BIOL 404: Molecular Evolution

Alignment

Manual alignment

\[
\begin{array}{cccc}
C & G & A & T \\
C & G & A & T \\
C & G & A & T \\
C & G & A & T \\
\end{array}
\]

match gap mis-match

Alignment

Distance and similarity indices

\[
\begin{array}{cccc}
C & G & A & T \\
C & G & A & T \\
C & G & A & T \\
C & G & A & T \\
\end{array}
\]

Specific penalties for gaps and mis-matches

match gap mis-match
Alignment

Distance and similarity indices

Distance = sum (# mismatches) x (mismatch penalty) + sum (# gaps) x (gap penalty)

Alignment algorithms use similarly of distance indexes and computationally solve for the optimal sequence alignment.

Alignment

Multiple alignments

Generally use a progressive alignment starting with pairwise comparison and adding one sequence at a time.

Alignment

Multiple alignments

BLAST

Basic Local Alignment Search Tool

BLAST

Basic BLAST

Choose a BLAST program to run.

nuclblat blast

Search a multiple database using a nucleotide query

protein blast

Search protein databases using a protein query

translatdb blast

Search translated nucleotide databases using a translated nucleotide query

Summary

The protein encoded by this gene is a member of the Fil-like receptor (FLR) family which shares a homologous structure in proteins recognized and activated by innate receptors. FLRs are highly conserved from Drosophila to humans and are involved in the recognition and signal transduction of pathogens and inflammation. The Fil-like receptor family contains members involved in the regulation of cell adhesion and innate immunity. The Fil-like receptor family also includes members that are involved in the regulation of cytokine production and the immune response. The expression of this receptor mediates the nuclear factor for kappa light chain activation and regulates nuclear factor kappa production (provided by RefSeq).
### For next class

**Project paragraphs**

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