A Computational Platform for Gene Expression Analysis

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Outline

Domain Problem I

Introduction

- 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.

Domain Problem II

Introduction

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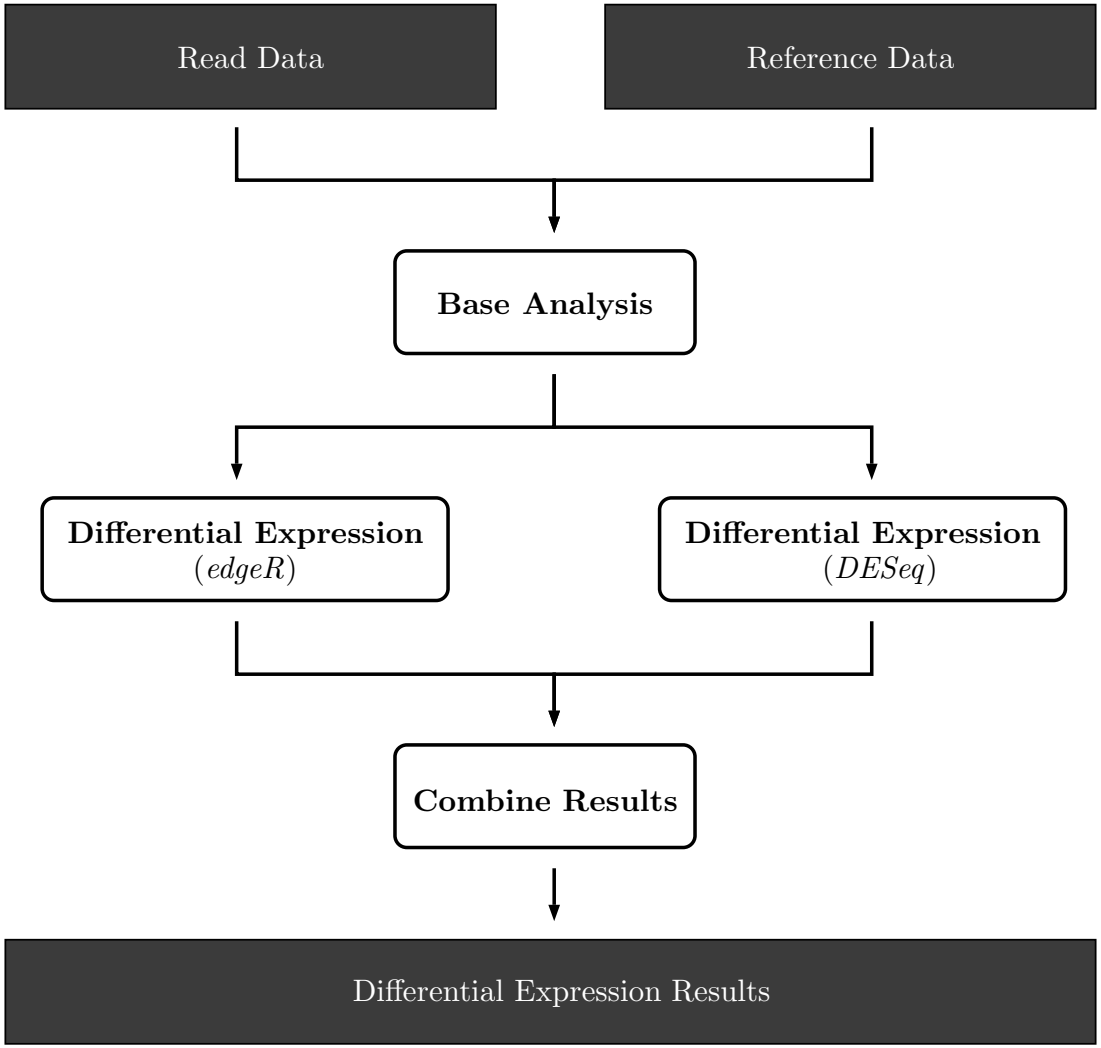
Gather information
Information should be contextually aggregated, allowing for quick access of relevant information.

- 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.

RNA-Seq Analysis Pipeline I

Developed Solution



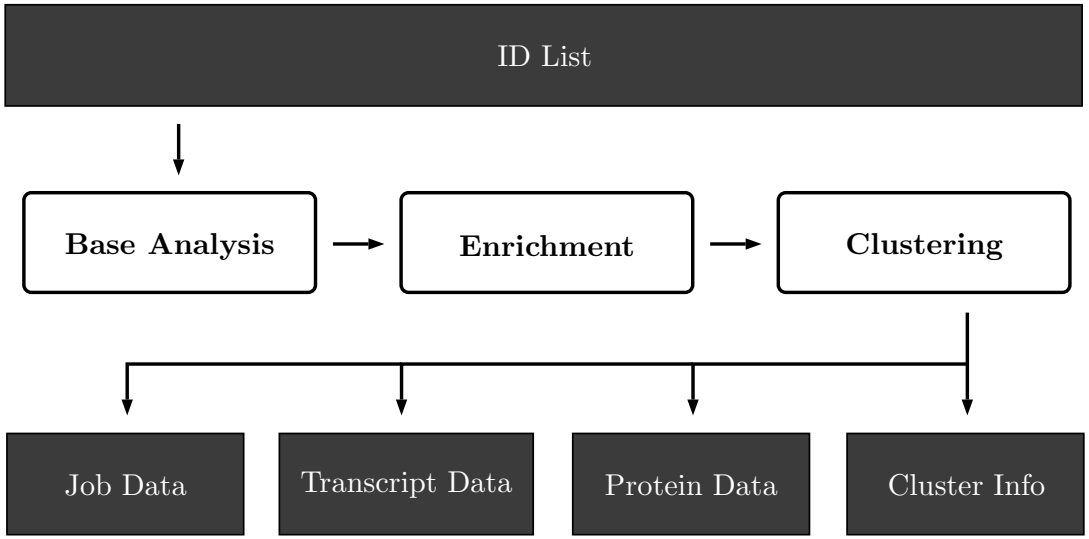
RNA-Seq Analysis Pipeline II

Developed Solution

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

RBP Analysis Pipeline (PBS Finder) I

Developed Solution

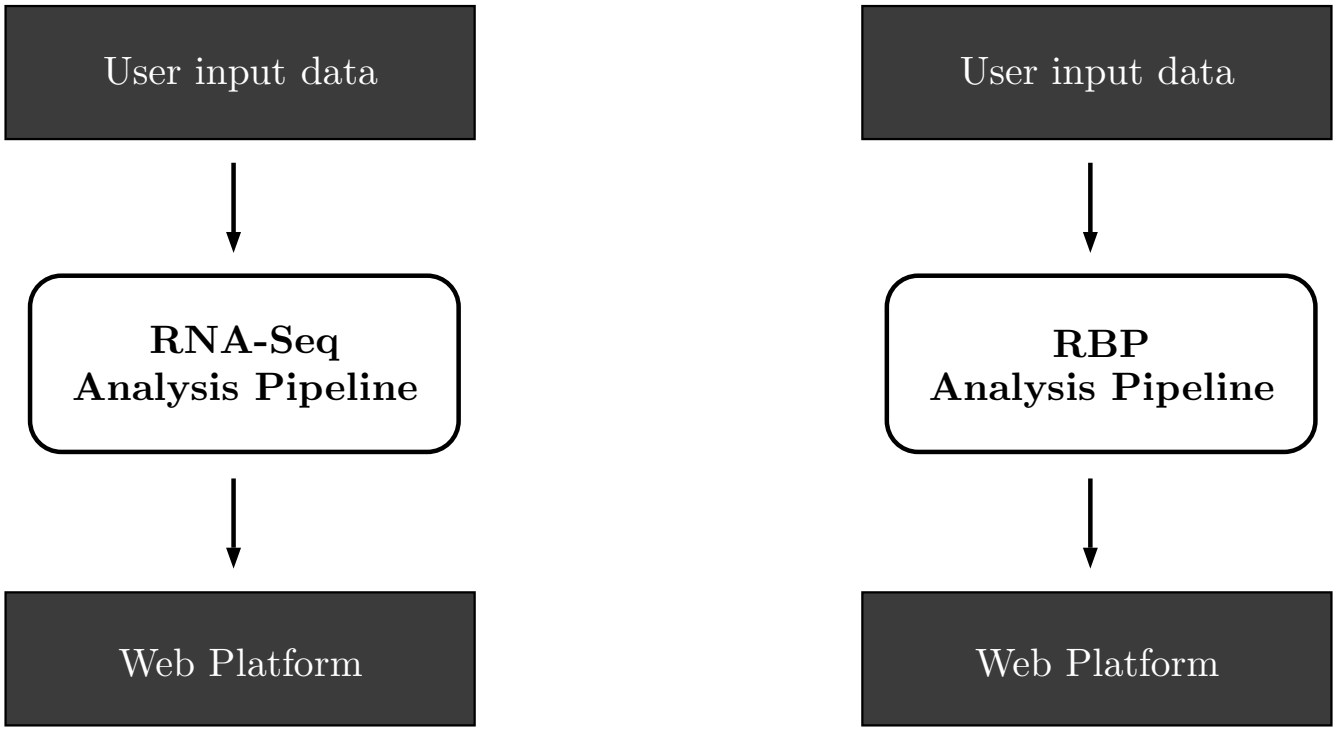


NOTES:
- Show scheme, RBP finding, gene enrichment, clustering.
- Refer web interface. - Refer that the tools is in production for several months, being extensively tested by experts.
- Refer user input and tool configuration.

Integration

Developed Solution

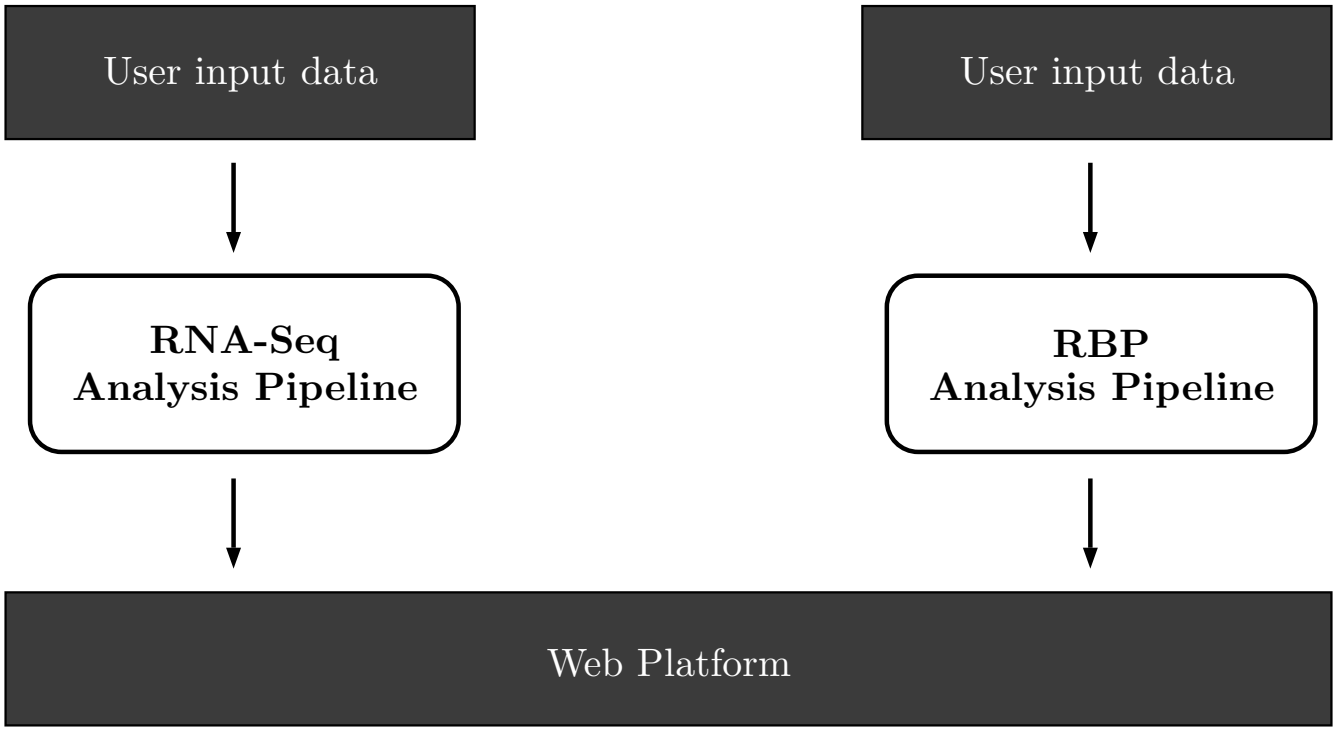
While focusing on aggregation and quick access to information, does it make sense to separate the results into two different platforms?



Integration

Developed Solution

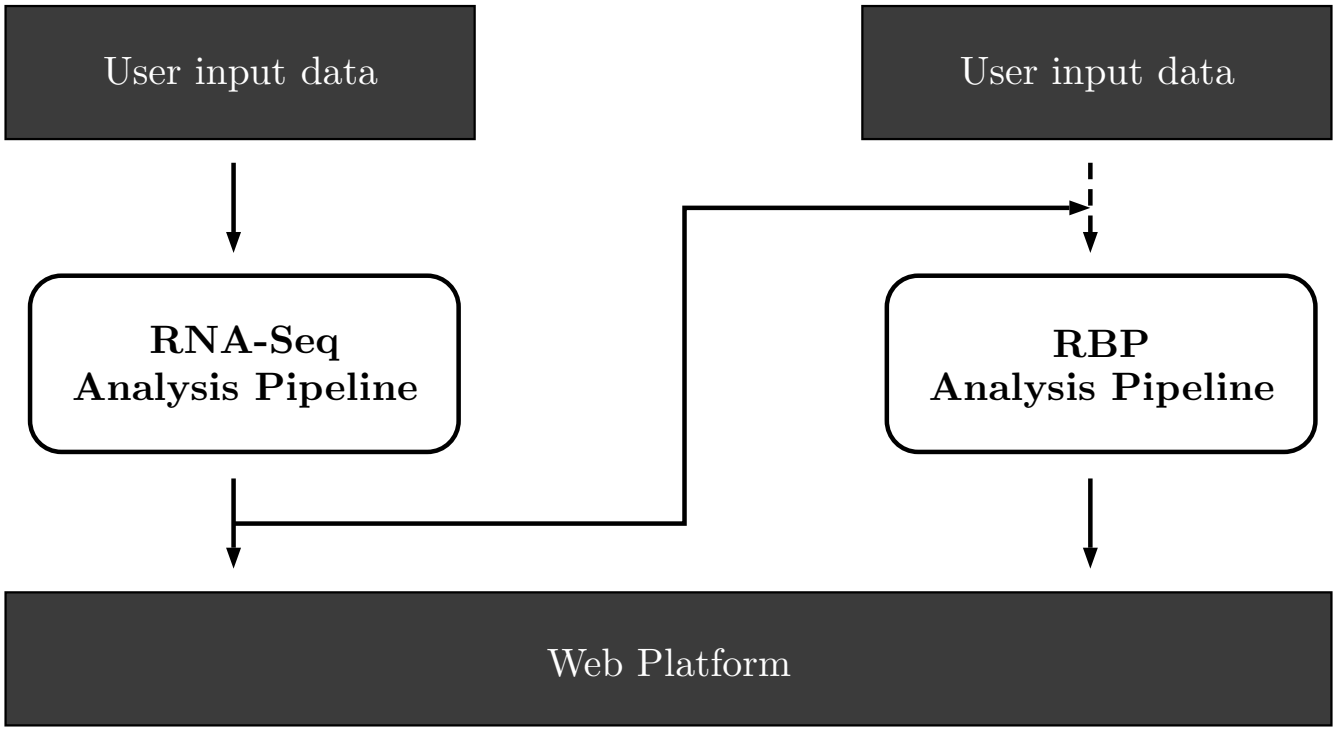
A list of differentially expressed genes is not very useful without further information about those genes. Does it make sense for a user to launch a new gene enrichment task by hand?



Integration

Developed Solution

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.

RBP Analysis Pipeline (PBS Finder)

Case Studies

Number of IDs	***Machine1***	***Machine2***	***Manual method***
100	$9m\ 56s$	$11m\ 1s$	$\approx 50h$
500	$41m\ 47s$	$55m\ 51s$	$\approx 250h$
900	$1h\ 33m\ 32s$	$2h\ 7m\ 4s$	$\approx 450h$

Objective Fulfilment

Conclusions

- 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.

Future Work

Conclusions

- 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

1. Introduction
   - Domain Problem
   - Motivation and Objectives
2. Developed Solution
   - Overview
   - RNA-Seq Analysis Pipeline
   - RBP Analysis Pipeline (PBS Finder)
   - Integration
3. Case Studies
   - RNA-Seq Analysis Pipeline
   - RBP Analysis Pipeline (PBS Finder)
4. Conclusions
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   - Future Work

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