# Introduction

Research sub-question: “ how does a co-assembler work, and what sort of data is produced? What are the steps the underlying algorithm takes in regard to de bruijn graphs?”

# Results

* “Stringit’s acceptance of multiple input formats, and use of a universally-accepted output format, makes it widely accessible, and unique in the field”
  + Features: different inputs and handling of them, exporting into .dot
  + Test: Compare my input/output system with that of other tools
  + In-depth: file formats, and their layout and uses (SAM/dot/asqg/454/others)
  + Answered research question: What is the best way to **manipulate** and present this sort of data?

* “Stringit has an intuitive visual representation for easy access to all information (that is provided by nodes)”
  + Features: node HUD, node sizes
  + Test: compare design with other tools
  + In-depth: How does the visual style of Stringit (and d3) benefit the user?
  + Answered research question: What is the best way to manipulate and **present** this sort of data?
* “The zooming feature of Stringit allows for both a grand overview and a detailed in-depth analysis for a full and unrivaled view of all the data”
  + Features: zooming
  + Test: user tests.
  + In-depth: Are user expectations of the functionalities of Stringit fulfilled?
  + Answered research question: What are other functionalities that are requisited for the functioning of Stringit?
* “Grouping the contig nodes based on sample read mapping readily shows regions of overlapping and/or diverging sequence”
* “Combining (co-)assembly and read map data into a single visualization is something that is not provided by other tools”
  + Features: data-translating code, coloring of nodes based on mapped reads (future: highlighting of co-mapped reads from different samples?)
  + Test: use cases. Show how easy it is to find regions of interest, compared to other tools
  + In-depth: niche of tool. When to use this, and when to use other tools.
    - (HP) diploid genomes/co-assemblies
    - Not: synteny, msa, read mapper?
  + Answered research question: What are the limitations of similar tools?

# Conclusion

Research main question: ”How is co-assembly data best visualized, so that it is suitable for analysis?”