



BLAST

Third Year (Medical Informatics Program)
Faculty of computer and information sciences

Team Members

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Introduction

- **BLAST** is one of the most common and useful tools for genetic research, this proposal describes a software flutter application we are working on it.

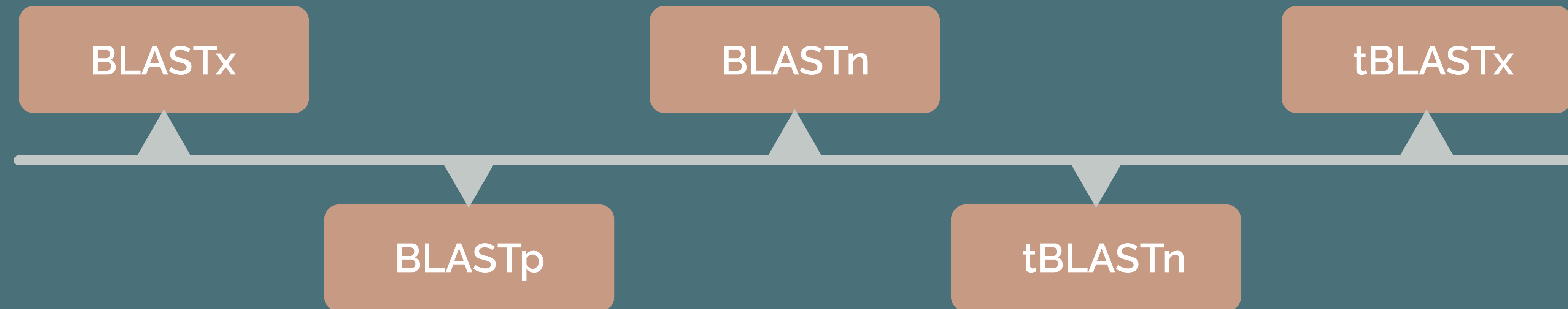
blast tool is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of different proteins or the nucleotides of dna sequences. a blast search enables a researcher to compare a query sequence with a library or database of sequences, and identify library sequences that resemble the query sequence above a certain threshold.

BLAST

- **BLAST Search** enables a researcher to compare a subject protein or nucleotide sequence (called a query) with a library or database of sequence, and indentify database sequences that resemble the query sequence above a certain threshold.
- **Algorithm:** align query sequence with genome , after cut query sequence Into 11 base length for DNA or 3 base length for protein find all alignments of each reads from library or database we prepare.

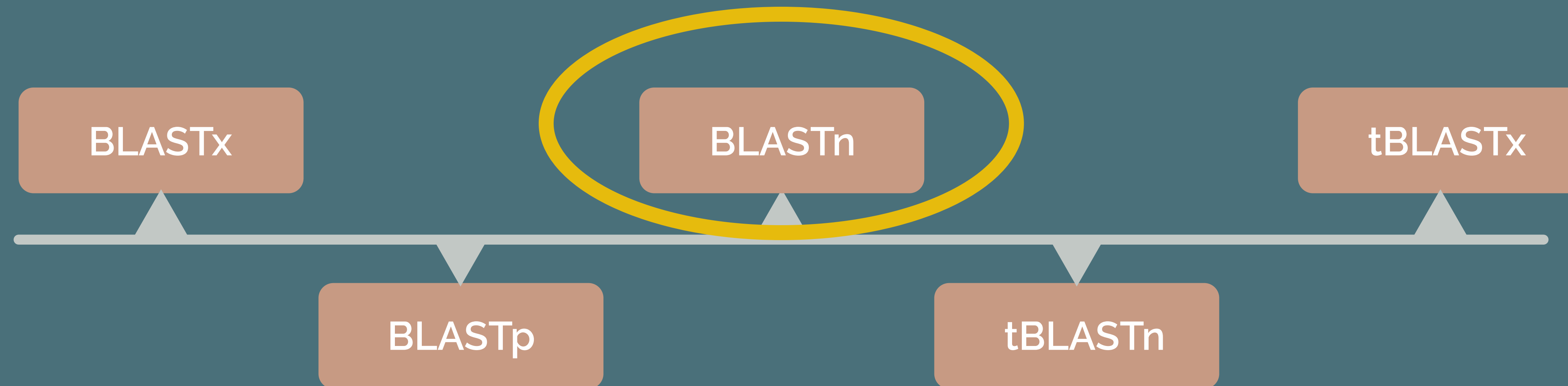
BLAST

- There are many different flavors of BLAST searches:



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Our application

- Our app focuses on **The BLASTn** nucleotide-nucleotide search looks for more distant sequences.



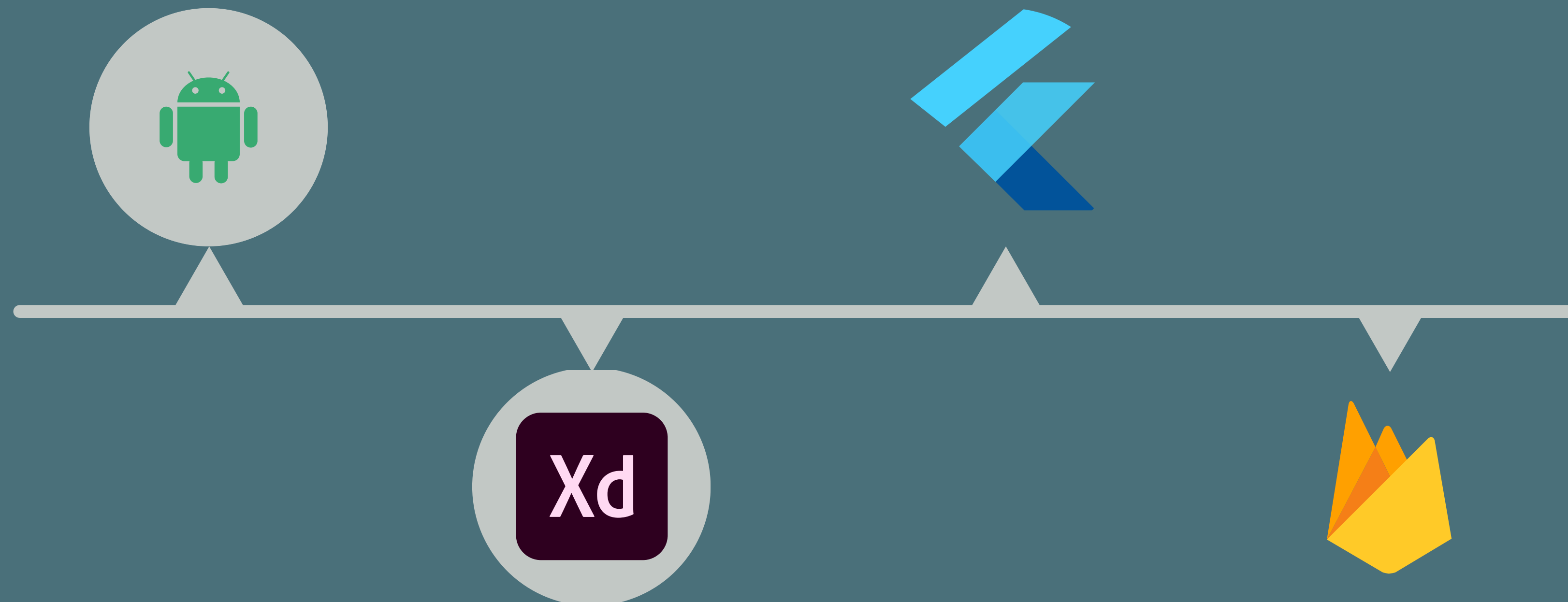
BLASTn

- **BLASTn** The query is a nucleotide sequence The database is a nucleotide database. No conversion is done on the query or the database
- **Alignment algorithms** : Mapping aligos to a genome, Annotating genomic DNA with transcriptome data from ESTs and RNA-Seq, Annotating untranslated regions.

Output

- List of local alignments between the query sequence and sequence in database.
- Alignment score.

Development and UI tools



References

- NCBI Bookshelf

Thank you



BLAST