A Computational Platform for Gene Expression Analysis

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Outline

- Molecular biology is a young field of study, with a lot of unknowns and partial knowledge.

- Studying gene expression is crucial to understand the mechanisms that control living organisms.

- We focused on two different areas:
  - differential expression analysis;
  - RNA-binding protein (RBP) discovery and analysis.

Three distinct problems:

- Read alignment against a reference genome and differential expression analysis on the aligned data.

- RBP discovery, analysis and information enrichment.

- Further result analysis using data mining techniques.

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Gather information
Information should be contextually aggregated, allowing for quick access of relevant information.

- Two distinct problems warrant two different solutions.

- The developed system should be available anywhere, through the internet.

- The system's footprint should be small enough to allow deployment in almost any available hardware.

NOTES:
- Show scheme, refer iRAP, the script and the web interface.
- Refer multiple differential expression tools.
- Refer user input and tool configuration.

NOTES:
- Show scheme, RBP finding, gene enrichment, clustering.
- Refer web interface. - Refer that the tools is in production for several months, being extensively tested by experts.
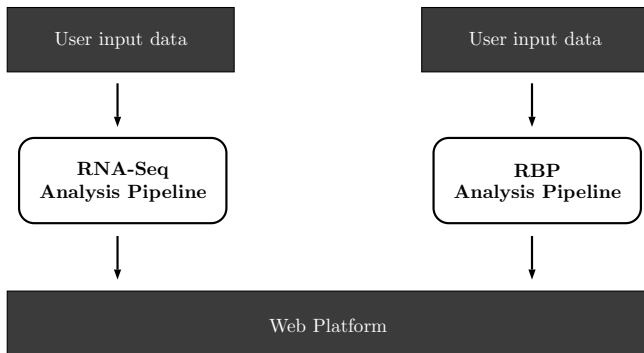- Refer user input and tool configuration.

While focusing on aggregation and quick access to information, does it make sense to separate the results into two different platforms?
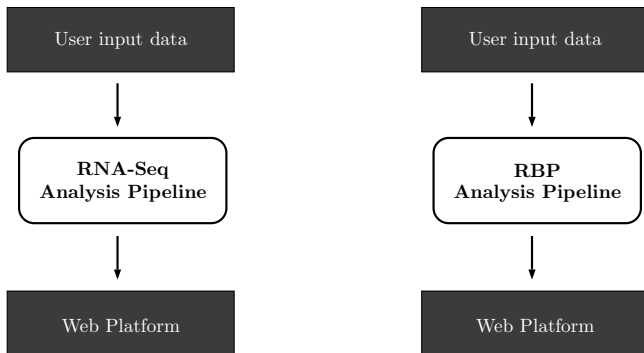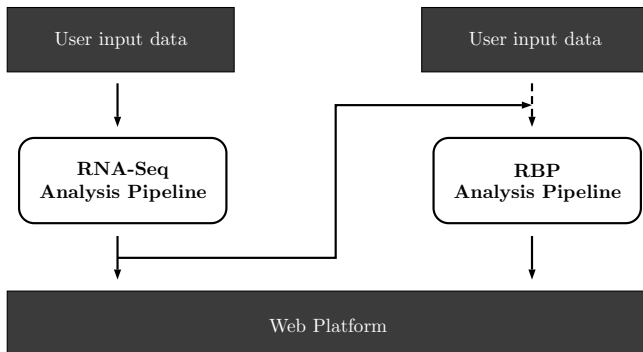
A list of differentially expressed genes is not very useful without further information about those genes. Does it make sense for a user to launch a new gene enrichment task by hand?

A fully integrated solution: the analysis pipelines can be used separately or automatically executed in sequence; result visualization for both pipelines is isolated.

NOTES:

- Refer objectives, data and experimental method.

- Refer results.

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- Refer results.
- Maybe show screenshot.

- RBP analysis pipeline and web platform (PBS Finder) fully implemented. PBS Finder has been in production for several months; during this time it was thoroughly tested by IBMC experts.

- RNA-Seq analysis pipeline partially implemented (iRAP deployed and result joining tool implemented).

- Integration of both tools could not be accomplished due to time constraints.

- Fully integrate the RNA-Seq analysis pipeline with the web platform (automatic job configuration, result visualization, etc.).

- Study the requirements for deploying the platform in large scale, and assess the feasibility of making it available internet-wide.

Review

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