Introduction to Blast

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What is BLAST

BLAST (basic local alignment search tool)

Use cases

1. Identify unknown sequences.

2. Build phylogenetic trees.

3. Find homologous proteins/species.

4. More

Advantages

1. Fast and accurate.

2. Reliable and flexiable.

Use the NCBI BLAST

Nucleotide BLAST

1. Understand the basic options.

2. Find homologous genes.

3. Identify an unknown sequence segment.

Protein BLAST

1. Understand the basic options.

2. Identify a unkown protein.

3. Find structure clues.

Use BLAST Locally

Why would we want to use it locally?

1. Download BLAST and understand the basic syntax.

2. Do the three searches that we previous did online.

3. Hint: use different blasts and search agaist online database.