
Counts File Library Documentation

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This library provides functions and classes to handle file conversion between standard formats (e.g., fasta or VCF files) to counts files that are used by [IQ-TREE](#) with [PoMo](#), and implementation of a polymorphism aware phylogenetic model.

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For a reference, please see and cite: Schrempf, D., Minh, B. Q., De Maio, N., von Haeseler, A., & Kosiol, C. (2016). Reversible Polymorphism-Aware Phylogenetic Models and their Application to Tree Inference. *Journal of Theoretical Biology*, in press.

Feel free to post any suggestions, doubts and bugs.

cflib contains several modules that ease the handling and preparation of data files in variant call format (vcf), fasta format and counts format (cf).

The *libPoMo* package is split into the following modules:

- *main*: Contains functions that are used by PoMo.
- *seqbase*: Provides basic functions and classes needed to work with sequence data.
- *fasta*: Provides functions to read, write and access fasta files.
- *vcf*: Provides functions to read, write and access vcf files.
- *cf*: Provides functions to read, write and access files that are in counts format.

CHAPTER 2

Contents

CHAPTER 3

Indices and tables

- `genindex`
- `modindex`
- `search`