

CSE 300 Online on Tikz and Beamer

Your roll

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Introduction

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Literature Review Sample

Summary of the relevant papers can be shown in presentation in elegant way using \LaTeX . Here is an example.

Grzegorz M. Boratyn, Jean Thierry-Mieg, Danielle Thierry-Mieg, Ben Busby and Thomas L. Madden; 2019

Magic-BLAST, an accurate RNA-seq aligner for long and short reads

- Next-generation sequencing technologies can produce tens of millions of reads, often paired-end, from transcripts or genomes.
- But few programs can align RNA on the genome and accurately discover introns, especially with long reads.
- Magic-BLAST is the best at intron discovery over a wide range of conditions and the best at mapping reads longer than 250 bases, from any platform.

A Flowchart

Flowchart of finding the sum of n natural numbers is shown below:

