

Data File:

The data file containing the abundance tables and the taxonomic information has to be in these three specific formats:

1. **QIIME Output TSV Format:** QIIME is a commonly used tool to find out, among other things, the abundance and the taxonomic information of the microbes which are present in a sample. QIIME offers the advantage that several samples can be processed and analysed in one run of their workflow. The output of QIIME can have a number of formats, the most common one being the BIOM format. The BIOM format is not readable by a normal text editor, but it can be easily converted to a TSV format file using the following command:

```
biom convert -i table.biom -o table.from_biom_w_taxonomy.txt --to-tsv --header-key taxonomy
```

The input file (“table.biom”) is converted to TSV format and the output TSV file (“table.from_biom_w_taxonomy.txt”) can be directly uploaded into TIME and the appropriate option must be selected.

```
1# Constructed from biom file
2 #OTU ID E22 E41 D25 D53 D1 D28 D20 D31 D23 E51 E10 taxonomy F24 F40 D42 F52 D9 D13 D40 D10 D19 D15 D48 D22 D21 F54
3 1808048 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Porphyrionadaceae; g_Parabacteroides; s_ 1.0 0.0
4 1036749 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Bacilli; o_Gemellales; f_Gemellaceae; g_ s_ 0.0 1.0 0.0 0.0 0.0 0.0
5 4376890 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Proteobacteria; c_Betaproteobacteria; o_Rhodocyclales; f_Rhodocyclaceae; g_Methyloversatilis; s_ 0.0
6 174924 91.0 2.0 1.0 0.0 2.0 2.0 2.0 1.0 1.0 2.0 5.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Ruminococcus; s_ 0.0 0.0 2.0
7 188753 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Blautia; s_ 0.0 0.0 0.0 0.0
8 189110 0.0 0.0 1.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Ruminococcus; s_ 0.0 0.0 0.0 0.0
9 193592 0.0 0.0 1.0 2.0 1.0 0.0 14.0 5.0 7.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Blautia; s_ 1.0 0.0 0.0 0.0
10 950828 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Streptococcaceae; g_ s_ 0.0 0.0 0.0 0.0 0.0
11 1974536 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Proteobacteria; c_Betaproteobacteria; o_Burkholderiales; f_Alcaligenaceae; g_Sutterella; s_ 302.0
12 177222 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales; f_Bacteroidaceae; g_Bacteroides; s_ 0.0 0.0 0.0 0.0
13 350297 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 5.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_ g_ s_ 0.0 0.0 0.0 0.0 0.0 0.0
14 981783 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Bacilli; o_Bacillales; f_Staphylococcaceae; g_Staphylococcus; s_epidermidis 0.0 2.0
15 196271 0.0 3.0 0.0 0.0 1.0 0.0 0.0 0.0 0.0 1.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_ g_ s_ 0.0 0.0 0.0 0.0 1.0 1.0
16 196270 3.0 1.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 3.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_ s_ 0.0 0.0 0.0 0.0 0.0
17 187248 0.0 4.0 4.0 0.0 4.0 0.0 0.0 0.0 3.0 2.0 24.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_ s_ 4.0 22.0 1.0 6.0
18 355450 1.0 4.0 0.0 0.0 0.0 0.0 0.0 0.0 1.0 11.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Oscillospira; s_ 0.0 0.0 0.0 0.0
19 179866 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Blautia; s_ 0.0 0.0 0.0 2.0
20 180563 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_ s_ 0.0 0.0 0.0 0.0
21 92874 0.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Actinomycetales; f_Actinomycetaceae; g_Actinomyces; s_ 0.0 0.0
22 179677 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Coproccoccus; s_ 0.0 0.0 0.0 0.0
23 288810 11.0 10.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 3.0 3.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_ s_ 0.0 0.0 7.0 0.0
24 181160 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae; g_Clostridium; s_ 0.0 0.0 0.0 0.0
25 183857 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Blautia; s_ 0.0 0.0 0.0 0.0
26 181167 0.0 1.0 1.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 1.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Dorea; s_ 1.0 0.0 0.0 0.0
27 337729 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_ s_ 0.0 0.0 0.0 0.0
28 1846997 0.0 0.0 0.0 0.0 1.0 0.0 0.0 1.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Veillonellaceae; g_Dialister; s_ 0.0 0.0 0.0 0.0
29 189571 0.0 0.0 0.0 0.0 2.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_Blautia; s_ 0.0 0.0 0.0 1.0
30 316892 0.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_ s_ 0.0 0.0 0.0 0.0
31 308491 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Ruminococcaceae; g_Oscillospira; s_ 0.0 0.0 0.0 0.0
32 4465985 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; g_ s_ 0.0 0.0 0.0 0.0
33 591285 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 k_Bacteria; p_Actinobacteria; c_Actinobacteria; o_Bifidobacteriales; f_Bifidobacteriaceae; g_Bifidobacterium; s_longum
34 108050 A A A A A A A A A A A A k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Lachnospiraceae; o_Blautia; s_ 0.0 0.0 0.0 0.0
```

Figure 1: Image of a sample QIIME output file

2. **TSV File:** Sometimes, if users have analysed the sequencing data using some software other than QIIME, they can upload their data in a slightly different format. This format is similar to the above format, with some major differences that provides flexibility to the user. The exact format (Sample File) can be downloaded from the TIME “Upload and Analyse Data” page.

Index	154	174	176	206	212	128	330	255	taxonomy
21	8	4	20	24	7	12	6	4	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Corynebacteriaceae; g__Corynebacterium; s__
32	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__
43	0	0	0	0	0	0	1	0	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Dermabacteraceae
54	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; s__
65	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__
76	0	1	0	0	0	0	0	0	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Corynebacteriaceae; g__Corynebacterium; s__
87	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__
98	0	1	0	0	2	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__
109	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__
1110	0	0	0	0	0	0	0	0	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Neisseriales; f__Neisseriaceae; g__Neisseria; s__subflava
1211	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Roseburia
1312	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Staphylococcaceae; g__Staphylococcus; s__aureus
1413	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__
1514	49	50	78	51	23	22	155	166	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Tisslerellaceae]; g__Anaerococcus; s__
1615	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__
1716	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Coprococcus; s__
1817	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; s__
1918	0	0	0	0	0	1	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__
2019	0	0	1	1	0	0	0	1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Dorea; s__formicigenerans
2120	0	0	0	0	0	0	0	2	k__Bacteria; p__Verrucomicrobia; c__Verrucomicrobiales; o__Verrucomicrobiales; f__Verrucomicrobiaceae; g__Akkermansia; s__muciniphila
2221	0	0	0	0	1	1	0	1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__
2322	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__
2423	0	0	0	0	0	0	0	0	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__
2524	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__
2625	0	0	0	1	0	0	0	1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__
2726	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Veillonellaceae; g__Veillonella; s__dispar
2827	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; s__
2928	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__
3029	0	0	0	0	1	0	1	1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__
3130	0	1	0	0	1	1	0	9	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Oscillospira; s__
3231	1152	1344	1315	3075	514	2739	1559	735	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__[Tisslerellaceae]; g__
3332	0	0	0	1	1	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Blautia; s__
3433	0	0	0	0	0	0	0	0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae; g__Coprococcus; s__

Figure 2: The TSV format with the taxonomic lineage information.

3. **Single Taxonomic Level TSV:** In some cases, only the taxonomic information at a specific taxonomic level can be obtained. In order to make the upload and analysis of these kinds of data files, this format is provided. The users are recommended to see the exact format in the Sample file in TIME “Upload” page.

Sample_Name	L. iners	L. crispatus	Atopobium	L. gasseri	Prevotella	Parvimonas	Sneathia	L. jensenii
2 400_010106	68.52	0.0	0.0	0.0	0.09	0.0	0.0	4.0
3 400_010506	87.45	0.0	0.0	0.0	0.0	0.0	0.0	0.09
4 400_010806	95.24	0.04	0.0	0.0	0.04	0.0	0.0	0.57
5 400_011206	93.9	0.0	0.0	0.0	0.0	0.0	0.0	0.29
6 400_011906	92.86	0.04	0.0	0.04	0.0	0.0	0.0	2.45
7 400_012206	98.95	0.0	0.0	0.04	0.0	0.0	0.0	0.22
8 400_012606	90.34	0.0	0.0	0.09	0.0	0.0	0.0	0.09
9 400_012906	0.44	0.0	0.0	0.0	0.05	0.0	0.0	0.1
10 400_020206	94.3	0.04	0.0	0.08	0.0	0.0	0.0	0.67
11 400_020506	97.28	0.0	0.0	0.13	0.04	0.0	0.0	1.1
12 400_020906	59.52	0.04	0.0	0.0	0.0	0.0	0.0	36.95
13 400_021206	64.94	0.0	0.0	0.0	0.0	0.0	0.0	31.5
14 400_021606	68.06	0.09	0.0	0.04	0.43	0.0	0.0	17.65
15 400_021906	86.76	0.04	0.0	0.08	0.0	0.0	0.0	12.16
16 400_022606	91.2	0.0	0.0	0.07	0.0	0.0	0.0	4.06
17 400_030206	94.8	0.0	0.0	0.0	0.03	0.0	0.0	3.96
18 400_030506	97.0	0.0	0.0	0.0	0.0	0.0	0.0	1.95
19 400_030906	85.4	0.04	0.02	0.02	0.02	0.0	0.0	13.23
20 400_031206	91.72	0.0	0.0	0.08	0.0	0.0	0.0	3.1
21 400_031606	90.6	0.0	0.0	0.04	0.0	0.0	0.0	4.39
22 400_031906	90.03	0.0	0.07	0.0	0.0	0.0	0.0	4.06
23 400_032306	12.44	0.0	0.0	0.0	6.32	0.0	0.0	1.05
24 400_032606	0.04	0.0	0.0	0.0	0.0	0.0	0.0	0.04
25 400_033006	69.61	0.0	0.0	0.04	4.09	0.0	0.0	8.52
26 400_040206	91.38	0.0	0.0	0.11	0.04	0.0	0.0	2.21
27 400_040606	94.23	0.04	0.0	0.04	0.0	0.0	0.0	1.13
28 400_040906	91.95	0.0	0.0	0.11	0.0	0.0	0.0	2.32
29 400_041306	92.84	0.0	0.0	0.13	0.0	0.0	0.0	2.19
30 400_041606	93.0	0.0	0.0	0.15	0.07	0.0	0.0	2.74
31 401_010706	86.81	0.0	0.0	0.04	0.0	0.0	0.0	11.93
32 401_011106	69.35	0.23	0.0	0.0	1.03	0.0	0.0	14.69
33 401_011406	84.04	0.0	0.0	0.0	0.0	0.0	0.0	10.81
34 401_011806	77.18	0.04	0.08	0.0	0.04	0.0	0.0	17.64

Figure 3: TSV file with the taxonomic information at only one taxonomic level.