Alignment-free tools for metagenomics-data analysis

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November 27, 2017

Overview

- Metagenomics
 - Metagenomes
 - NGS and Alignment
- 2 Alignment-based
- 3 Alignment-free methods
- Second Section

Metagenomics

- A metagenome is the whole set of transcripts found in a sample.
- Metagenomics is the study of those
- > 90% uncultureable microorganisms
- design of antibiotics, analysis of microorganismal life

NGS and Alignment

- Advances in sequencing made metagenomics possible
- NGS generates comparable reads

Metagenomics

Goals

- insight in microorganismal life
- first evidence of origin and function
- independent from databases and coding regions

Alignment-based approach

Advantages

- Align sequences against database
- Profiles can be analyzed
- BLAST > 80% accuracy

Alignment-based approach

Advantages

- Align sequences against database
- Profiles can be analyzed
- BLAST > 80% accuracy

Disadvantages

- Low speed
- Dependent of databases
- Unsequenced transcripts cannot be matched
- Databases mostly consist of coding sequences

Blocks of Highlighted Text

Block 1

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Block 2

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Block 3

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Multiple Columns

Heading

- Statement
- 2 Explanation
- Example

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Table

Treatments	Response 1	Response 2
Treatment 1	0.0003262	0.562
Treatment 2	0.0015681	0.910
Treatment 3	0.0009271	0.296

Table: Table caption

Theorem

Theorem (Mass-energy equivalence)

 $E = mc^2$

Verbatim

Example (Theorem Slide Code)

```
\begin{frame}
\frametitle{Theorem}
\begin{theorem}[Mass--energy equivalence]
$E = mc^2$
\end{theorem}
\end{frame}
```

Figure

Uncomment the code on this slide to include your own image from the same directory as the template .TeX file.

Citation

An example of the \cite command to cite within the presentation:

This statement requires citation [Smith, 2012].

References



John Smith (2012)

Title of the publication

Journal Name 12(3), 45 - 678.

The End