**Domcut**

Domcut[1] is a program which predicts inter-domain linker regions based on the difference in amino acid composition between domain and linker regions. Only those sequences which have a length in range 50-500 are considered as domains. On the other hand, a linker region must be: (1) connecting two adjacent domains defined above; (2) in the range from 10 to 100 residues; and (3) not containing membrane spanning regions. To represent the preference of amino acid residues in linker regions, the linker index Si for amino acid residue *i* is calculated as follows:

no formula!

Where filinker/fidomain is the frequency of amino acid residue *i* in the linker/domain region respectively. The negative value of Si means the residue preferably exists in the linker region. something about linker profile which would help in identifying the domain boundaries?

**References**

[1]: Suyama M, Ohara O (2003): DomCut: prediction of inter-domain linker regions in amino acid sequences. Bioinformatics 19:673–674.