Usage of EMBL2checklists

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ABSTRACT

The submission of DNA sequences to public sequence databases is an essential, but insufficiently automated step in the process of generating and disseminating novel DNA sequence data. A user-friendly software tool is needed that streamlines the file preparation for database submissions of DNA sequences that are commonly generated in plant and fungal DNA barcoding. A Python package was developed that converts DNA sequences from the common EMBL and GenBank flat file formats to submission-ready, tab-delimited spreadsheets (so-called "checklists") for a subsequent upload to the annotated sequence section of the European Nucleotide Archive (ENA). The package, titled "EMBL2checklists", automatically converts DNA sequences, their annotation features, and associated metadata into the idiosyncratic format of marker-specific ENA checklists and, thus, generates output that can be uploaded via the interactive Webin submission system of ENA. Here, we present a step-by-step protocol of the bioinformatic steps necessary to generate submission-ready checklist files from raw DNA sequence data and associated metadata via EMBL2checklists.

EXTERNAL LINK

https://www.biorxiv.org/content/early/2018/10/05/435644

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Gruenstaeudl M., Hartmaring Y. (2018). EMBL2checklists: A Python package to facilitate the user-friendly submission of plant DNA barcoding sequences to ENA. bioRxiv 435644; doi: https://doi.org/10.1101/435644

PDF

Gruenstaeudl.and.Hartmaring.2018_EMBL2checklists_PREPRINT.pdf

PROTOCOL STATUS

Working

We use this protocol in our group and it is working

1 Annotation of DNA sequences

Add sequence features and feature qualifiers to each DNA sequence using INSDC-compatible feature table keywords.
Use *any* of the following software tools:

SOFTWARE

Geneious

by Kearse et al. (2012) Geneious Basic: An integrated and extendable desktop software platform for ... Bioinformatics 28: 1647-1649

Geneious is among the most efficient and best-documented tools to adding sequence features and feature qualifiers to DNA sequences.
For more information regarding the automatic annotation of sequences with Geneious, see the following video tutorial on Youtube:

SOFTWARE
Artemis
by Rutherford et al. (2000) Artemis: Sequence visualization and annotation. Bioinformatics 16: 944–945

SOFTWARE
DnaSP
by Rozas et al. (2017) DnaSP v6: DNA Sequence Polymorphism Analysis of Large Datasets. Mol. Biol. Evol. 34: 3299-3302

For exporting annotated DNA sequences as GenBank- or EMBL-formatted flat files, see pages 44 to 46 of the user manual of DnaSP v.6.12.

2 **Saving sequences as flat file**
Save multiple DNA sequences of the same barcoding marker as an single, multi-sequence flat file in EMBL or GenBank format. Use *any* of the following software tools:

SOFTWARE
Geneious
by Kearse et al. (2012) Geneious Basic: An integrated and extendable desktop software platform for ... Bioinformatics 28: 1647-1649

Geneious is among the most efficient and best-documented tools to export annotated DNA sequences as a GenBank flat file format.

SOFTWARE
Artemis
by Rutherford et al. (2000) Artemis: Sequence visualization and annotation. Bioinformatics 16: 944–945

SOFTWARE
DnaSP
by Rozas et al. (2017) DnaSP v6: DNA Sequence Polymorphism Analysis of Large Datasets. Mol. Biol. Evol. 34: 3299-3302

For exporting annotated DNA sequences as GenBank- or EMBL-formatted flat files, see page 93 of the user manual of DnaSP v.6.12.

3 **Validation of flat file**
Test the validity of the file format, the feature table syntax or the taxonomic status of organism names, among other aspects, using one of two software tools.

For validation of *EMBL-formatted flat files*, use:

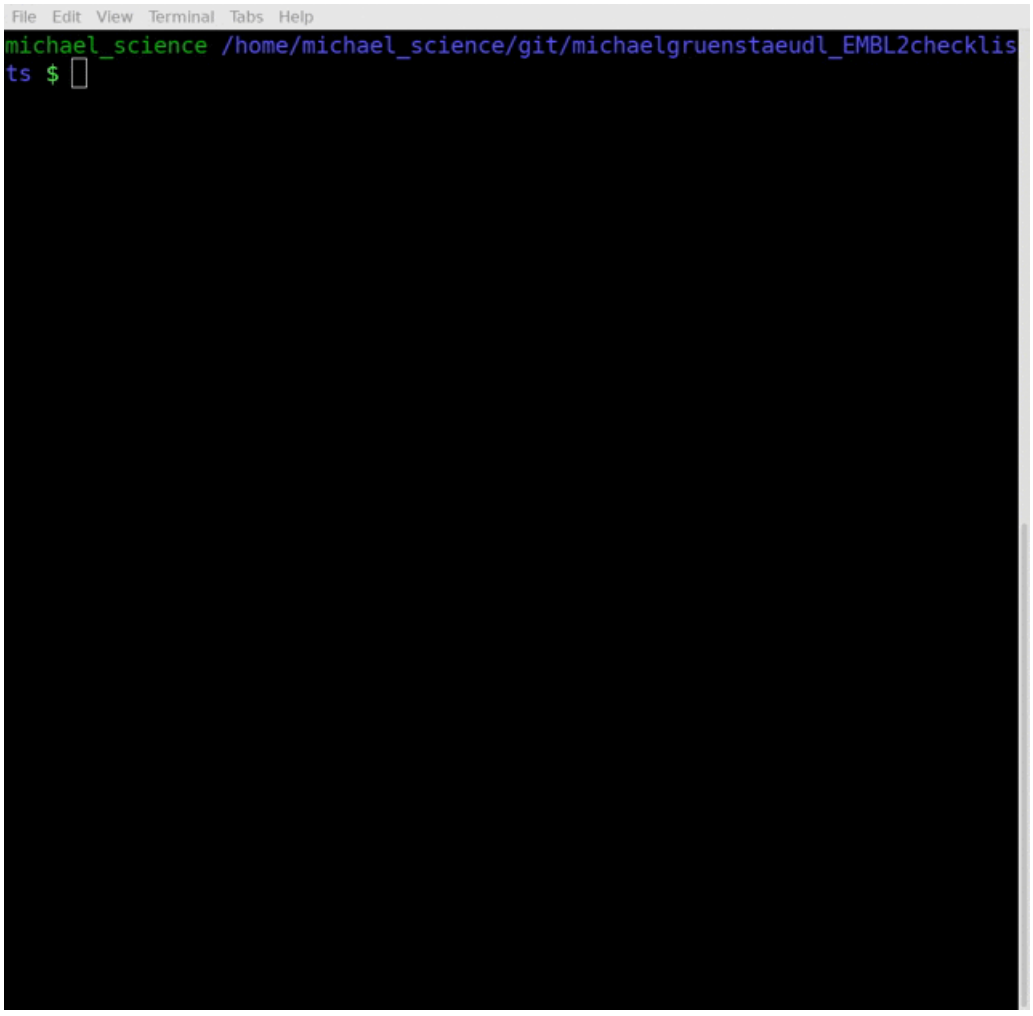
SOFTWARE

EMBL flat file validator

COMMAND

```
java -jar embl-api-validator-1.1.155.jar example_ITS.embl
```

Command to validate the format and content of an EMBL-formatted flat file (which is used as input to EMBL2checklists in the subsequent protocol step) via the EMBL flat file validator.



Video tutorial of the correct execution of the EMBL flat file validator on an input file to EMBL2checklists.

For validation of *GenBank-formatted flat files*, use:

SOFTWARE

SBOL Validator

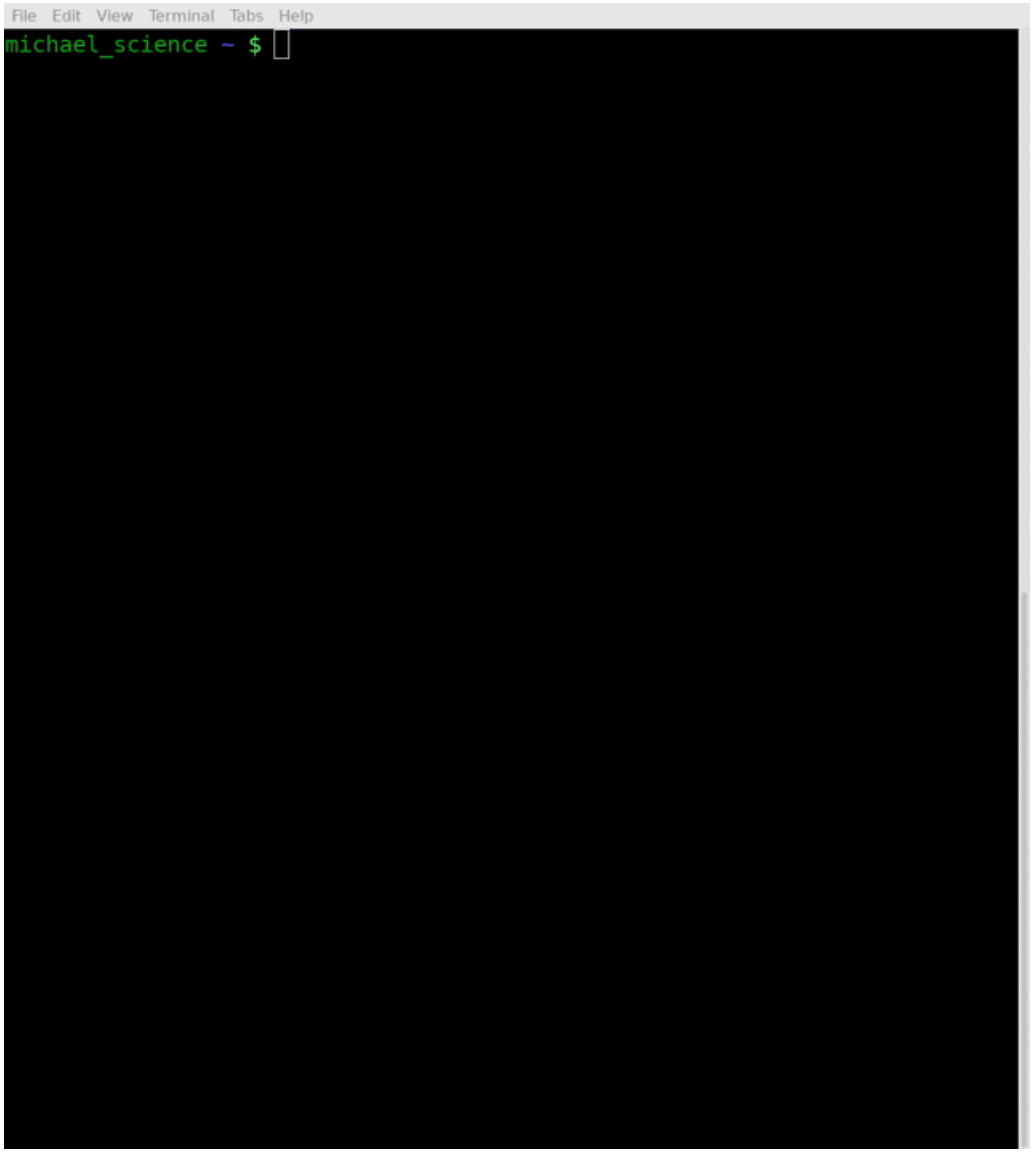
4 Installation of EMBL2checklists

It is recommended that you install EMBL2checklists via pip (i.e., the recommended installer of the Python Package Index). On Linux and MacOS, this can be achieved via the following command:

COMMAND

(sudo) pip2 install EMBL2checklists

Command to install EMBL2checklists via the default Python installer.



Video tutorial of the correct installation of EMBL2checklists, including the testing of software initialization upon installation.

Conversion from flat file to checklist

Convert the EMBL- or GenBank-formatted flat file into the Webin checklist file format using the software:

SOFTWARE

EMBL2checklists

COMMAND

```
EMBL2checklists_CLI \
  -i example/input/example_trnK_matK.embl \
  -o example/temp/example_trnK_matK.tsv \
  -c trnK_matK \
  -e no
```

Command to run EMBL2checklists on an example dataset provided as part of the Python package.

Video tutorial of the correct execution of EMBL2checklists via the command-line on an example dataset provided as part of the Python package.

COMMAND

```
EMBL2checklists_GUI
```

Command to run EMBL2checklists on an example dataset provided as part of the Python package.

Video tutorial of the correct execution of EMBL2checklists via the GUI on an example dataset provided as part of the Python package.

5 Upload checklist to ENA

Upload the resulting checklist to the sequence section of ENA using the interactive route of the Webin submission system.