**Function 'BLAST+SWNW'**

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**Depends** MATLAB 2013a or higher

**Description**

BLAST+SNW is an function programmed in MATLAB environment, aiming to predict mono subcellular location for a protein with known amino acid sequence. It uses BLAST 2.2.31+ to filter candidate proteins from drill set, then apply Smith-Waterman algorithm and Needleman Wunsch algorithm to determine the maximum-likelihood result.

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**Usage**

**[output] = BLAST\_SWNW(input\_file, drill, output\_pwd, Blastpath)**

'**input\_file**' is an fasta file that includes comments and amino acid sequences as test dataset.

'**drill**' is an fasta file that includes comments and amino acid sequences as drill dataset.

'**output\_pwd**' is the path where temporary files are going to be placed.

'**Blastpath**' is the working path of BLAST.

'**output**' is a 3-vector cell array, **column 1** contains input protein comments, **column 2** contains their corresponding prediction results, **column 3** contains P\_SWNW, an parameter indicating result credibility.