Benchmark of *de novo* Short Read Assembly Strategies for Metagenomics

Ino de Bruijn

Content

- Introduction on Assembly
  - What is assembly?
  - Popular methods
- Benchmark Method
  - Which assemblers have been validated?
  - How have they been validated?
- Benchmark Results
  - What is the most awesome assembler?

Introduction on Assembly

- Different technologies to sequence your sample
  - Sanger (400-600nt, error rate 0.001-1.0%)
  - 454 (400nt, error rate 1-4%)
  - Illumina (100nt, error rate 0.1-1%)
  - PacBio (3k-5knt, error rate 13-20%)
  - Ion Torrent (200-400nt, error rate 0.5-2.5%)
- Assembly turns reads into contigs and/or scaffolds
- Algorithms fit sequencing technologies
- Three general approaches
  - Overlap-Layout-Consensus (Long reads Celera 2000, Newbler 2005)
  - Greedy (Short reads, SSAKE 2007)
  - de Bruijn Graph (Short reads, Velvet 2008)

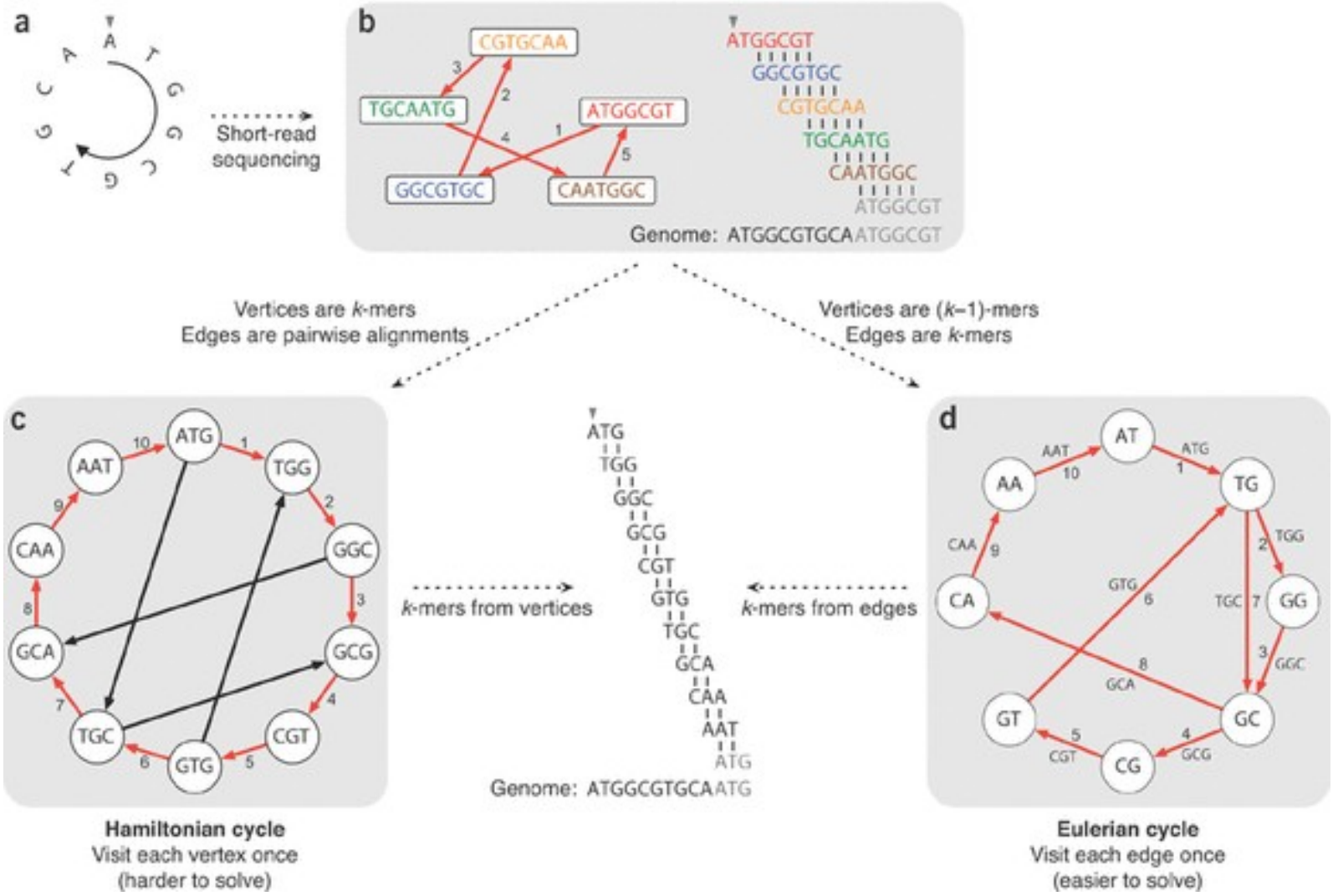
Introduction on Assembly

- Different technologies to sequence your sample
  - Sanger (400-600nt, error rate 0.001-1.0%)
  - 454 (400nt, error rate 1-4%)
  - Illumina (100nt, error rate 0.1-1%)
  - PacBio (3k-5knt, error rate 13-20%)
  - Ion Torrent (200-400nt, error rate 0.5-2.5%)
- Assembly turns reads into contigs and/or scaffolds
- Algorithms fit sequencing technologies
- Three general approaches
  - Overlap-Layout-Concensus (Long reads Celera 2000, Newbler 2005)
  - Greedy (Short reads, SSAKE 2007)
  - de Bruijn Graph (Short reads, Velvet 2008)

FYI, this man is not my grandpa

Introduction on Assembly

De Bruijn Graph



Introduction on Assembly

- Choosing the right K...
  - larger K more specific less coverage (span repeats, regions occurring twice, less connections in the graph)
  - Smaller K more sensitive more coverage (more connections in the graph)
  - Ideally combine both
- De Bruijn Graph potential information available
  - Overlap between kmers
  - Kmer coverage (how often does a kmer occur)
  - Read that created the kmer (choose between paths)
  - Insert size distribution between pairs (if paired reads were used)
- Programs differ in
  1) how the graph is stored
  2) how the graph is traversed

Introduction on Assembly

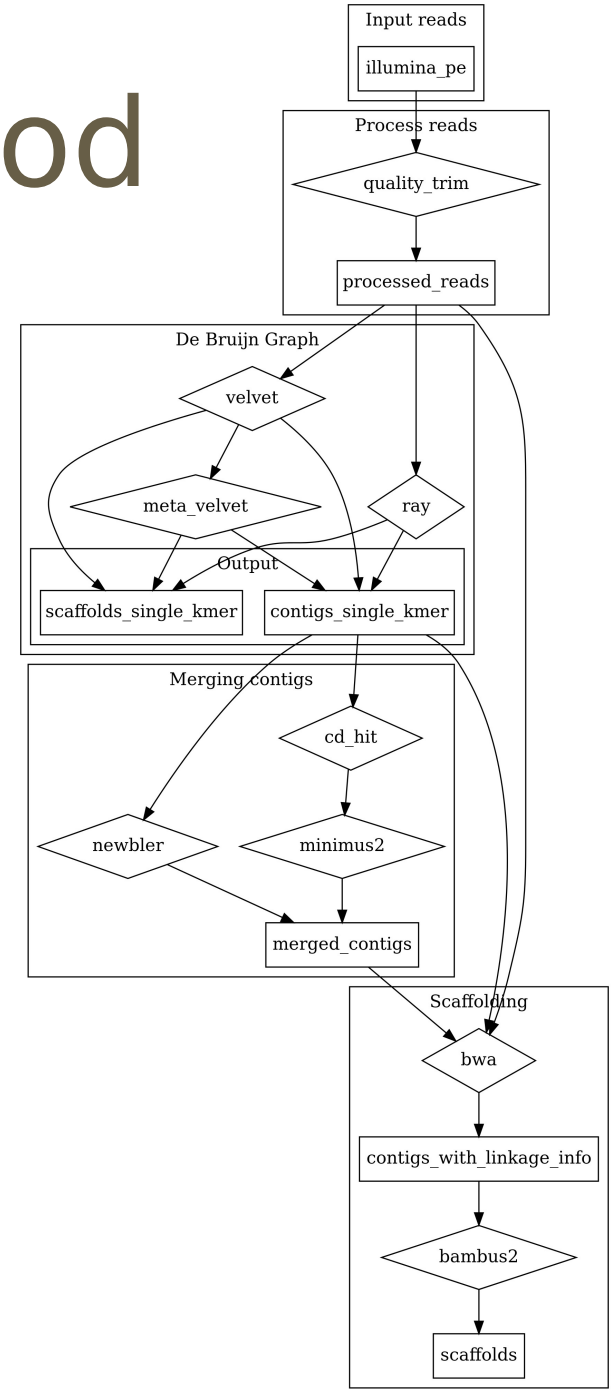
- Metagenomics uses DNA from environmental sample
  - Not all microbes can be cultured in the lab
  - Study microbial communities in their natural environment
- Metagenomic assembly more difficult than single genome assembly
  - Number of genomes unknown (maybe a rough idea)
  - Coverage of genomes differs (different abundances of genomes)
  - Closely related strains complicate the graph (in de Bruijn: anything that shares stretches of DNA longer than K)

Benchmark Method

- Use an *in vitro* simulated metagenome with known species
  - 59 species, total size 195Mb
  - Two abundance distributions of genomes
    - Even, approximately the same genome copy numbers
    - Uneven, log-normal distribution of phyla similar to soil
    - Assemblies can be validated by aligning them against the reference genomes (we used nucmer for this)
- Use Illumina paired end reads since that is currently one of the most popular sequencing techniques for metagenomic samples

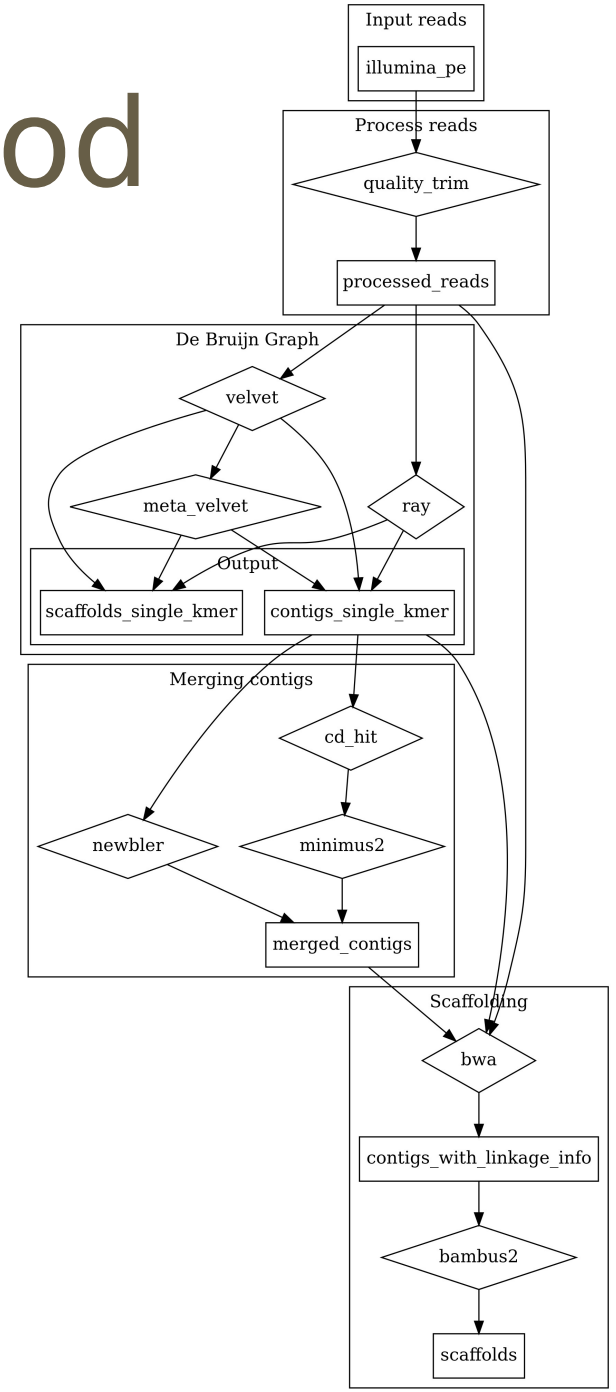
Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test



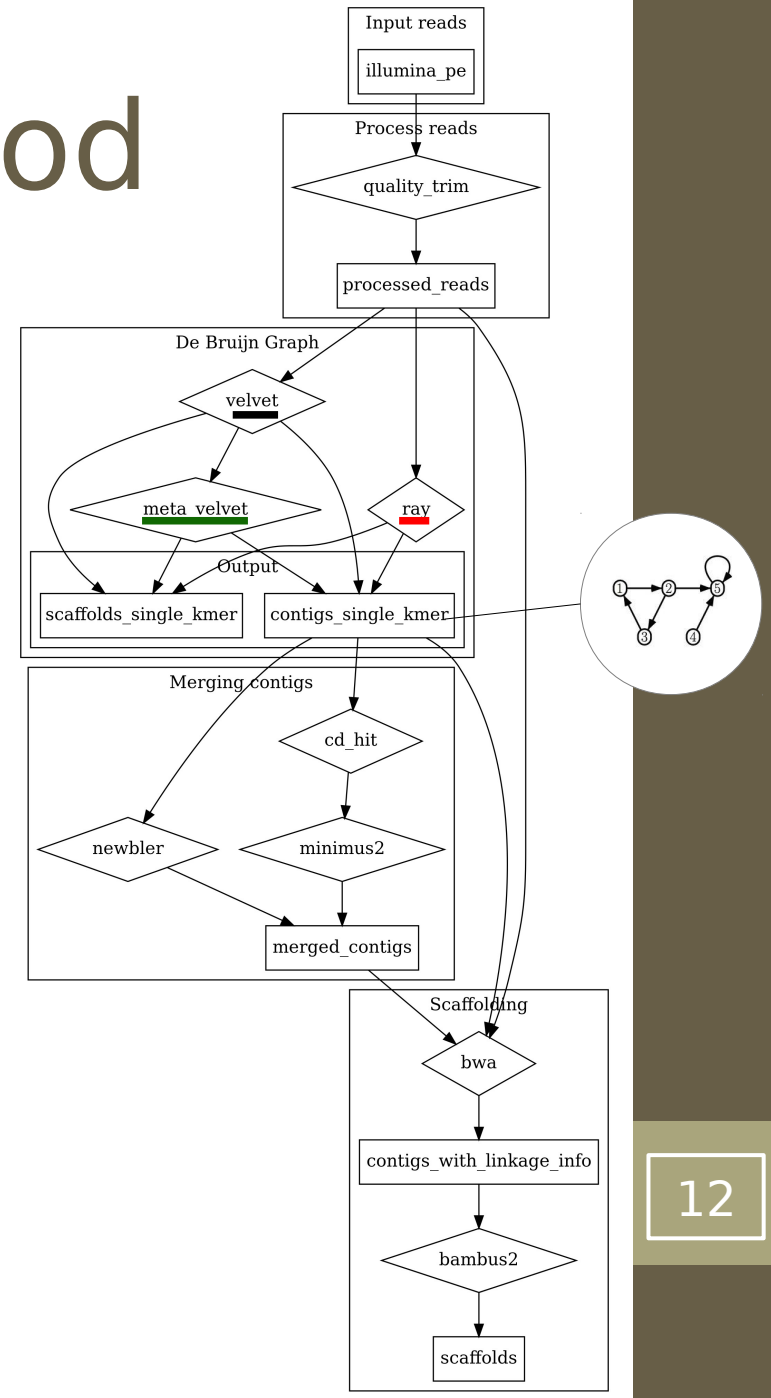
Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test



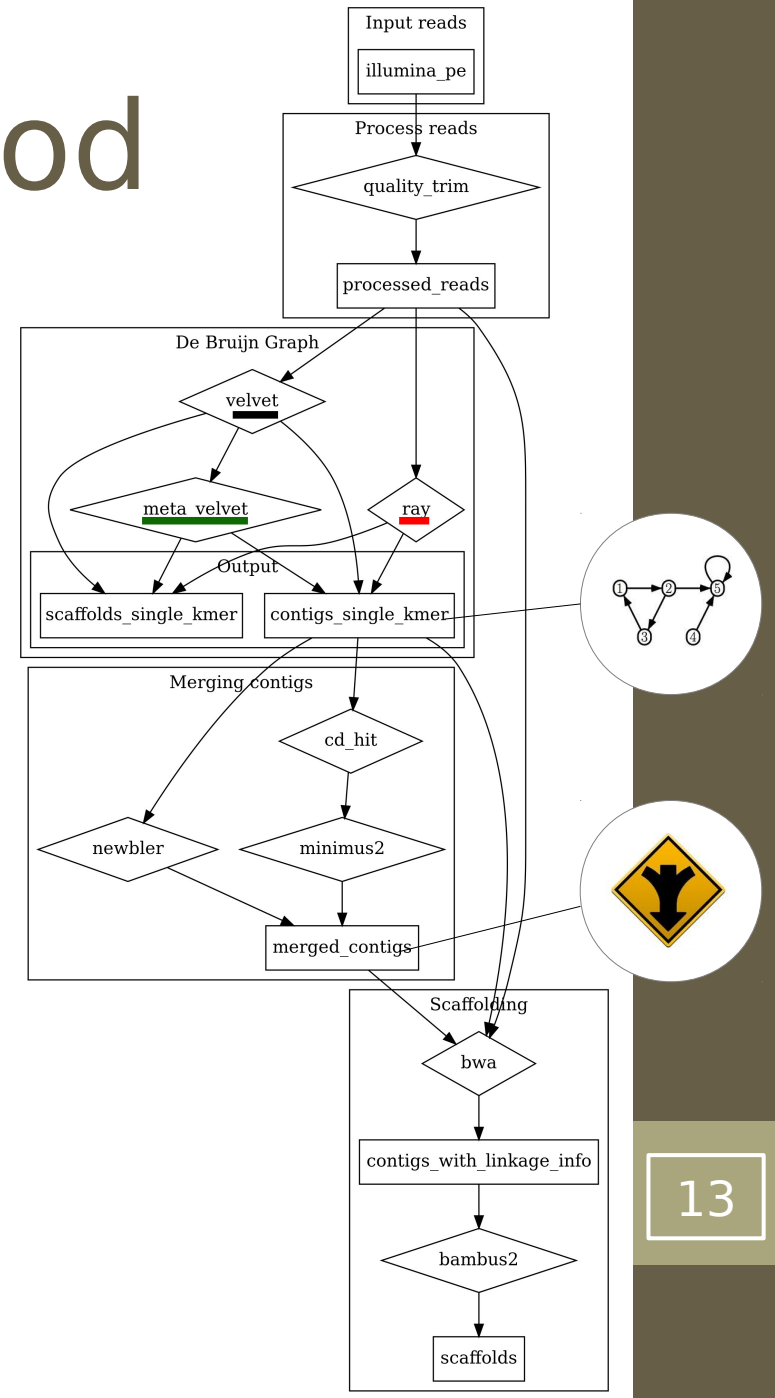
Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test
- Contiging with
  - Velvet
  - Meta-Velvet
  - Ray



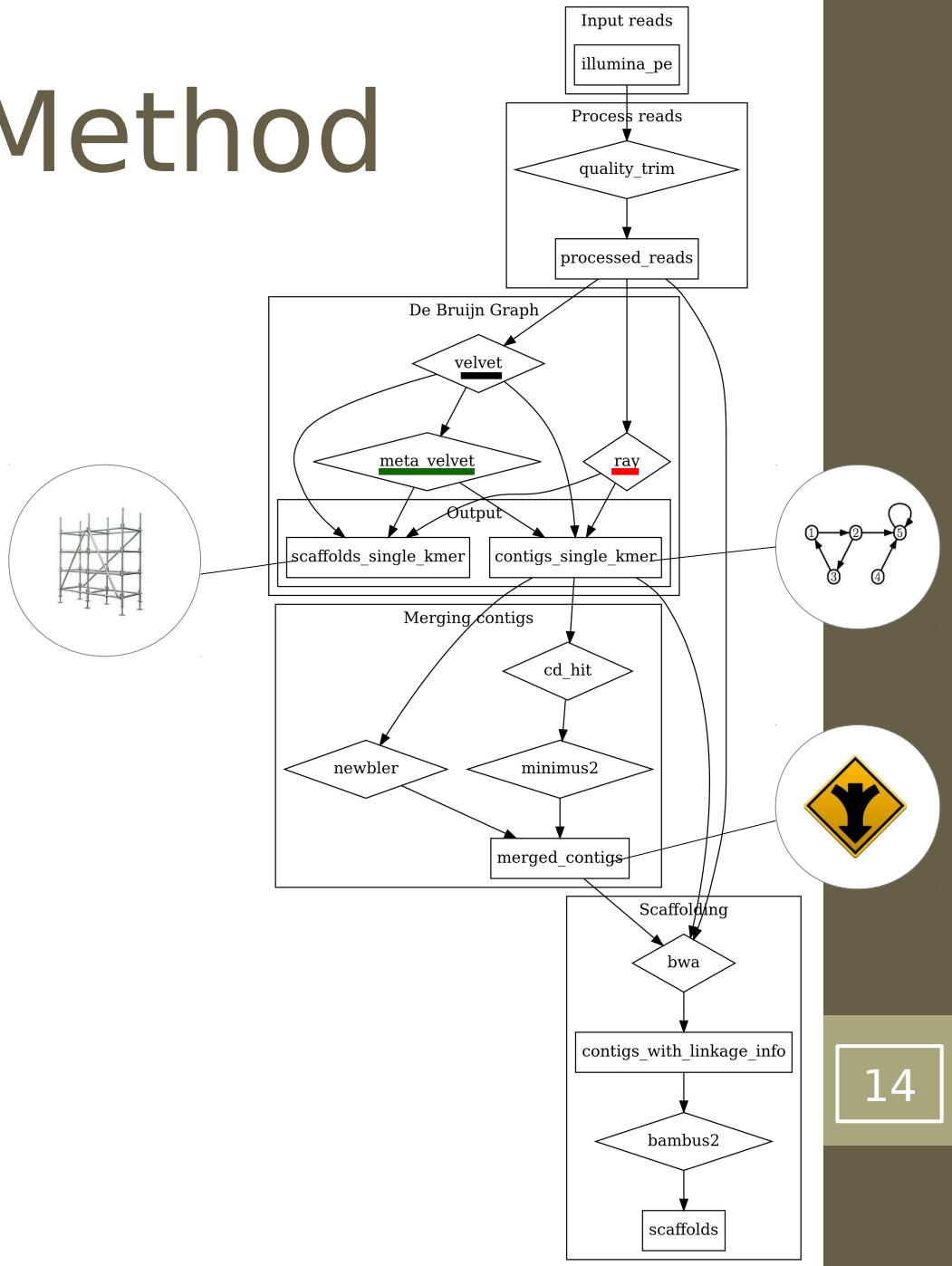
Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test
- Contiging with
  - Velvet
  - Meta-Velvet
  - Ray
- Merging with
  - Newbler
  - Minimus2



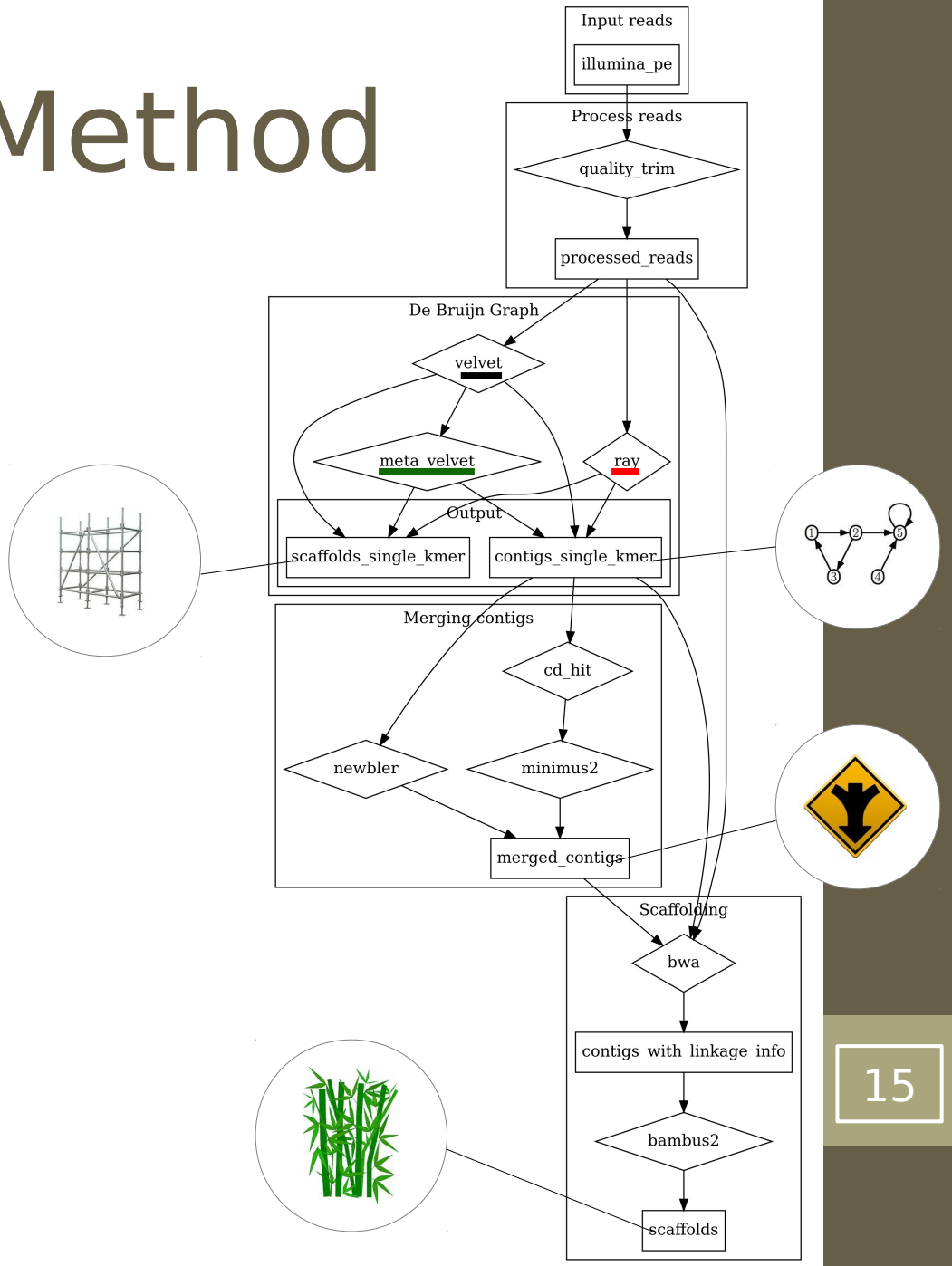
Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test
- Contiging with
  - Velvet
  - Meta-Velvet
  - Ray
- Merging with
  - Newbler
  - Minimus2
- Scaffolding with
  - Velvet
  - Meta-Velvet
  - Ray



Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test
- Contiging with
  - Velvet
  - Meta-Velvet
  - Ray
- Merging with
  - Newbler
  - Minimus2
- Scaffolding with
  - Velvet
  - Meta-Velvet
  - Ray
  - Bambus2



Benchmark Method

- Enormous amount of assembly strategies possible
  - Select a number of assembly strategies to test
- Contiging with
  -  Velvet
  -  Meta-Velvet
  -  Ray

  = 3 strategies
- Merging with
  -  Newbler
  -  Minimus2

  = 2 x 3 stragies = 6 strategies
- Scaffolding with
  -  Velvet
  -  Meta-Velvet
  -  Ray
  -  Bambus2

  = 3 strategies

  = (6 merge + 3 contig) strategies = 9 strategies

Total of 21 strategies

Benchmark Method

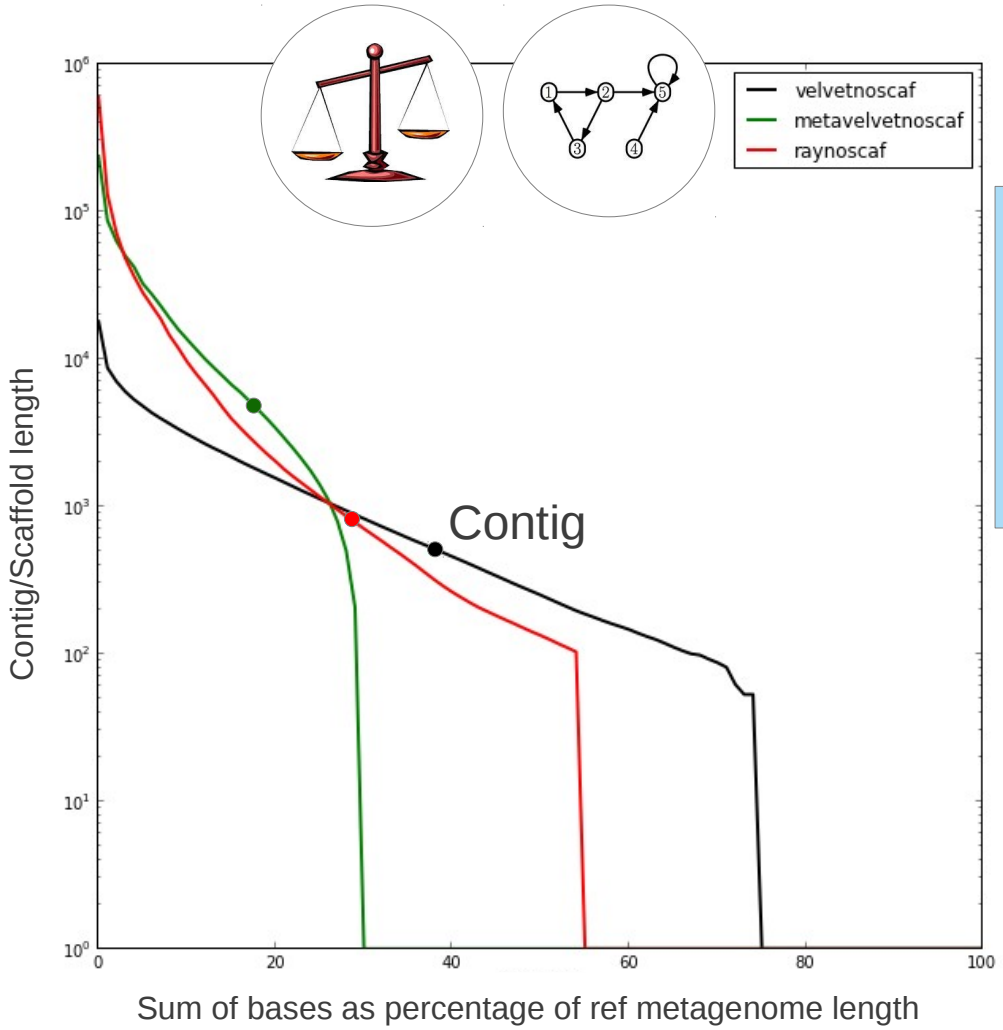
- How to compare all these different strategies?
- Validation of metagenomic assembly often focuses on one or more of the following points:
  1) contig/scaffold length distribution
  2) contig/scaffold coverage of the reference metagenome
  3) chimericity and erroneousness of the contigs/scaffolds
  4) functional annotation
  5) phylogenetic classification
- We focus on the first three since those also tend to improve 4 and 5 as shown by Mende et al (2012)
- Select winner in three categories

Benchmark Results

1) contig/scaffold length distribution
   - Popular statistic: N50 length (or L50)
     - Weighted median of contig lengths (contigs weighted by length)
     - 50% of all bases in the assembly are in contigs >= L50
     - Bigger is better
   - Problem when comparing between different assemblers: cut-off length matters and sum of bases between assemblies differs
     - Advantage for assemblers that only output long contigs

Benchmark Results

1) contig/scaffold length distribution

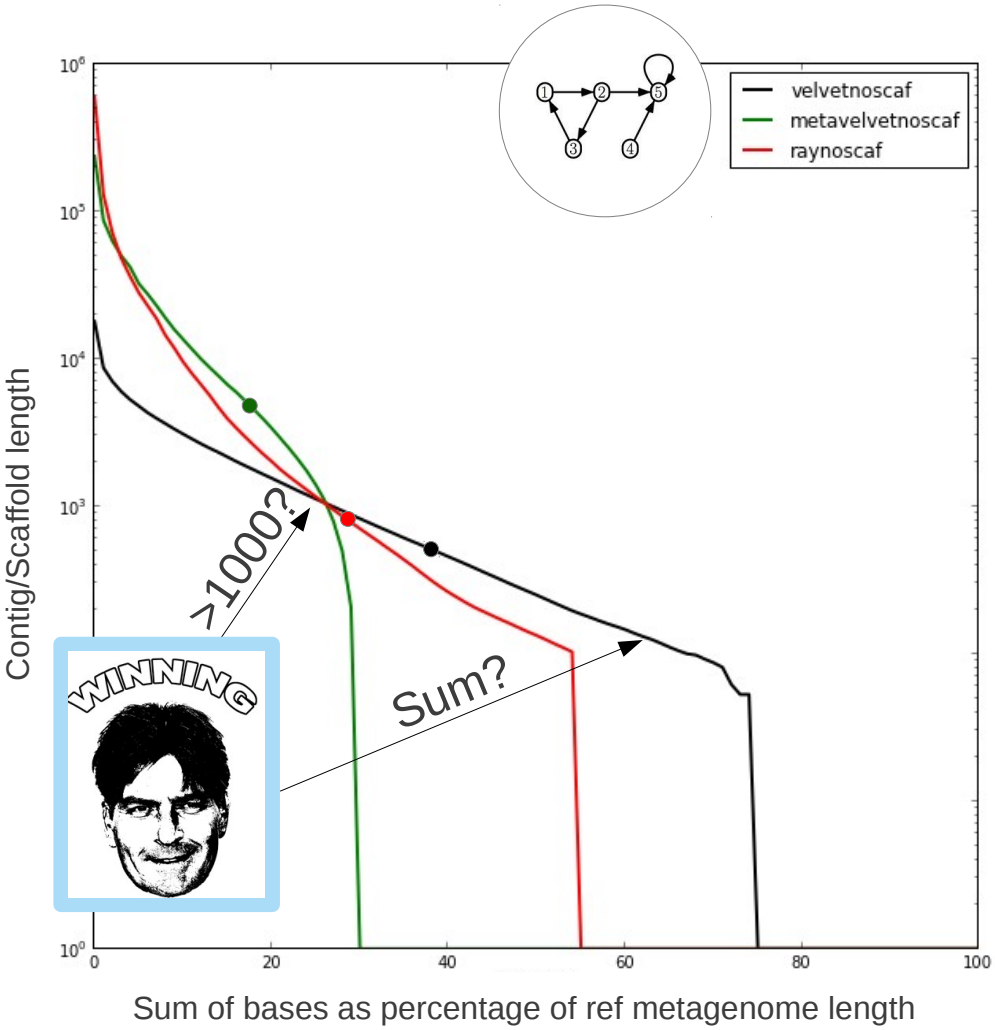


Shows best single kmer strategy per assembler based on L50

Dots are L50 values at cut-off 100

Benchmark Results

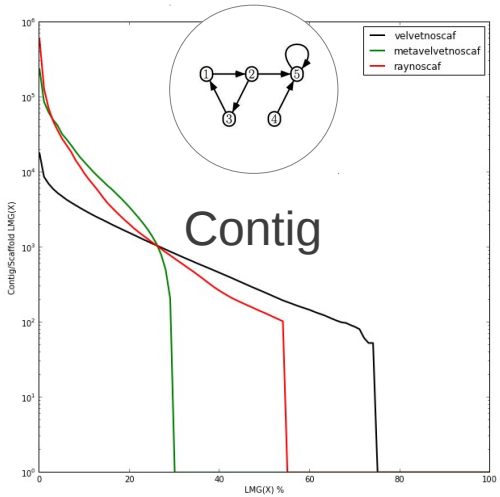
1) contig/scaffold length distribution

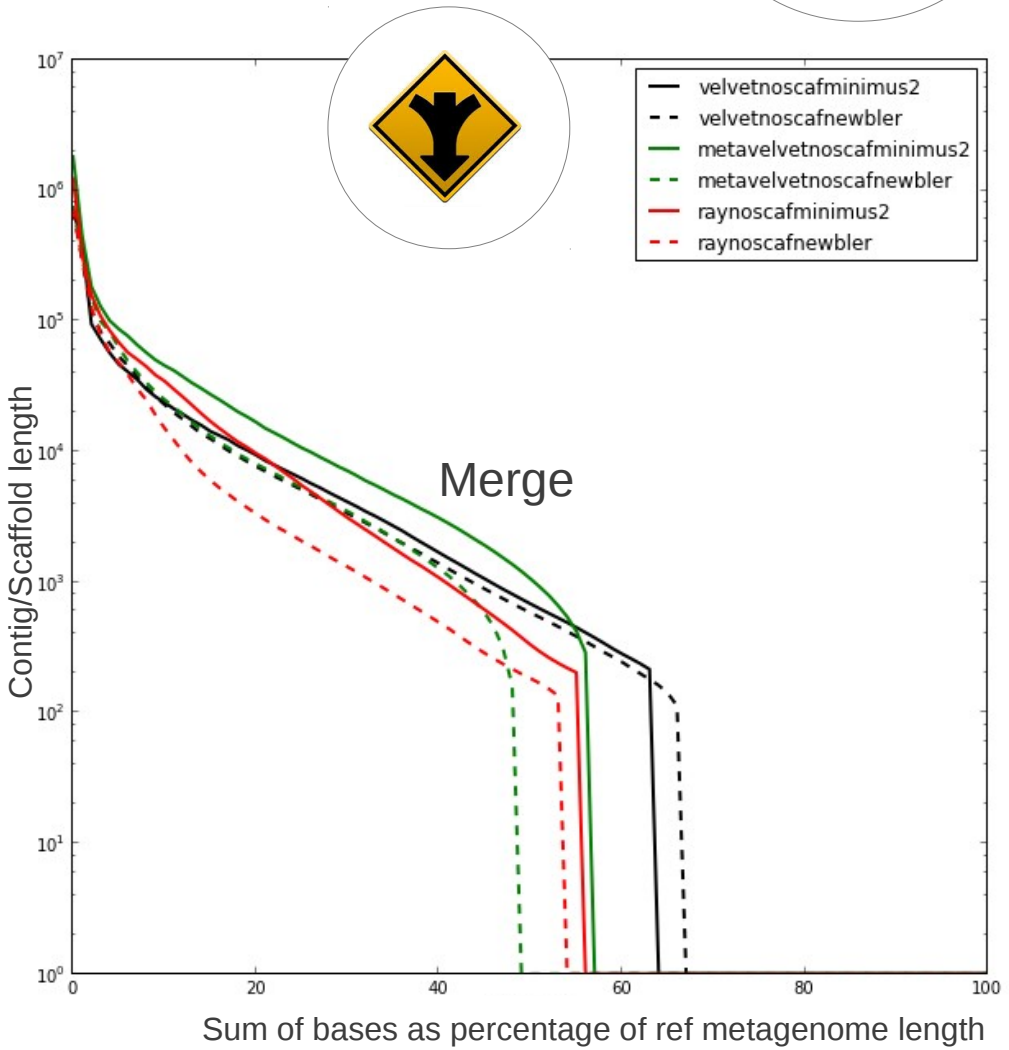


Difficult to say which is winning based on length distribution alone.

Benchmark Results

1) contig/scaffold length distribution



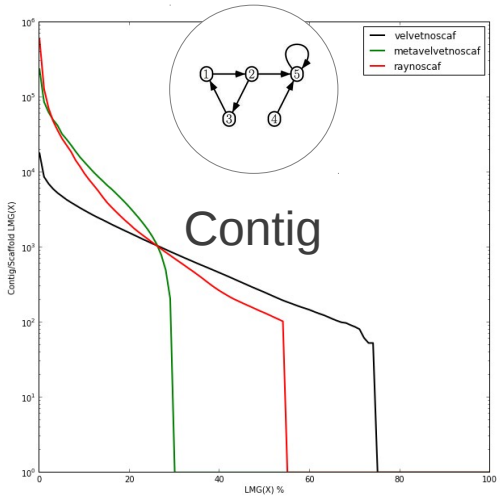


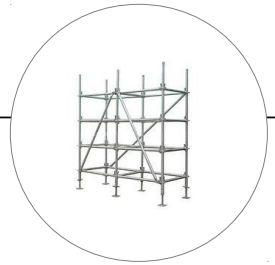
Merging increases lengths and makes length distributions more similar.

L50 before → after
V 665 → 3487 / 2553
M-V 6892 → 43685 / 45085
R 919 → 4076 / 1731

Benchmark Results

1) contig/scaffold length distribution





Scaffolding most notable with Velvet and Meta-Velvet

L50 before → after
V 665 → 4453
M-V 6892 → 12604
R 919 → 1002

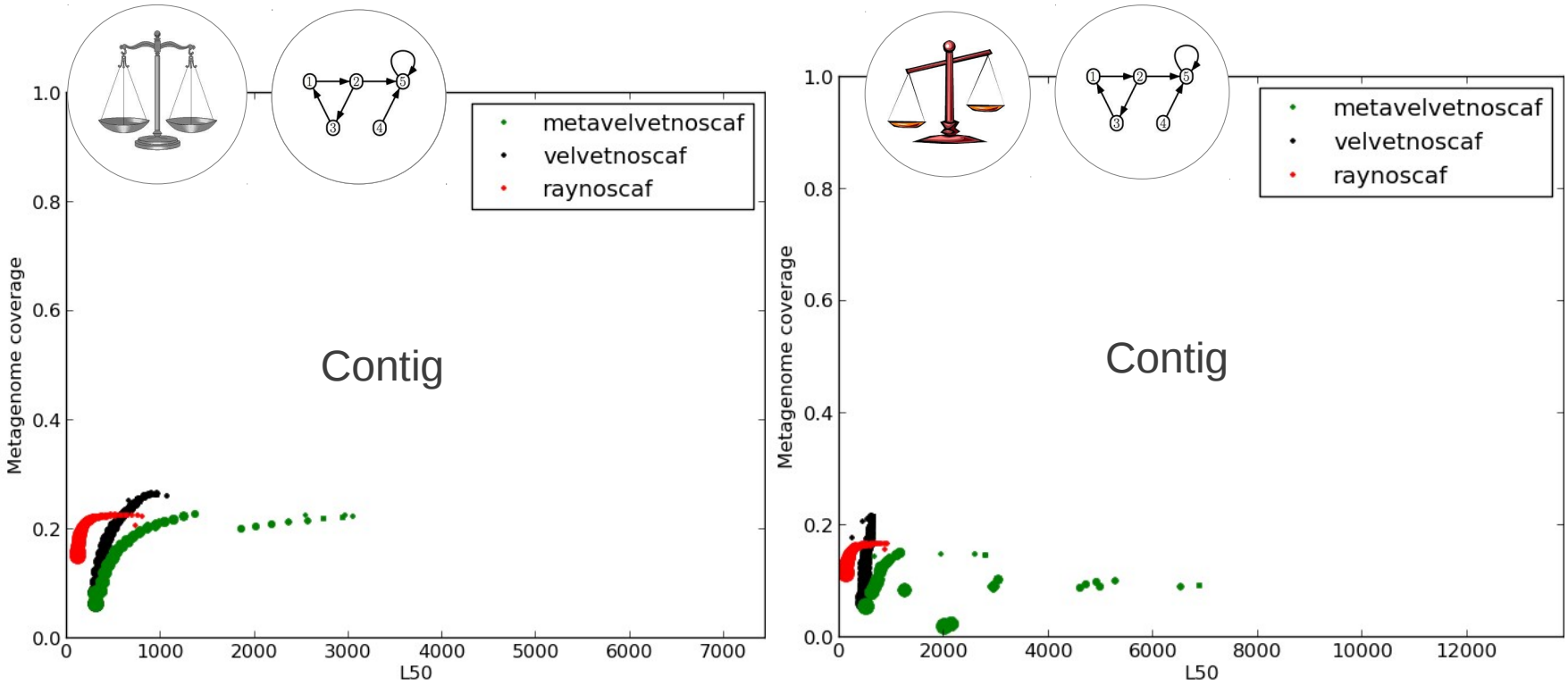
Benchmark Results

2) contig/scaffold coverage of the reference metagenome

- So the length distributions don't say a lot, how much of the reference metagenome is actually covered?

Benchmark Results

2) contig/scaffold coverage of the reference metagenome



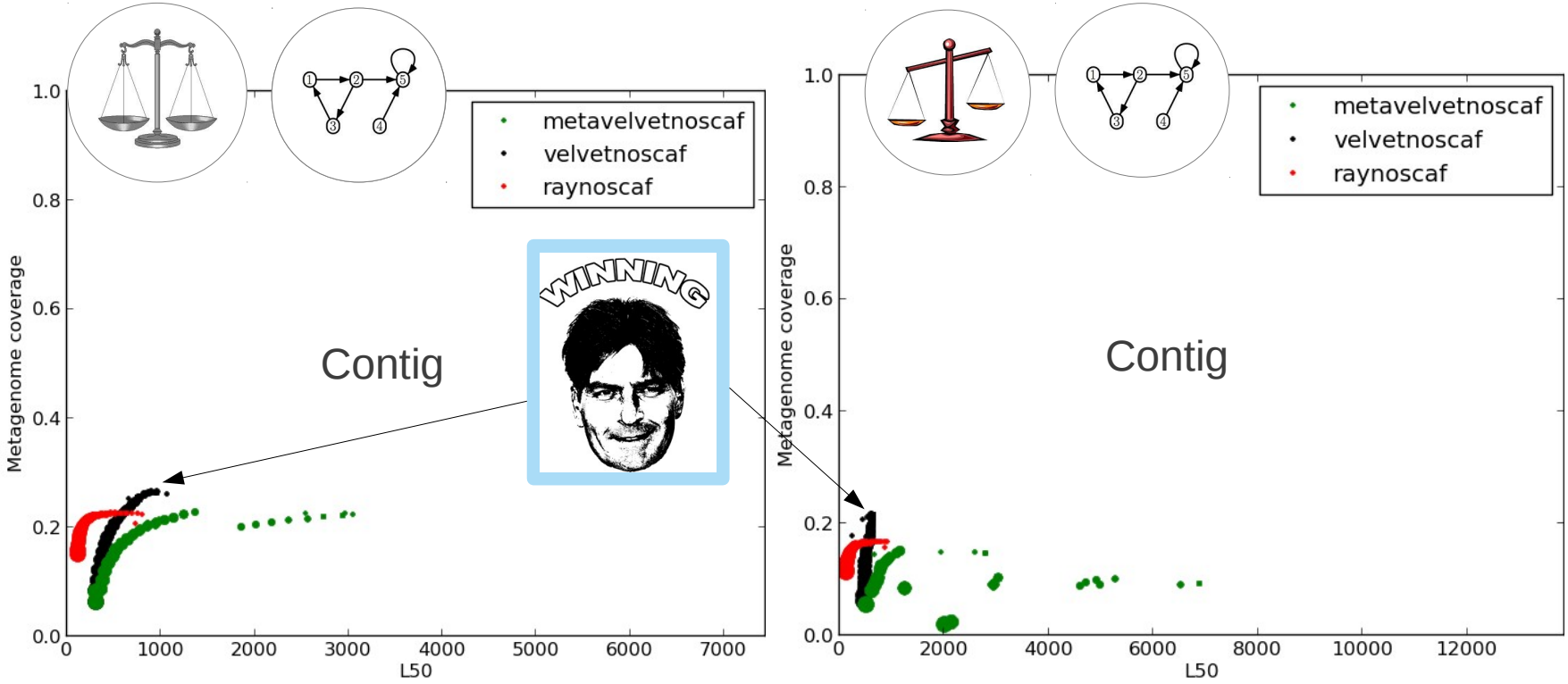
Metagenome coverage:
Number of non-overlapping bases covered by the assembly expressed as ratio of entire metagenome

Each dot is an assembly

Point size indicates kmer size (21-79)

Benchmark Results

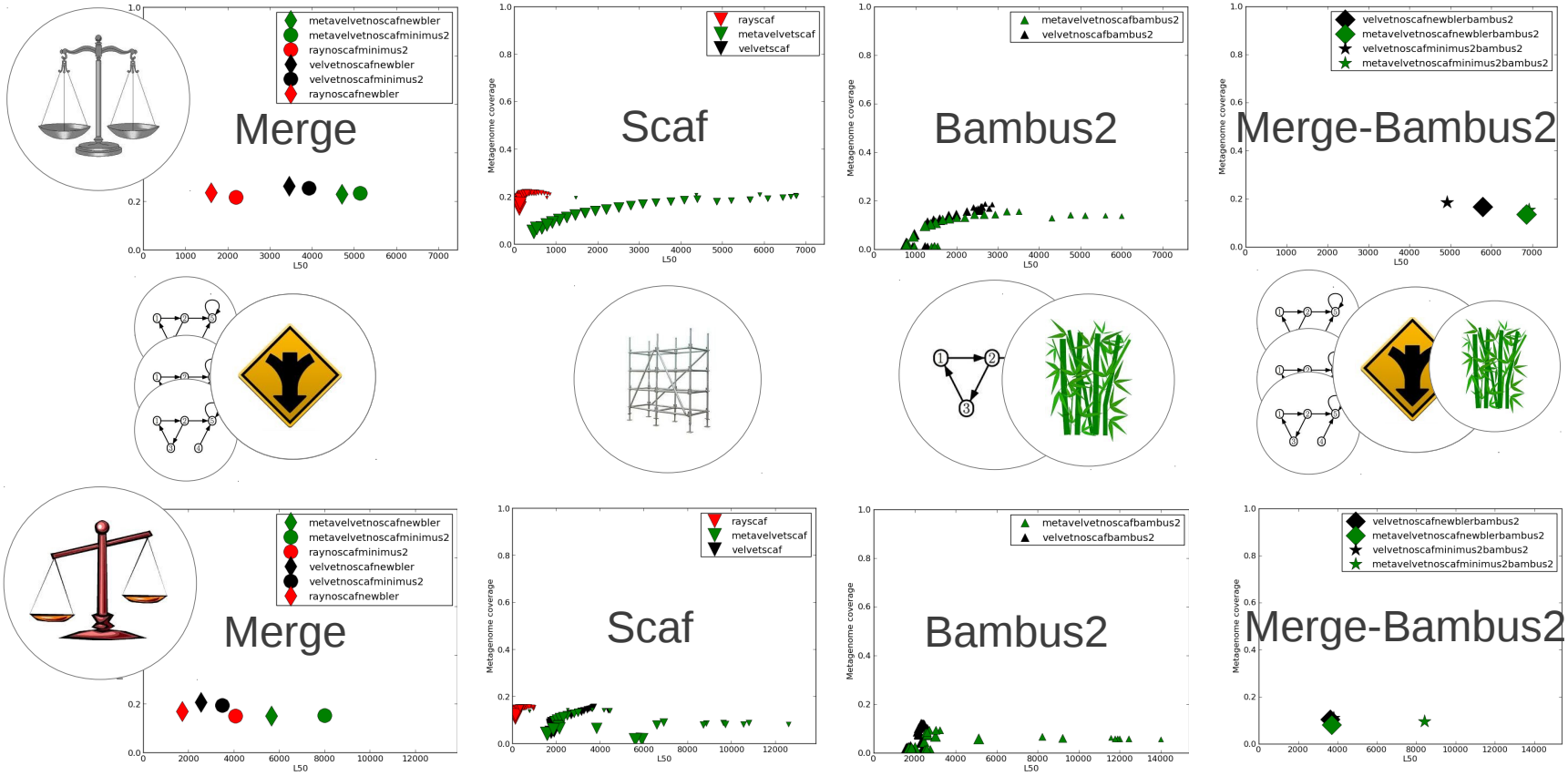
2) contig/scaffold coverage of the reference metagenome



Velvet does a good job covering the metagenome.

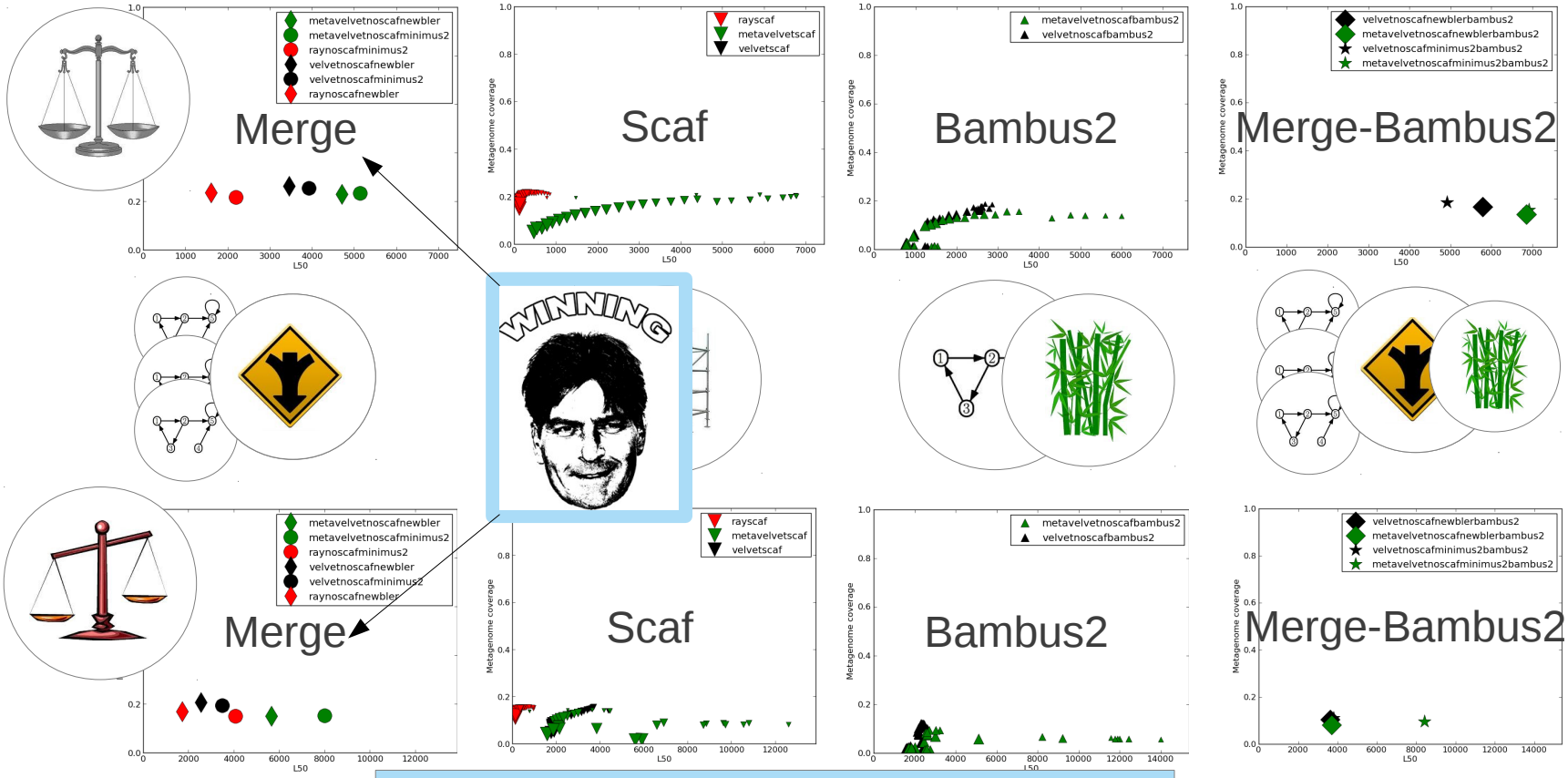
Benchmark Results

2) contig/scaffold coverage of the reference metagenome



Benchmark Results

2) contig/scaffold coverage of the reference metagenome



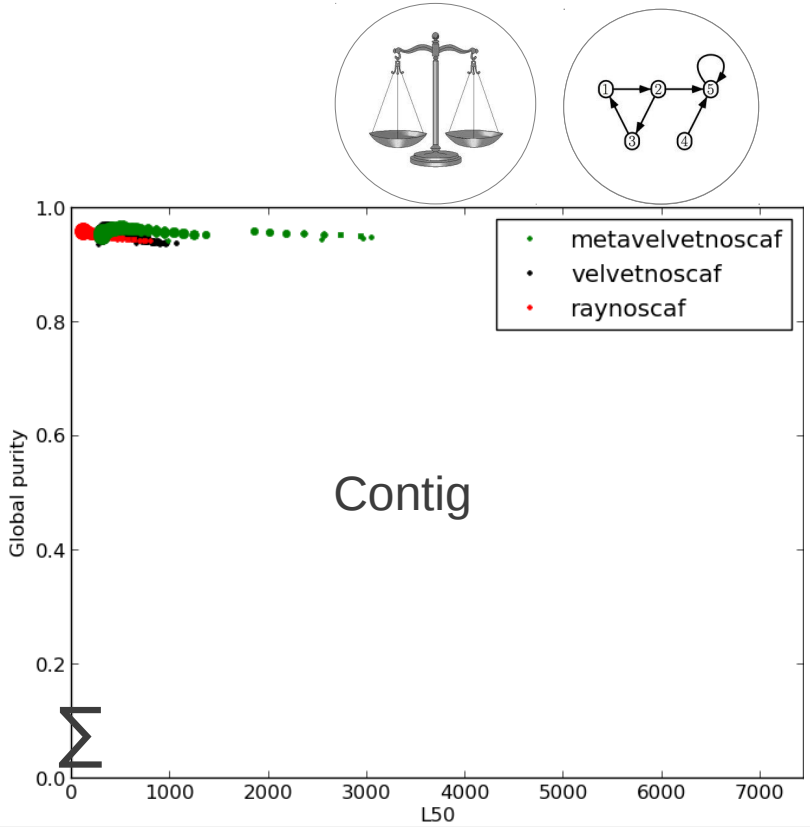
Merging increases length while keeping coverage high. Still original Velvet contigs win overal

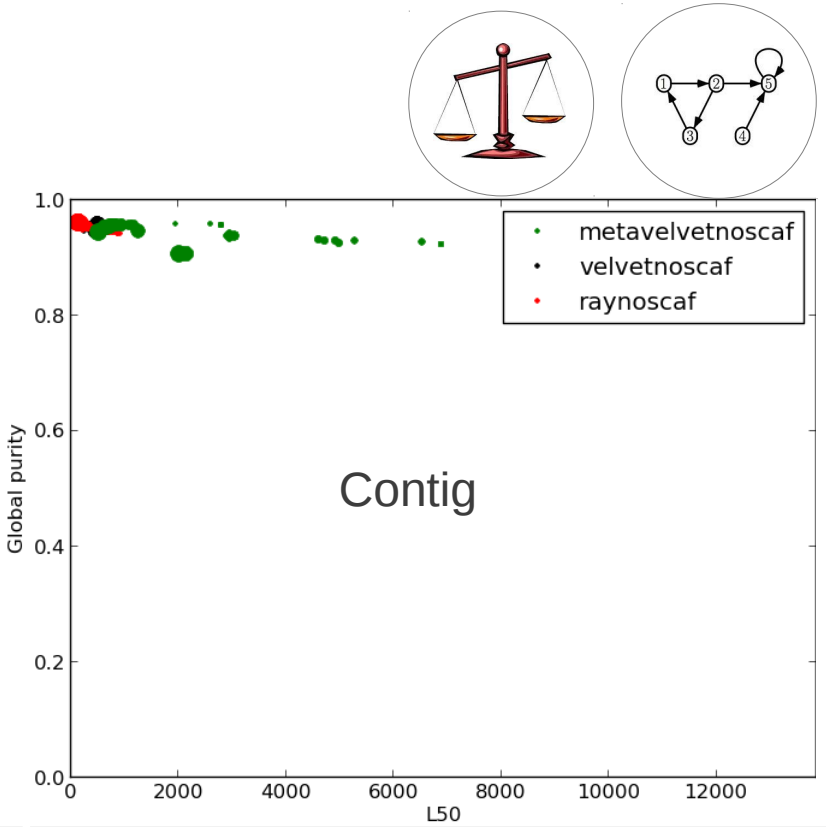
Benchmark Results

3) chimericity and erroneousness of the contigs/scaffolds
   - If lengths increase, but coverage doesn't. Do we have duplicate contigs or erroneous contigs?

Benchmark Results

3) chimericity and erroneousness of the contigs/scaffolds





Global purity:

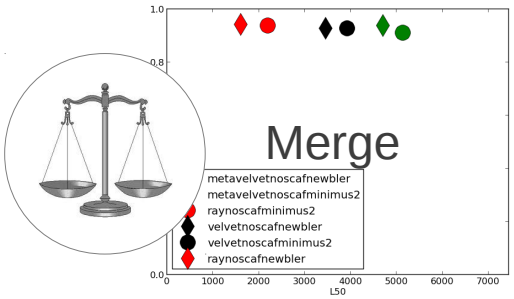
$$\sum_{\text{contigs}} \frac{\#\text{ bases in best alignment contig}}{\text{total nr of bases assembly}}$$

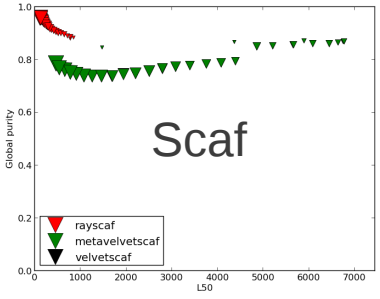
Each dot is an assembly

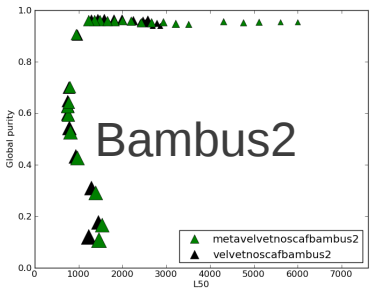
Point size indicates kmer size (21-79)

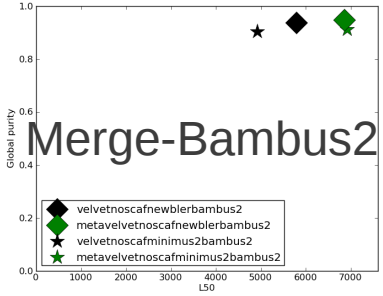
Benchmark Results

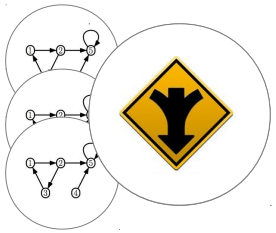
3) chimericity and erroneousness of the contigs/scaffolds

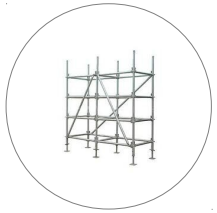


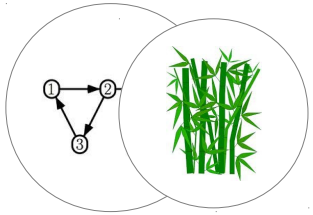


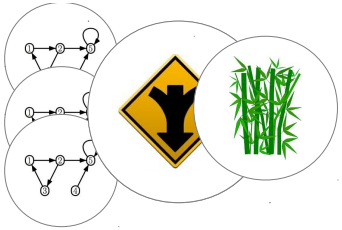


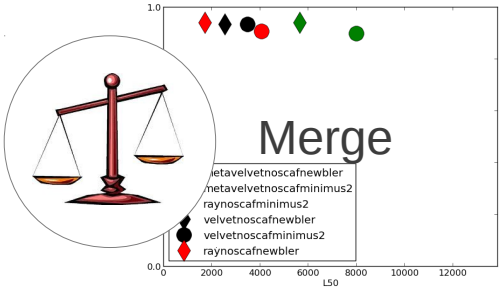


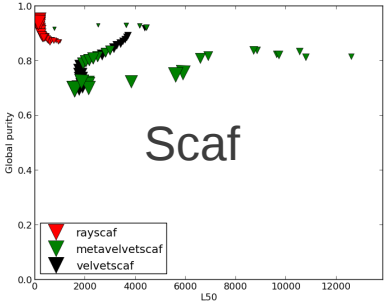


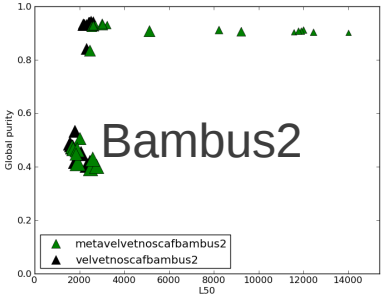


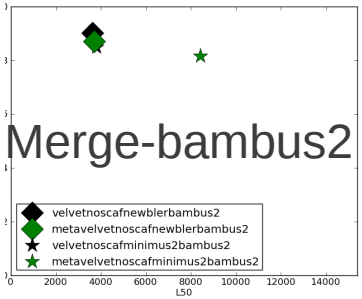






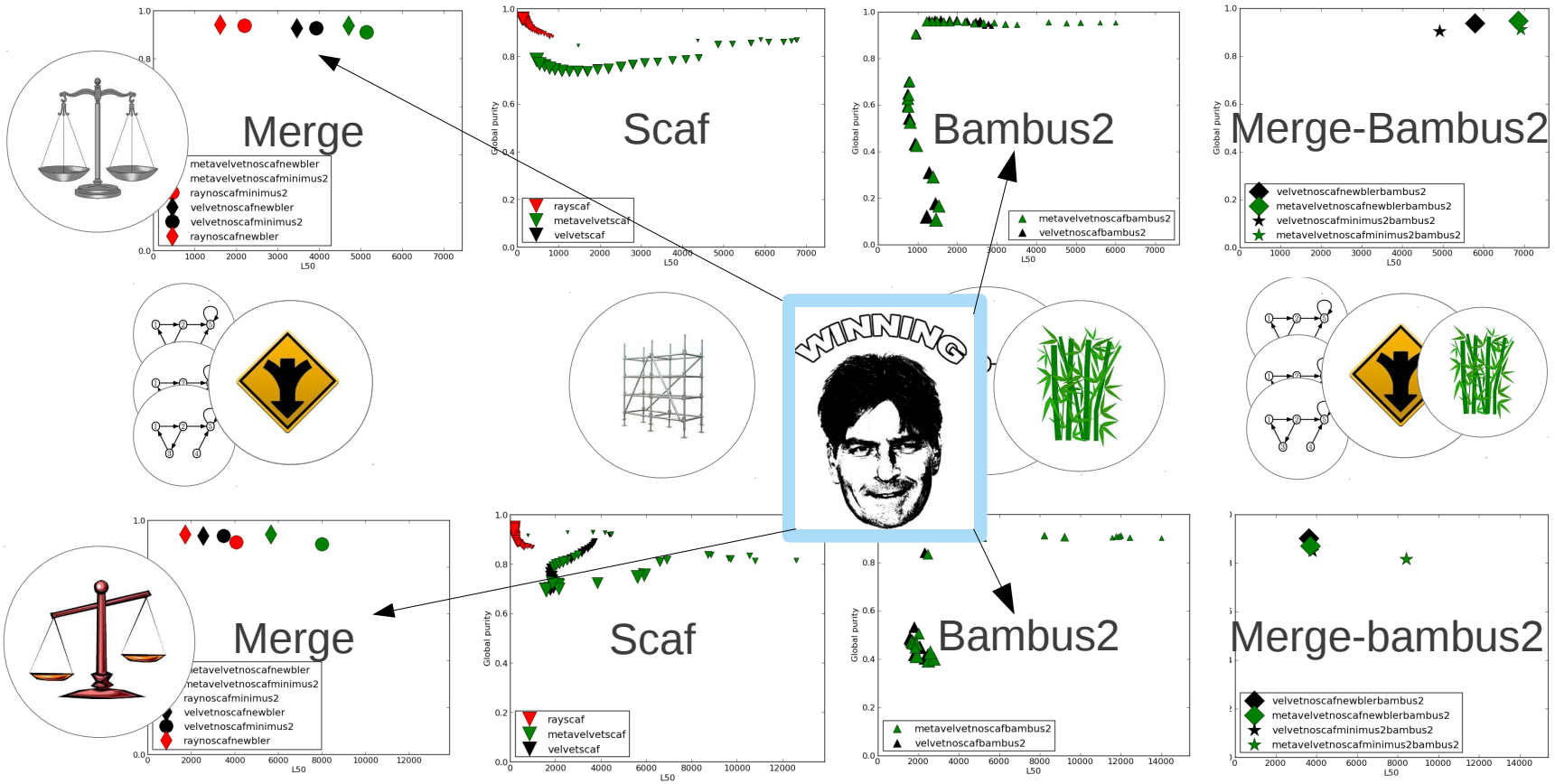






Benchmark Results

3) chimericity and erroneousness of the contigs/scaffolds

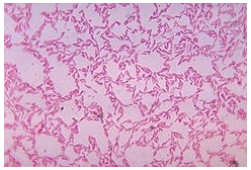


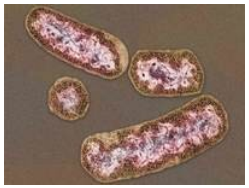
Ergo, Merging and Bambus2 both perform well purity-wise

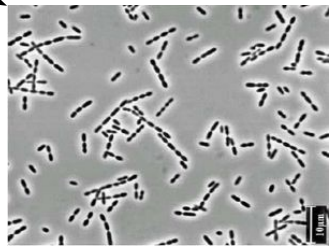
Conclusions

- Difficult to name one true winner. Depends on what the post-processing will be like
  -  If interested in functional annotation: Ray or Velvet. Velvet preferred if annotation works on really short contigs 100-1000 (more coverage of metagenome).
  -  If only interested in long contigs and less so in their purity, perhaps choose Meta-Velvet.
  -  Merging seems to work quite well although you lose some metagenome coverage
    - Might want to avoid scaffolding since it doesn't work that well
      -  bambus2 in particular loses a lot of metagenome coverage
      -  Internal scaffolding works better than bambus2, but merging alone does a better job

I was gonna put your picture as well, but I got lazy so here are some pictures of possibly highly expressed bacteria in your gut instead that I'm equally grateful to







Stockholms universitet

University of Glasgow

SciLifeLab

Thanks!
Tack!
Obrigado!
Kiitos!
Teşekkürler!
धन्यवाद!
நன்றி!
Amesegënallô
Hvala!
Gracias!
謝謝
ขอบคุณ
شكرا

Questions?