IgFamily v0.9.9

Key features

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**- FASTA utility tools:**

Read FASTA files into runtime. Custom FASTA creation utility provides functionality for tailored output files. This utlility can be used to create required FASTA format –

>[ACCESSION]|[NAME]|[TYPE]|[SPECIES]|

Accession field is a housekeeping field and is not required for runtime. Name, type, and species fields are used in data structure creation, association, and function.

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| --- | --- |
| FASTA parse function | pp. |
| FASTA file utilities | pp. |

**- Peptide file parsing:**

Read peptide files into runtime. Currently supported are *PEAKS v8.0 DE NOVO* de novo peptides .csv export, *PEAKS v8.0 SPIDER* protein peptide .csv export, and *NOVOR v1.1* de novo peptides .csv export.

*PEAKS v8.0 DE NOVO* de novo peptides peptide file assigns peptide with modification and amino acid local confidence score. Note that here *PEAKS* *v8.0 DE NOVO* assigns individual export accesions to replicate peptide assignments.

*PEAKS v8.0 SPIDER* protein peptide file assigns peptide with modification, spectral count, and -10IgP certainty score.

*NOVOR v1.1* de novo peptides file assigns peptide with modification and amino acid local confidence score. Note that here *NOVOR v1.1* assigns individual export accesions to replicate peptide assignments.

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| Peptide file parse functions | pp. |

**- *msconvert* external integration**

Production

Version: v0.9.6

Release: 2016-09-17

Codebase: 4,857 source lines of code

Dependency: 18 files

Version history: 139 commits

Codebase additions: 21,040 source lines of code

Codebase deletions: 16,083 source lines of code

Development environment: Microsoft Visual Studio Community 2015

Version control: Git