



Workflows in Galaxy

Exercise II: Modify and run a workflow in Galaxy

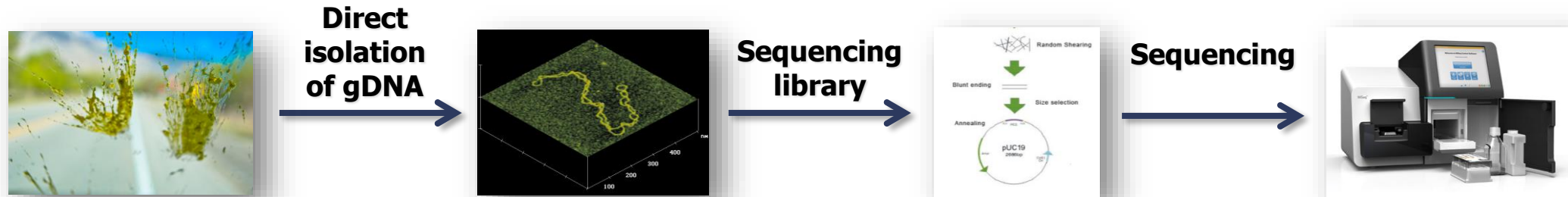
Taxonomic profiling of metagenomic sample

Erik Hjerde



Metagenomics

The study of genetic material directly from a sample



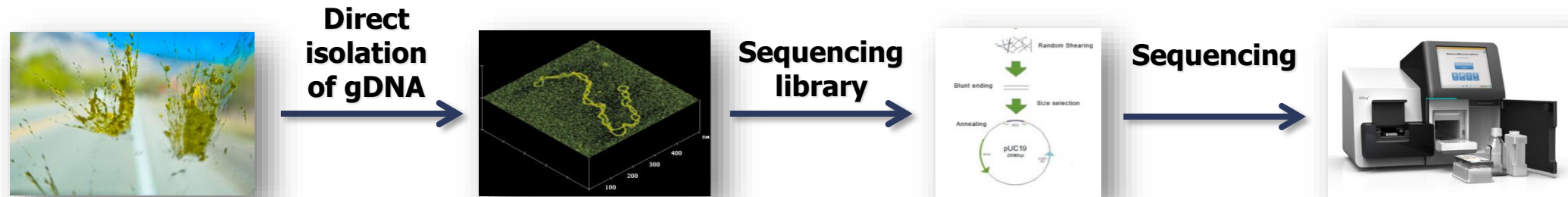
Metagenomics



Mariam Quiñones

Metagenomics

The study of genetic material directly from a sample



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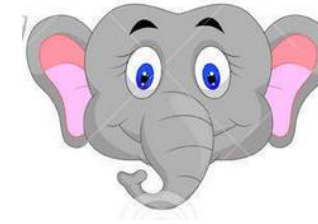




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How do we study the taxonomy in a sample?

Each sequence read is a tiny genomic fragment from a specie in the sample



In a metagenome a sequence read is basically representing a specie

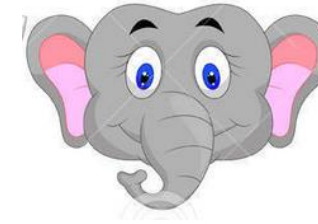
AGTCCAGGTAACGTTACAACG

[illegible]

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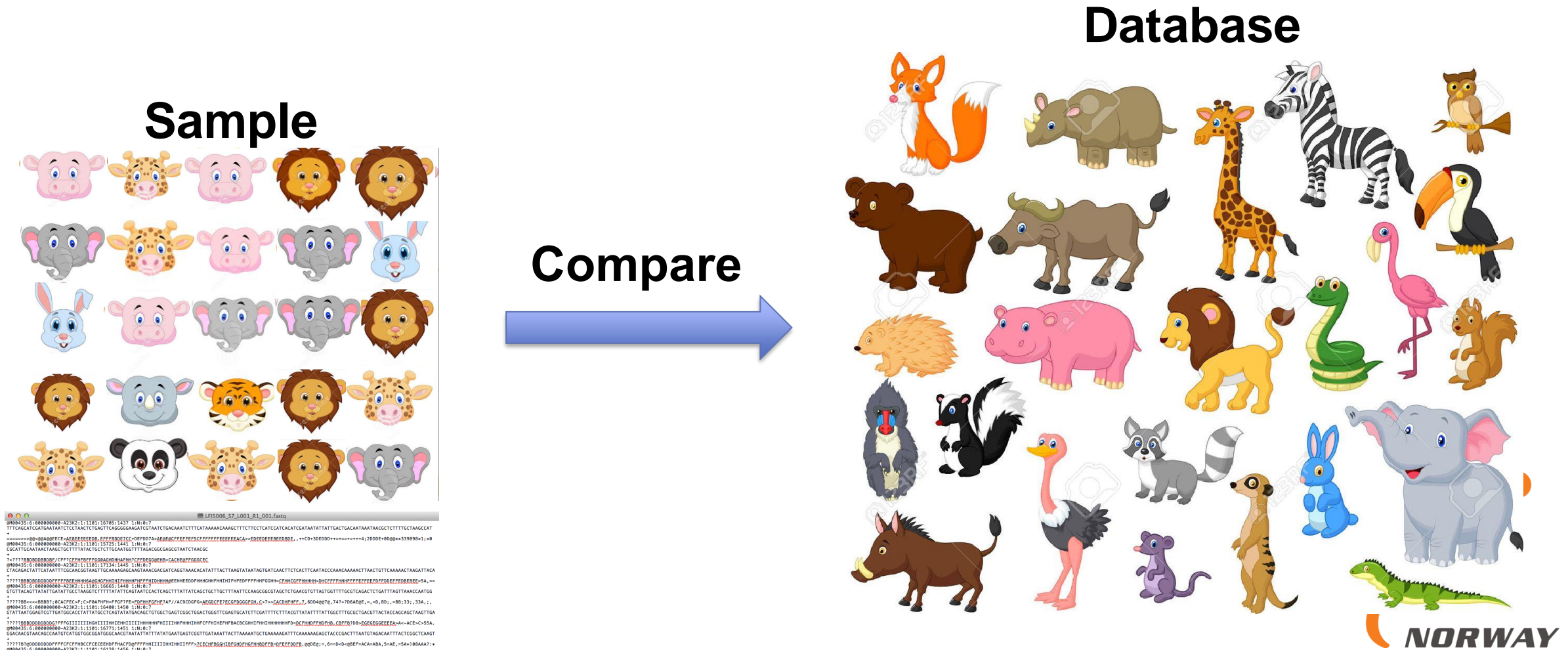


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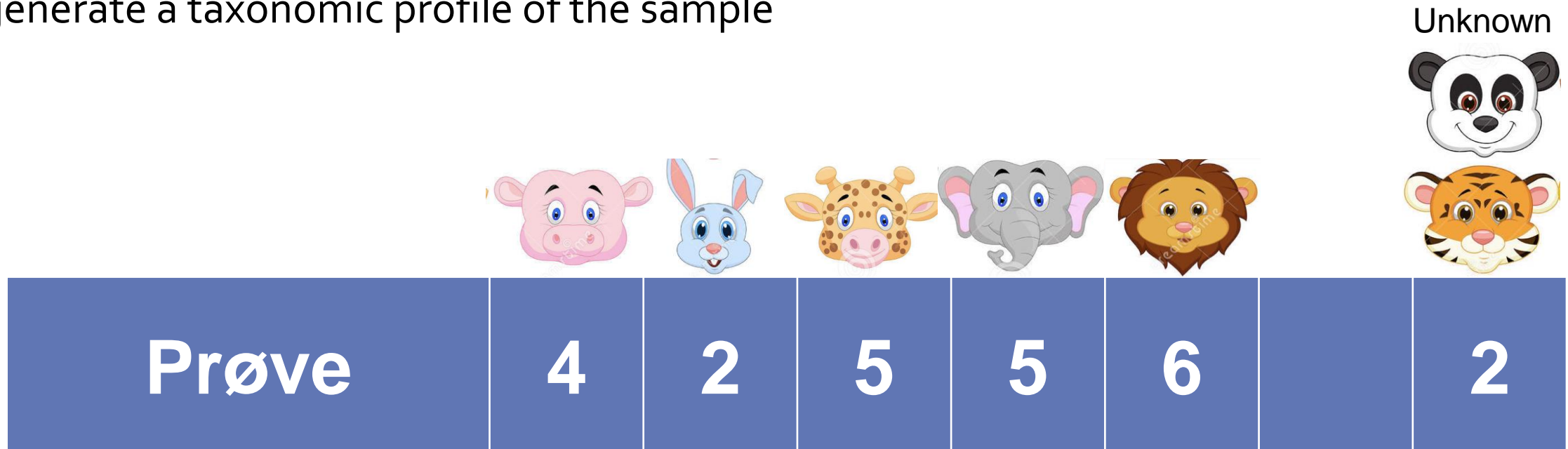
How do we study the taxonomy in a sample?

The sequence reads are compared to known sequences in databases



How do we study the taxonomy in a sample?

By comparing all the sequences in the sample and counting the occurrences, we can generate a taxonomic profile of the sample

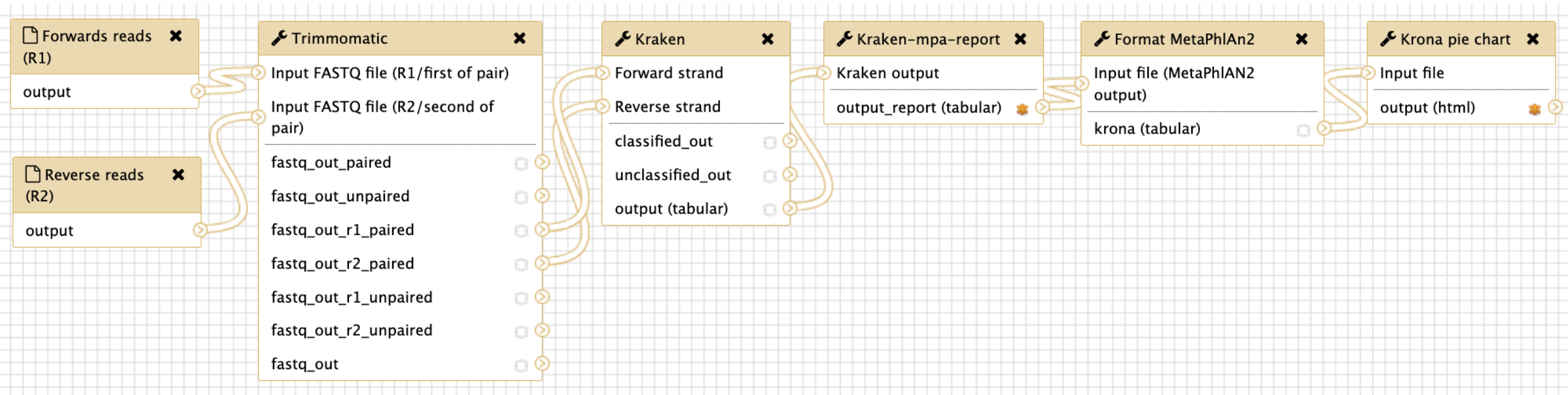


Exercise II

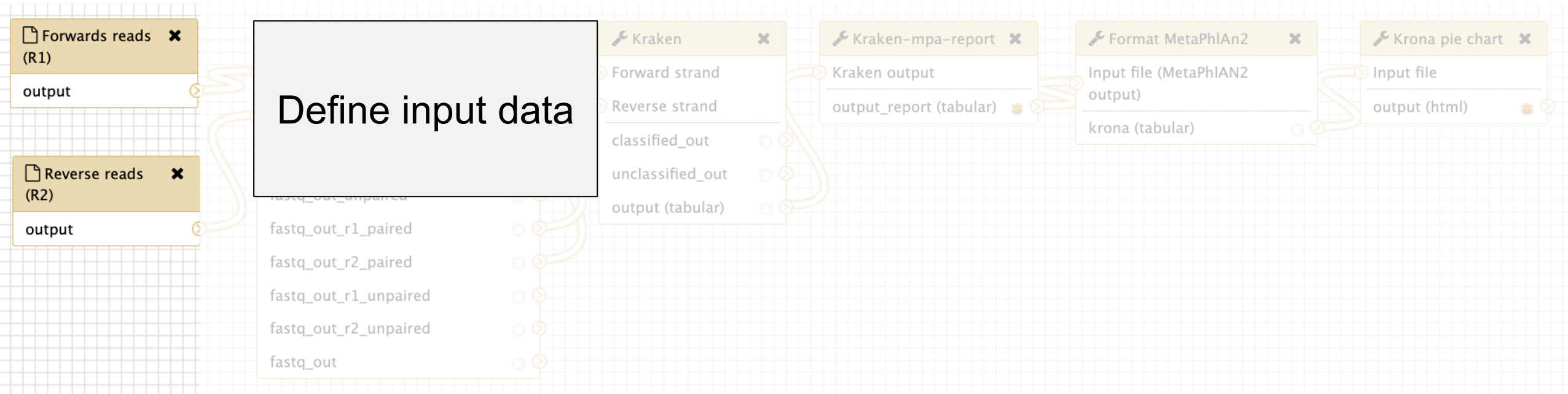
TASK:

1. Modify a workflow
2. Import data from NeLS
3. Run analysis on proper data using the workflow

The existing workflow



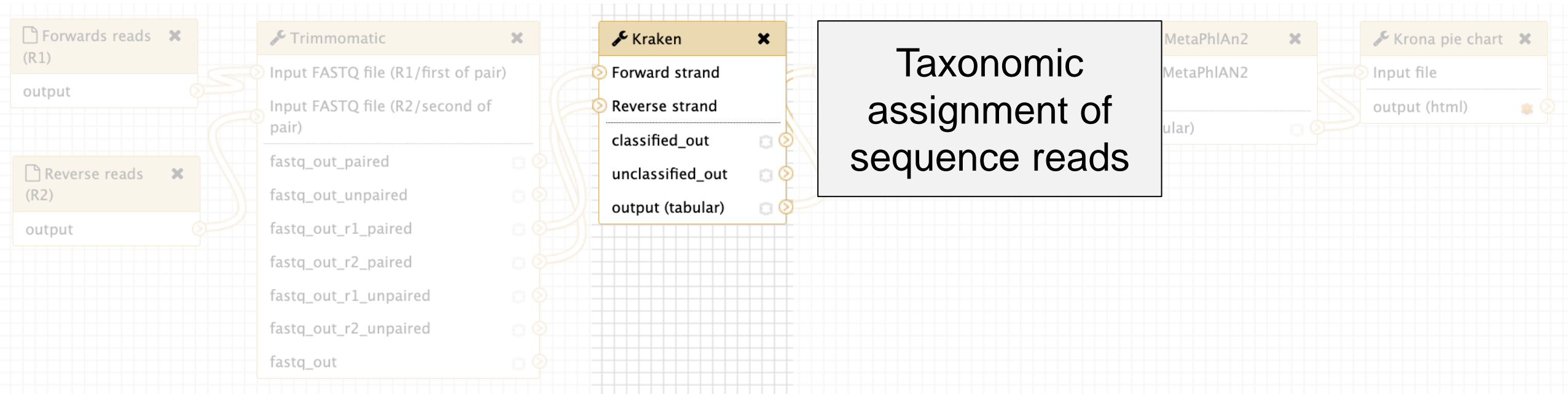
The existing workflow



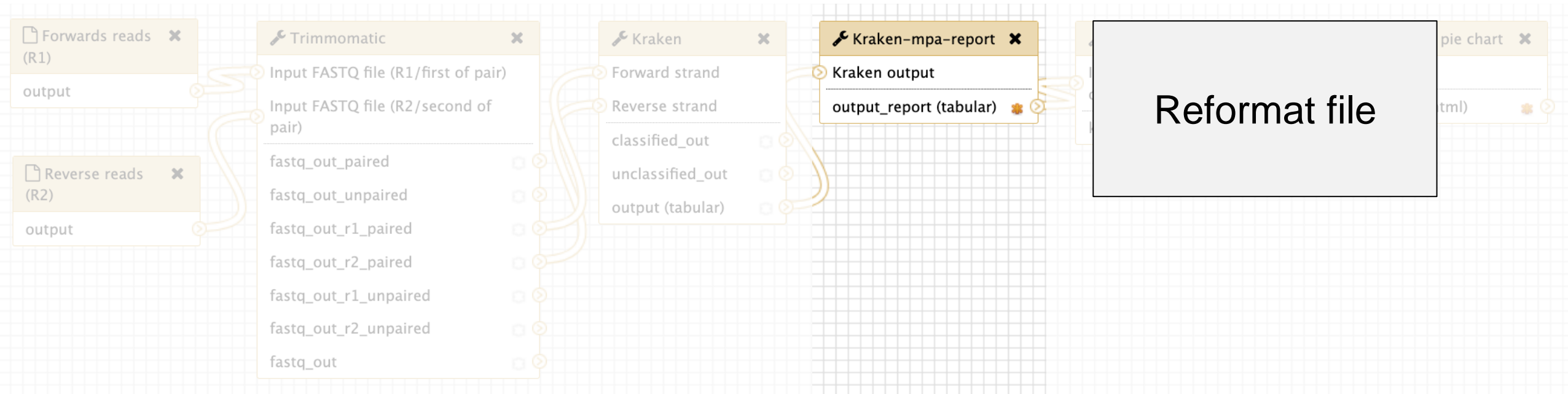
The existing workflow



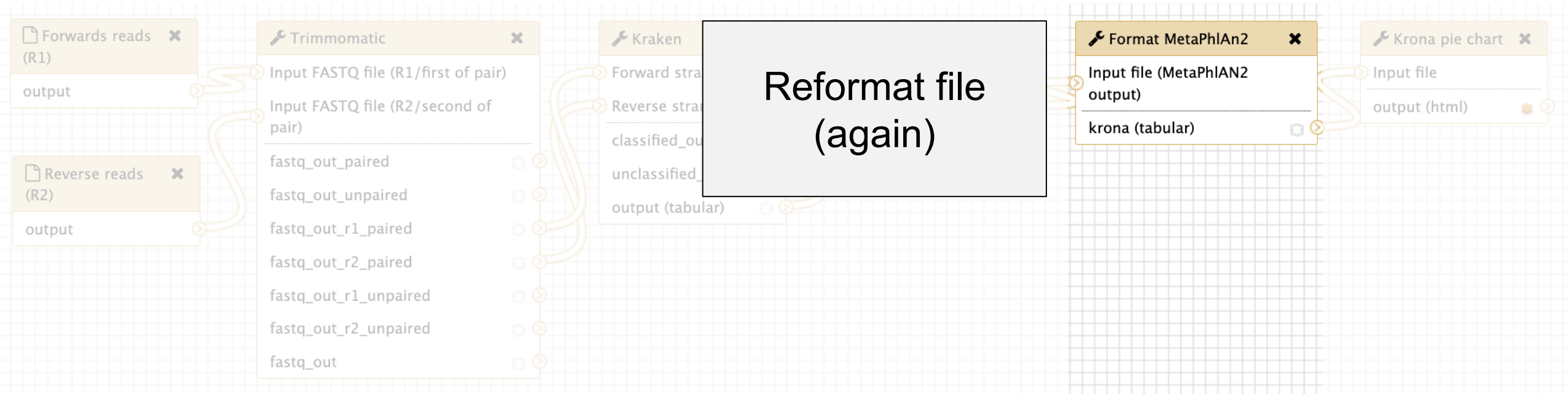
The existing workflow



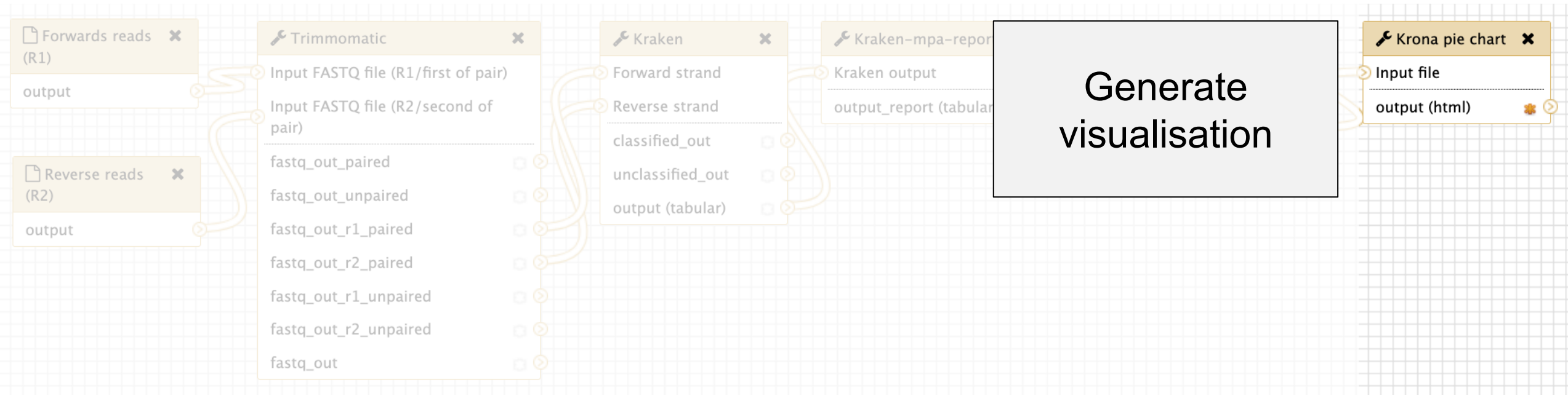
The existing workflow



The existing workflow



The existing workflow



The final workflow

