

Fold-Filter & scripts – User Manual

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Description about what it does and what is it good for.

Explanation of the filtering options and of the filter format.

Example Filter

More detailed explanation on examples.

Installation / Usage

Mainly discuss all the prerequisites that are needed - Python2.x, Perl, ViennaRNA [LBZS⁺11], DotKnot [SD10, SDW11] with its own custom ViennaRNA instance, optionally UCLUST [Edg10].

Available Options:

..options..

More Scripts

Short description of the other scripts.

`parse_rnarobo.pl`

`weights_tool.pl`

Example Usage in Pipeline with RNARobo

References

- [Edg10] Robert C Edgar. Search and clustering orders of magnitude faster than BLAST. *Bioinformatics*, 26(19):2460–2461, 2010.
- [LBZS⁺11] Ronny Lorenz, Stephan HF Bernhart, Christian Hoener Zu Siederdisen, Hakim Tafer, Christoph Flamm, Peter F Stadler, Ivo L Hofacker, et al. ViennaRNA Package 2.0. *Algorithms for Molecular Biology*, 6(1):26, 2011.
- [SD10] Jana Sperschneider and Amitava Datta. DotKnot: pseudoknot prediction using the probability dot plot under a refined energy model. *Nucleic acids research*, 38(7):e103–e103, 2010.
- [SDW11] Jana Sperschneider, Amitava Datta, and Michael J Wise. Heuristic RNA pseudoknot prediction including intramolecular kissing hairpins. *RNA*, 17(1):27–38, 2011.