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AHRD_Snakemake - Automatically Update Function Annotation on a Multi-Proteome-Scale

Genome-scale protein annotation can be performed by the transfer of functions from known proteins matched via sequence similarity. Errors can propagate when annotations falsely generated in this manner make their way into public databases and are used as basis for subsequent function transfers. Our program "Automatic assignment of Human Readable Descriptions" (AHRD) can overcome these pitfalls by avoiding previously transferred annotations. It emulates the decision process of a human curator to select a description and GO terms from similarity search results. Through integration into a Snakemake workflow AHRD can now be easily applied to many proteomes at the same time. New annotations submitted to public databases can increase the annotation completeness and quality of stale proteomes released by past research projects. So the re-annotation quantity AHRD_Snakemake is capable of providing has a quality all of its own because it is able to keep a data base of genome-scale protein collections up to date with the current public knowledge.

Primary authors: BOECKER, Florian (uni-bonn); Prof. SCHOOF, Heiko (uni-bonn)

Presenter: BOECKER, Florian (uni-bonn)

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