

Phylogenetic data management

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2018-01-30

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Introduction

Typical usages of the command *taxon-frequencies*

Installing dyad frequencies for a single taxon

```
## Adapt the variable depending on your taxon of interest
export TAXON=Pseudomonadales

## Compute and install strand-insensitive dyad frequencies
taxon-frequencies -v 1 -taxon ${TAXON} -type dyad -ml 3 -2str -install

## Compute and install strand-sensitive dyad frequencies
taxon-frequencies -v 1 -taxon ${TAXON} -type dyad -ml 3 -1str -install

## Check the resulting taxonomic frequency file
zless ${RSAT}/public_html/data/taxon_frequencies/${TAXON}/dyads_3nt_sp0-20_upstream-noorf_${TAXON}-noov
```

Installing dyad frequencies for all sub-taxa of a given taxon

```
## Adapt the variable depending on your taxon of interest
export TAXON=Pseudomonadales

## Install dyad frequencies for all sub-taxa of a given taxon
taxon-frequencies -v 2 -type dyad -ml 3 -2str -install -sub_taxa \
    -taxon ${TAXON}
```

Install all the background models for a given taxon

```
## Adapt the variable depending on your taxon of interest
export TAXON=Pseudomonadales
```

```
## Install background models for oligonucleotides and dyads
taxon-frequencies -v 1 -all_models -install -taxon ${TAXON}
```