"
[1] "Replacing: NMNAT_nadD_v2 NA values with FALSE"
[1] "Replacing: NNT_pntA NA values with FALSE"
[1] "Replacing: NUDT12_nudC NA values with FALSE"
[1] "Replacing: PHO_Pho NA values with FALSE"
[1] "Replacing: QPRT_nadC NA values with FALSE"
[1] "Replacing: ribC NA values with FALSE"
[1] "Replacing: THI4_THI4_v1 NA values with FALSE"
[1] "Replacing: Thiamine phosphatase_Thiamine phosphatase NA values with
FALSE"

```
[1] "Replacing: TPK / THI80_thiN NA values with FALSE"
[1] "Replacing: AO_nadB NA values with FALSE"
[1] "Replacing: BIOA_bioA_v2 NA values with FALSE"
[1] "Replacing: BIOC_bioC NA values with FALSE"
[1] "Replacing: BIOD_bioD NA values with FALSE"
[1] "Replacing: BIOF_bioF NA values with FALSE"
[1] "Replacing: BIOH_bioH NA values with FALSE"
[1] "Replacing: BtuB NA values with FALSE"
[1] "Replacing: BtuC NA values with FALSE"
[1] "Replacing: BtuF NA values with FALSE"
[1] "Replacing: CobA_cobA NA values with FALSE"
[1] "Replacing: CobA/CobO/BtuR_cobA/cobO/btuR NA values with FALSE"
[1] "Replacing: CobC/PhpB_cobC/phpB NA values with FALSE"
[1] "Replacing: CobS/CobV_cobS/cobV NA values with FALSE"
[1] "Replacing: CobT/CobU_cobT/cobU NA values with FALSE"
[1] "Replacing: CobU/CobP_cobU/cobP NA values with FALSE"
[1] "Replacing: CysG_cysG NA values with FALSE"
[1] "Replacing: CysG_cysG_altered_threshold NA values with FALSE"
[1] "Replacing: Dxs_dxs NA values with FALSE"
[1] "Replacing: FABB_fabB NA values with FALSE"
[1] "Replacing: FABF_fabF NA values with FALSE"
[1] "Replacing: FABZ_fabZ NA values with FALSE"
[1] "Replacing: FBAI_fabI NA values with FALSE"
[1] "Replacing: HemA_hemA_v1 NA values with FALSE"
[1] "Replacing: HemL_hemL NA values with FALSE"
[1] "Replacing: HemX_hemX NA values with FALSE"
[1] "Replacing: HMPK_thiD NA values with FALSE"
[1] "Replacing: HMPPS_ThiC NA values with FALSE"
[1] "Replacing: MazG_mazG NA values with FALSE"
[1] "Replacing: NADS_nadE NA values with FALSE"
[1] "Replacing: NADTH_sthA NA values with FALSE"
[1] "Replacing: NMNAT_nadD_v1 NA values with FALSE"
[1] "Replacing: NMNAT_nadR NA values with FALSE"
[1] "Replacing: NNT_pntB NA values with FALSE"
[1] "Replacing: PNCC_pncC NA values with FALSE"
[1] "Replacing: QS_nadA NA values with FALSE"
[1] "Replacing: RSGA_RsgA NA values with FALSE"
[1] "Replacing: THIF_thiF NA values with FALSE"
[1] "Replacing: THIG_thiG NA values with FALSE"
[1] "Replacing: THIH_thiH NA values with FALSE"
[1] "Replacing: THII_thiI NA values with FALSE"
[1] "Replacing: ThiK_ThiK NA values with FALSE"
[1] "Replacing: THIL_ThiL NA values with FALSE"
[1] "Replacing: THIS_thiS NA values with FALSE"
[1] "Replacing: CbiB/CobD_cbiB/cobD NA values with FALSE"
[1] "Replacing: CbiD_cbiD NA values with FALSE"
[1] "Replacing: CbiE_cbiE NA values with FALSE"
[1] "Replacing: CbiE_cbiE_altered_threshold NA values with FALSE"
[1] "Replacing: CbiG_cbiG NA values with FALSE"
[1] "Replacing: CbiH/CbiJ_cbiH/cbiJ NA values with FALSE"
[1] "Replacing: CbiH/CbiJ_cbiH/cbiJ_altered_threshold NA values with
FALSE"
[1] "Replacing: CbiK_cbiK NA values with FALSE"
[1] "Replacing: CbiP/CobQ_cbiP/cobQ NA values with FALSE"
[1] "Replacing: CbiT_cbiT NA values with FALSE"
[1] "Replacing: CbiT_cbiT_altered_threshold NA values with FALSE"
[1] "Replacing: CobB-CbiA_cobB-cbiA NA values with FALSE"
[1] "Replacing: CobD_cobD NA values with FALSE"
```

```
[1] "Replacing: CobH-CbiC_cobH-cbiC NA values with FALSE"
[1] "Replacing: CobI-CbiL_cobI-cbiL NA values with FALSE"
[1] "Replacing: CobK-CbiJ_cobK-cbiJ NA values with FALSE"
[1] "Replacing: CobK-CbiJ_cobK-cbiJ_altered_threshold NA values with
FALSE"
[1] "Replacing: CobM, CbiF_cobM, cbiF NA values with FALSE"
[1] "Replacing: CobM/CbiF_cobM/cbiF NA values with FALSE"
[1] "Replacing: PduO/MMAB_pduO/mmab NA values with FALSE"
[1] "Replacing: PduX_pduX NA values with FALSE"
[1] "Replacing: BluB_bluB NA values with FALSE"
[1] "Replacing: CobC_cobC NA values with FALSE"
[1] "Replacing: CobF_cobF NA values with FALSE"
[1] "Replacing: CobG_cobG_altered_threshold NA values with FALSE"
[1] "Replacing: CobL_cobL NA values with FALSE"
[1] "Replacing: CobN_cobN NA values with FALSE"
[1] "Replacing: CobR_cobr NA values with FALSE"
[1] "Replacing: CobS_cobS NA values with FALSE"
[1] "Replacing: CobT_cobT NA values with FALSE"
[1] "Replacing: THIO_thiO NA values with FALSE"
[1] "Replacing: BIOA_bioA_v1 NA values with FALSE"
[1] "Replacing: BIOI_bioI NA values with FALSE"
[1] "Replacing: BIOW_bioW NA values with FALSE"
[1] "Replacing: CbiX_cbiX NA values with FALSE"
[1] "Replacing: CobA-HemD_cobA-hemD NA values with FALSE"
[1] "Replacing: TENA_TenA NA values with FALSE"
[1] "Replacing: TENI_tenI NA values with FALSE"
[1] "Replacing: ASPDH_nadX NA values with FALSE"
[1] "Replacing: CobG_cobG NA values with FALSE"
[1] "Replacing: CbiGH-CobJ_cbiGH-cobJ NA values with FALSE"
[1] "Replacing: HMP(P)K / TMP-Ppse_thiDE NA values with FALSE"
[1] "Replacing: HMPK_thiDE NA values with FALSE"
[1] "Replacing: ACP1_Acp1 NA values with FALSE"
[1] "Replacing: HMPK_Thi20 NA values with FALSE"
[1] "Replacing: HMPK_THI20 NA values with FALSE"
[1] "Replacing: NMNAT_POF1 NA values with FALSE"
[1] "Replacing: NMT1_THI5 NA values with FALSE"
[1] "Replacing: NNT_NNT NA values with FALSE"
[1] "Replacing: Thiamine pyridinylase_Thiamine pyridinylase NA values
with FALSE"
[1] "Replacing: BIOG_bioG NA values with FALSE"
[1] "Replacing: BIOJ_bioJ NA values with FALSE"
[1] "Replacing: BIOK_bioK NA values with FALSE"
[1] "Replacing: BTD_btd NA values with FALSE"
[1] "Replacing: CbiH60_cbiH60 NA values with FALSE"
[1] "Replacing: CbiZ_cbiZ NA values with FALSE"
[1] "Replacing: CfbA_cfbA NA values with FALSE"
[1] "Replacing: CobIJ_cobIJ NA values with FALSE"
[1] "Replacing: CobY_cobY NA values with FALSE"
[1] "Replacing: ENPP1_3_CD203 NA values with FALSE"
[1] "Replacing: EPRS_EPRS NA values with FALSE"
[1] "Replacing: HemDX_hemDX NA values with FALSE"
[1] "Replacing: HPAB_hpaB_v1 NA values with FALSE"
[1] "Replacing: HPAB_hpaB_v2 NA values with FALSE"
[1] "Replacing: NMNAT_nadM_v1 NA values with FALSE"
[1] "Replacing: NMNAT_nadM_v2 NA values with FALSE"
[1] "Replacing: PHO5_11_12_PHO5_11_12 NA values with FALSE"
[1] "Replacing: RhnA-CobC_rhnA-cobC NA values with FALSE"
[1] "Replacing: TH2_Th2 NA values with FALSE"
```

```
[1] "Replacing: THI4_thi4_v2 NA values with FALSE"
[1] "Replacing: THIDN_ThiDN NA values with FALSE"
[1] "Replacing: THIN_ThiN NA values with FALSE"


4.4 08_generate_list_of_fasta.py
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/search_output/*/accs/unique_hits.fa
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/fasta/08_fasta_hits_eslsfetch.fasta


4.5 09_join_with_taxonomy_and_fasta.R
Warning message:
package 'optparse' was built under R version 4.0.5
Warning messages:
1: package 'ggplot2' was built under R version 4.0.5
2: package 'tibble' was built under R version 4.0.5
3: package 'tidyr' was built under R version 4.0.5
4: package 'readr' was built under R version 4.0.5
5: package 'dplyr' was built under R version 4.0.5
6: package 'stringr' was built under R version 4.0.5
7: package 'forcats' was built under R version 4.0.5
[1] "nrow():
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/summary_spreadsheets/07_output_df_organism_targe
ts'_query_scores_and_significance.csv 58350"
[1] "Importing fasta file to df..."
[1] "--> Using Esl-sfetch fasta sequences"
[1] "1. 0 Instances of a non-blank header / target name (TRUE, rows) with
no fasta (FALSE, cols)"
[1] "2. Success: All the headers / target names have fasta information"
[1] "3. Success: No headers have been duplicated"
[1] "Resulting dataframe contains 26 different organisms"
[1] "--> Saving this dataframeto:
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/summary_spreadsheets/09_output_df_organism_targe
ts'_query_scores_and_significance_metadata_faa.csv"

4.6 10_significant_Proteins_per_Template_Name.R
Warning message:
package 'optparse' was built under R version 4.0.5
Warning messages:
1: package 'ggplot2' was built under R version 4.0.5
2: package 'tibble' was built under R version 4.0.5
3: package 'tidyr' was built under R version 4.0.5
4: package 'readr' was built under R version 4.0.5
5: package 'dplyr' was built under R version 4.0.5
6: package 'stringr' was built under R version 4.0.5
7: package 'forcats' was built under R version 4.0.5
Warning message:
package 'RColorBrewer' was built under R version 4.0.5
`summarise()` has grouped output by 'organism', 'Protein', 'Pathway',
'target_name'. You can override using the `.groups` argument.
 [1] "Pathway"
 [2] "reactant"
 [3] "product"
 [4] "Protein"
 [5] "Query"
```

```
 [6] "Required_for_positive_protein_classification"
 [7] "full_e_value"
 [8] "full_bitscore"
 [9] "domain_e_value"
[10] "domain_bitscore"
[11] "Reaction_number"
[12] "EC_number"
`summarise()` has grouped output by 'Pathway'. You can override using the
`.groups` argument.
Joining, by = c("organism", "Pathway", "Protein")
Joining, by = c("organism", "Pathway", "Protein")
`summarise()` has grouped output by 'organism', 'Pathway', 'Protein',
'reactant', 'product', 'target_name', 'fa', 'geomean_full_bitscore'. You
can
override using the `.groups` argument.
```

4.7 11_summarise_vitamin_graphs.py

```
('GCA_905232135.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCA_905232135.1_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: False
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: False
Path between C15814 and C20246: False
Path between C00022 and C20246: False
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Path between C00003 and C20247: True
Path between C00037 and C20247: True
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C20246': False, 'C20247-C01081': True, 'C00003-C20247': True, 'C00037-
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B1
('GCA_905232135.1_protein', 'B12')
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Path between C05772 and C06504: False
Path between C02463 and C05778: True
Path between C11538 and C06504: False
Path between C06504 and C06507: False
Path between C06507 and C06508: False
Path between C06508 and C00194: False
Path between C06507 and C06509: False
Path between C00188 and C06509: False
```

```
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Path between C03114 and C05775: False
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'C01847-C03114': False, 'C03114-C05775': False}
B12
('GCA_905232135.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCA_905232135.1_protein_B3
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B3
('GCA_905232135.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C00037 and C20246: False
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B1
('GCF_000005845.2_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C02463 and C05772: False
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Path between C06509 and C00194: True
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Path between C03114 and C05775: True
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'C01847-C03114': False, 'C03114-C05775': True}
B12
('GCF_000005845.2_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000005845.2_protein_B3
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Saving graph to
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B1
('GCF_000006945.2_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C01847 and C03114: False
Path between C03114 and C05775: True
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B12
('GCF_000006945.2_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Saving graph to
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B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000006965.1_protein_B1
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Path between C04752 and C01081: True
Path between C01081 and C00068: False
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
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Path between THIS and C15810: True
Path between C15814 and C20246: True
Path between C00022 and C20246: True
Path between C00118 and C20246: True
Path between C20247 and C01081: True
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'C00037-C20247': False}
B1
('GCF_000006965.1_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C06508 and C00194: True
Path between C06507 and C06509: True
Path between C00188 and C06509: False
Path between C06509 and C00194: True
Path between C01847 and C03114: True
Path between C03114 and C05775: False
{'C00025-C02463': False, 'C00037-C02463': True, 'C02463-C05772': True,
'C05772-C06504': True, 'C02463-C05778': True, 'C11538-C06504': False,
'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_000006965.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B3
('GCF_000006965.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
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B1
('GCF_000009045.1_protein', 'B12')
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B12
('GCF_000009045.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B3
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B7
('GCF_000009265.1_protein', 'B1')
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Saving graph to
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Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
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Path between C00037 and C20247: False
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B1
('GCF_000009265.1_protein', 'B12')
Saving graph to
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Path between C03114 and C05775: False
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B12
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('GCF_000009265.1_protein', 'B7')
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Saving graph to
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Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
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Path between C15814 and C20246: True
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Path between C00003 and C20247: False
Path between C00037 and C20247: False
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C20247': False}
B1
('GCF_000009625.1_protein', 'B12')
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'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': False, 'C03114-C05775': False}
B12
('GCF_000009625.1_protein', 'B3')
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/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B3
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B7
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Saving graph to
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Path between C04752 and C01081: True
Path between C01081 and C00068: False
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: True
Path between C15814 and C20246: True
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Path between C00037 and C20247: False
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'C00118-C20246': True, 'C20247-C01081': True, 'C00003-C20247': False,
'C00037-C20247': False}
B1
('GCF_000014045.1_protein', 'B12')
Saving graph to
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Path between C06507 and C06509: True
Path between C00188 and C06509: False
Path between C06509 and C00194: True
Path between C01847 and C03114: True
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'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_000014045.1_protein', 'B3')
Saving graph to
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Path between C01185 and C00003: False
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Saving graph to
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Path between C01092 and C00120: False
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B7
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Saving graph to
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is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000018145.1_protein_B1
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Path between C04752 and C01081: True
Path between C01081 and C00068: False
Path between C00378 (Thiamine) and C00068: True
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Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
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Path between C00037 and C20247: False
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B1
('GCF_000018145.1_protein', 'B12')
Saving graph to
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Path between C05772 and C06504: False
Path between C02463 and C05778: True
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Path between C06508 and C00194: True
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Path between C01847 and C03114: True
Path between C03114 and C05775: False
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B12
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Saving graph to
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Saving graph to
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
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Path between C15814 and C20246: False
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B1
('GCF_000018865.1_protein', 'B12')
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Saving graph to
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Path between C06504 and C06507: True
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Path between C01847 and C03114: False
Path between C03114 and C05775: True
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Saving graph to
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is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000021945.1_protein_B1
Path between C00018 and C04752: False
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Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
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Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: False
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B1
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Saving graph to
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Path between C03114 and C05775: False
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B1
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Path between C03114 and C05775: False
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Saving graph to
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Path between C01185 and C00003: True
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B3
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Path between C00082 and C20246: False
Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
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B1
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B3
('GCF_000092065.1_protein', 'B7')
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Path between C03373 and C04752: False
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: False
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Path between C15814 and C20246: False
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B1
('GCF_000146045.2_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000146045.2_protein_B12
Path between C00025 and C02463: False
Path between C00037 and C02463: True
Path between C02463 and C05772: False
Path between C05772 and C06504: False
Path between C02463 and C05778: True
Path between C11538 and C06504: False
Path between C06504 and C06507: False
Path between C06507 and C06508: False
Path between C06508 and C00194: False
Path between C06507 and C06509: False
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Path between C01847 and C03114: False
Path between C03114 and C05775: False
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'C06504-C06507': False, 'C06507-C06508': False, 'C06508-C00194': False,
'C06507-C06509': False, 'C00188-C06509': False, 'C06509-C00194': False,
'C01847-C03114': False, 'C03114-C05775': False}
B12
('GCF_000146045.2_protein', 'B3')
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000146045.2_protein_B3
Path between C00049 and C01185: False
Path between C01185 and C00003: True
{'C00049-C01185': False, 'C01185-C00003': True}
B3
('GCF_000146045.2_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000146045.2_protein_B7
Path between C19845 and C01092: False
Path between C01092 and C00120: True
{'C19845-C01092': False, 'C01092-C00120': True}
B7
('GCF_000151265.2_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000151265.2_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: False
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: False
Path between C15814 and C20246: False
Path between C00022 and C20246: False
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Path between C00003 and C20247: False
Path between C00037 and C20247: False
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B1
('GCF_000151265.2_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000151265.2_protein_B12
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Path between C02463 and C05772: False
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Path between C06504 and C06507: False
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Path between C06508 and C00194: False
Path between C06507 and C06509: False
Path between C00188 and C06509: False
Path between C06509 and C00194: False
Path between C01847 and C03114: False
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'C06507-C06509': False, 'C00188-C06509': False, 'C06509-C00194': False,
'C01847-C03114': False, 'C03114-C05775': False}
B12
('GCF_000151265.2_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000151265.2_protein_B3
Path between C00049 and C01185: True
Path between C01185 and C00003: False
{'C00049-C01185': True, 'C01185-C00003': False}
B3
('GCF_000151265.2_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000151265.2_protein_B7
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Path between C01092 and C00120: True
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B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000154785.2_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: False
Path between C04752 and C01081: True
Path between C01081 and C00068: False
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: True
Path between C15814 and C20246: True
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Path between C00003 and C20247: False
Path between C00037 and C20247: False
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'C00118-C20246': True, 'C20247-C01081': True, 'C00003-C20247': False,
'C00037-C20247': False}
B1
('GCF_000154785.2_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000154785.2_protein_B12
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Path between C02463 and C05772: True
Path between C05772 and C06504: True
Path between C02463 and C05778: True
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Path between C03114 and C05775: False
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'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_000154785.2_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000154785.2_protein_B3
Path between C00049 and C01185: False
Path between C01185 and C00003: False
{'C00049-C01185': False, 'C01185-C00003': False}
B3
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000154785.2_protein_B7
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B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
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B1
('GCF_000330885.1_protein', 'B12')
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Saving graph to
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Path between C01847 and C03114: True
Path between C03114 and C05775: False
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B3
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000330885.1_protein_B7
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{'C19845-C01092': True, 'C01092-C00120': False}
B7
('GCF_000372725.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_000372725.1_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: False
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: False
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Path between C00022 and C20246: False
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Path between C20247 and C01081: True
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Path between C00037 and C20247: False
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B1
('GCF_000372725.1_protein', 'B12')
Saving graph to
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B12
('GCF_000372725.1_protein', 'B3')
Saving graph to
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B3
('GCF_000372725.1_protein', 'B7')
Saving graph to
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('GCF_000373425.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C03373 and C04752: True
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True

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Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: True
Path between C15814 and C20246: True
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C20246': True, 'C20247-C01081': True, 'C00003-C20247': False, 'C00037-
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B1
('GCF_000373425.1_protein', 'B12')
Saving graph to
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B12
('GCF_000373425.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C00049 and C01185: True
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B3
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Saving graph to
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Path between C01092 and C00120: False
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B7
('GCF_000427765.1_protein', 'B1')
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Saving graph to
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Path between C00018 and C04752: False
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: False
Path between NifS_and_cysteine and C15812: True
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B1
('GCF_000427765.1_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C00025 and C02463: False
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Path between C01847 and C03114: True
Path between C03114 and C05775: False
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'C05772-C06504': True, 'C02463-C05778': True, 'C11538-C06504': False,
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'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
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B12
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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('GCF_000427765.1_protein', 'B7')
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C01092 and C00120: False
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B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_001664385.1_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: True
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
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Path between C00003 and C20247: False
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C20246': True, 'C20247-C01081': True, 'C00003-C20247': False, 'C00037-
C20247': False}
B1
('GCF_001664385.1_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_001664385.1_protein_B12
Path between C00025 and C02463: False
Path between C00037 and C02463: True
Path between C02463 and C05772: True
Path between C05772 and C06504: True
Path between C02463 and C05778: True
Path between C11538 and C06504: False
Path between C06504 and C06507: True
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Path between C06507 and C06509: True
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Path between C06509 and C00194: True
Path between C01847 and C03114: True
Path between C03114 and C05775: False
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'C05772-C06504': True, 'C02463-C05778': True, 'C11538-C06504': False,
'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_001664385.1_protein', 'B3')
```

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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B3
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B7
('GCF_002417665.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_002417665.1_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: False
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: False
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
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'C00118-C20246': True, 'C20247-C01081': True, 'C00003-C20247': False,
'C00037-C20247': False}
B1
('GCF_002417665.1_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_002417665.1_protein_B12
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Path between C02463 and C05778: True
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Path between C06504 and C06507: True
Path between C06507 and C06508: True
Path between C06508 and C00194: True
Path between C06507 and C06509: True
Path between C00188 and C06509: False
Path between C06509 and C00194: True
Path between C01847 and C03114: True
```

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'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': True}
B12
('GCF_002417665.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_002417665.1_protein_B3
Path between C00049 and C01185: True
Path between C01185 and C00003: True
{'C00049-C01185': True, 'C01185-C00003': True}
B3
('GCF_002417665.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_002417665.1_protein_B7
Path between C19845 and C01092: True
Path between C01092 and C00120: True
{'C19845-C01092': True, 'C01092-C00120': True}
B7
('GCF_007827425.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_007827425.1_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: True
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: True
Path between C15814 and C20246: True
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Path between C00003 and C20247: False
Path between C00037 and C20247: False
{'C00018-C04752': False, 'C03373-C04752': True, 'C04752-C01081': True,
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C15810': True, 'C15814-C20246': True, 'C00022-C20246': True, 'C00118-
C20246': True, 'C20247-C01081': True, 'C00003-C20247': False, 'C00037-
C20247': False}
B1
('GCF_007827425.1_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_007827425.1_protein_B12
Path between C00025 and C02463: False
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Path between C02463 and C05772: True
Path between C05772 and C06504: False
Path between C02463 and C05778: False
```

```
Path between C11538 and C06504: True
Path between C06504 and C06507: True
Path between C06507 and C06508: True
Path between C06508 and C00194: True
Path between C06507 and C06509: True
Path between C00188 and C06509: False
Path between C06509 and C00194: True
Path between C01847 and C03114: True
Path between C03114 and C05775: False
{'C00025-C02463': False, 'C00037-C02463': True, 'C02463-C05772': True,
'C05772-C06504': False, 'C02463-C05778': False, 'C11538-C06504': True,
'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_007827425.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_007827425.1_protein_B3
Path between C00049 and C01185: True
Path between C01185 and C00003: True
{'C00049-C01185': True, 'C01185-C00003': True}
B3
('GCF_007827425.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_007827425.1_protein_B7
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Path between C01092 and C00120: True
{'C19845-C01092': True, 'C01092-C00120': True}
B7
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Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_010365265.1_protein_B1
Path between C00018 and C04752: False
Path between C03373 and C04752: True
Path between C04752 and C01081: True
Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
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Path between C15814 and C20246: True
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Path between C00037 and C20247: False
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C15810': True, 'C15814-C20246': True, 'C00022-C20246': True, 'C00118-
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B1
('GCF_010365265.1_protein', 'B12')
```

```
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C06504 and C06507: True
Path between C06507 and C06508: True
Path between C06508 and C00194: True
Path between C06507 and C06509: True
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Path between C06509 and C00194: True
Path between C01847 and C03114: True
Path between C03114 and C05775: False
{'C00025-C02463': False, 'C00037-C02463': True, 'C02463-C05772': True,
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'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_010365265.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_010365265.1_protein_B3
Path between C00049 and C01185: True
Path between C01185 and C00003: True
{'C00049-C01185': True, 'C01185-C00003': True}
B3
('GCF_010365265.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_010365265.1_protein_B7
Path between C19845 and C01092: False
Path between C01092 and C00120: False
{'C19845-C01092': False, 'C01092-C00120': False}
B7
('GCF_013752735.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_013752735.1_protein_B1
Path between C00018 and C04752: False
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: True
Path between C00082 and C20246: False
Path between C00037 and C20246: True
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: True
Path between C15814 and C20246: True
Path between C00022 and C20246: True
Path between C00118 and C20246: True
Path between C20247 and C01081: True
Path between C00003 and C20247: False
Path between C00037 and C20247: False
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B1
('GCF_013752735.1_protein', 'B12')
Saving graph to
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Path between C06507 and C06508: True
Path between C06508 and C00194: True
Path between C06507 and C06509: True
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Path between C01847 and C03114: True
Path between C03114 and C05775: False
{'C00025-C02463': False, 'C00037-C02463': True, 'C02463-C05772': True,
'C05772-C06504': True, 'C02463-C05778': True, 'C11538-C06504': False,
'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_013752735.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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Path between C00049 and C01185: True
Path between C01185 and C00003: True
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B3
('GCF_013752735.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
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B7
('GCF_014194605.1_protein', 'B1')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_014194605.1_protein_B1
Path between C00018 and C04752: False
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Path between C01081 and C00068: True
Path between C00378 (Thiamine) and C00068: False
Path between C00082 and C20246: False
Path between C00037 and C20246: True
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```
Path between NifS_and_cysteine and C15812: True
Path between THIS and C15810: True
Path between C15814 and C20246: True
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Path between C00037 and C20247: False
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C20246': False, 'C00037-C20246': True, 'NifS_and_cysteine-C15812': True,
'THIS-C15810': True, 'C15814-C20246': True, 'C00022-C20246': True,
'C00118-C20246': True, 'C20247-C01081': True, 'C00003-C20247': False,
'C00037-C20247': False}
B1
('GCF_014194605.1_protein', 'B12')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_014194605.1_protein_B12
Path between C00025 and C02463: False
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Path between C02463 and C05772: True
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Path between C06504 and C06507: True
Path between C06507 and C06508: True
Path between C06508 and C00194: True
Path between C06507 and C06509: True
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Path between C06509 and C00194: True
Path between C01847 and C03114: True
Path between C03114 and C05775: False
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'C05772-C06504': True, 'C02463-C05778': True, 'C11538-C06504': False,
'C06504-C06507': True, 'C06507-C06508': True, 'C06508-C00194': True,
'C06507-C06509': True, 'C00188-C06509': False, 'C06509-C00194': True,
'C01847-C03114': True, 'C03114-C05775': False}
B12
('GCF_014194605.1_protein', 'B3')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_014194605.1_protein_B3
Path between C00049 and C01185: True
Path between C01185 and C00003: True
{'C00049-C01185': True, 'C01185-C00003': True}
B3
('GCF_014194605.1_protein', 'B7')
Saving graph to
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/vitamin_graphs/GCF_014194605.1_protein_B7
Path between C19845 and C01092: True
Path between C01092 and C00120: True
{'C19845-C01092': True, 'C01092-C00120': True}
B7


4.8 12_join_vitamin_predictions_to_search_results.R
Warning message:
```

package 'optparse' was built under R version 4.0.5
Warning messages:
1: package 'ggplot2' was built under R version 4.0.5
2: package 'tibble' was built under R version 4.0.5
3: package 'tidyr' was built under R version 4.0.5
4: package 'readr' was built under R version 4.0.5
5: package 'dplyr' was built under R version 4.0.5
6: package 'stringr' was built under R version 4.0.5
7: package 'forcats' was built under R version 4.0.5
Joining, by = "organism"

4.9 13_join_with_mags_metadata.R
Warning message:
package 'optparse' was built under R version 4.0.5
Warning messages:
1: package 'ggplot2' was built under R version 4.0.5
2: package 'tibble' was built under R version 4.0.5
3: package 'tidyr' was built under R version 4.0.5
4: package 'readr' was built under R version 4.0.5
5: package 'dplyr' was built under R version 4.0.5
6: package 'stringr' was built under R version 4.0.5
7: package 'forcats' was built under R version 4.0.5

Polish data structure
Log file was saved at:
/Users/ah830/Documents/GitHub/MAGsearcher/benchmarking/MAGsearcher_analys
is/SOKS_anaylsis/B1_run1/MAGsearcher_analysis.log

End of MAGsearcher analysis

X.1 Deactivate Conda environment
DeprecationWarning: 'source deactivate' is deprecated. Use 'conda
deactivate'.
Error: "source deactivate" command filed with exit code 0.
     Command being timed: "./MAGsearcher_wrapper.sh"
     User time (seconds): 4529.91
     System time (seconds): 359.68
     Percent of CPU this job got: 346%
     Elapsed (wall clock) time (h:mm:ss or m:ss): 23:29.49
     Average shared text size (kbytes): 0
     Average unshared data size (kbytes): 0
     Average stack size (kbytes): 0
     Average total size (kbytes): 0
     Maximum resident set size (kbytes): 1497636
     Average resident set size (kbytes): 0
     Major (requiring I/O) page faults: 12853
     Minor (reclaiming a frame) page faults: 79170508
     Voluntary context switches: 158401
     Involuntary context switches: 4487480
     Swaps: 0
     File system inputs: 0
     File system outputs: 0
     Socket messages sent: 260
     Socket messages received: 867
     Signals delivered: 3029
     Page size (bytes): 4096
     Exit status: 0