

Guide to Turning an RDP File into a Data Set

Berkley Shands, Patricio S. La Rosa, Elena Deych, William Shannon

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Below we will define the basic steps required to generate a data set from an RDP file

1. Take an RDP file such as this example:

```
;Root:1.0;Bacteria:1.0;Firmicutes:1.0;Bacilli:1.0;Bacillales:1.0;Staphylococcaceae:1.0;  
;Root:1.0;Bacteria:1.0;Firmicutes:1.0;Bacilli:1.0;Lactobacillales:1.0;Carnobacteriaceae:0.8;  
;Root:1.0;Bacteria:1.0;Bacteroidetes:1.0;Bacteroidia:1.0;Bacteroidales:1.0;Prevotellaceae:1.0;  
;Root:1.0;Bacteria:1.0;Bacteroidetes:1.0;Bacteroidia:1.0;Bacteroidales:1.0;Prevotellaceae:1.0;  
;Root:1.0;Bacteria:1.0;Bacteroidetes:1.0;Bacteroidia:1.0;Unclassified:0.5;Unclassified:0.5;
```

2. Take the first entry and separate each level into its own row, while separating levels by a period:

```
Root, 1  
Root.Bacteria, 1  
Root.Bacteria.Firmicutes, 1  
Root.Bacteria.Firmicutes.Bacilli, 1  
Root.Bacteria.Firmicutes.Bacilli.Bacillales, 1  
Root.Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae, 1
```

3. Do the same with each following row, adding to the number at the end if it is the same:

```
Root, 5  
Root.Bacteria, 5  
Root.Bacteria.Firmicutes, 2  
Root.Bacteria.Firmicutes.Bacilli, 2  
Root.Bacteria.Firmicutes.Bacilli.Bacillales, 1  
Root.Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae, 1  
Root.Bacteria.Firmicutes.Bacilli.Lactobacillales, 1  
Root.Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae, .8  
Root.Bacteria.Bacteroidetes, 3  
Root.Bacteria.Bacteroidetes.Bacteroidia, 3  
Root.Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales, 2  
Root.Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae, 2  
Root.Bacteria.Bacteroidetes.Bacteroidia.Unclassified, .5  
Root.Bacteria.Bacteroidetes.Bacteroidia.Unclassified.Unclassified, .5
```

4. Change any unclassifieds or anything else that could appear under mul-

tuple different parents (we prefer adding a 'U' to the parents name):

Root.Bacteria.Bacteroidetes.Bacteroidia.BacteroidiaU, .5

Root.Bacteria.Bacteroidetes.Bacteroidia.BacteroidiaU.BacteroidiaUU, .5

5. Remove the 'Root' level since we are only looking at Bacteria in this example:

Bacteria, 5

Bacteria.Firmicutes, 2

Bacteria.Firmicutes.Bacilli, 2

Bacteria.Firmicutes.Bacilli.Bacillales, 1

Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae, 1

Bacteria.Firmicutes.Bacilli.Lactobacillales, 1

Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae, 1

Bacteria.Bacteroidetes, 3

Bacteria.Bacteroidetes.Bacteroidia, 3

Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales, 2

Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae, 2

Bacteria.Bacteroidetes.Bacteroidia.BacteroidiaU, .5

Bacteria.Bacteroidetes.Bacteroidia.BacteroidiaU.BacteroidiaUU, .5

6. Repeat for any additional RDP files and add them as new columns (and rows as needed) in our data set:

Taxa, Sample 1, Sample 2

Bacteria, 5, 5

Bacteria.Firmicutes, 2, 5

Bacteria.Firmicutes.Bacilli, 2, 5

Bacteria.Firmicutes.Bacilli.Bacillales, 1, 5

Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaceae, 1, 5

Bacteria.Firmicutes.Bacilli.Lactobacillales, 1, 0

Bacteria.Firmicutes.Bacilli.Lactobacillales.Carnobacteriaceae, 1, 0

Bacteria.Bacteroidetes, 3, 0

Bacteria.Bacteroidetes.Bacteroidia, 3, 0

Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales, 2, 0

Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Prevotellaceae, 2, 0

Bacteria.Bacteroidetes.Bacteroidia.BacteroidiaU, .5, 0

Bacteria.Bacteroidetes.Bacteroidia.BacteroidiaU.BacteroidiaUU, .5, 0

Bacteria.Firmicutes.Bacilli.Lactobacillales.Streptococcaceae, 0, 5

7. Save the file as a .csv (or anything other file readable by R) and load it in R:

Notes:

- Any symbol can be used as a taxa level separator except colons.
- There can only be one top level node, if we were looking at Archaea too we would need to keep the Root level in.