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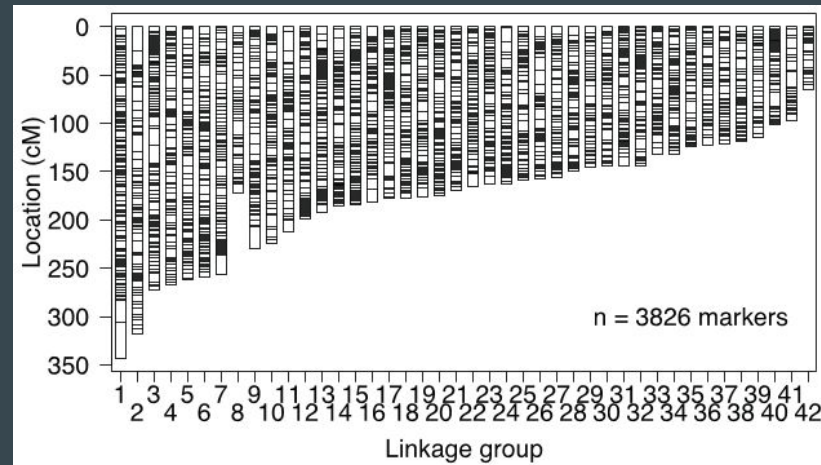
## Linkage Map Comparison made Easy

Presentation authors: Eric normandeau, Ben Sutherland, Louis Bernatchez

# Creating Maps

# The Story behind MapComp

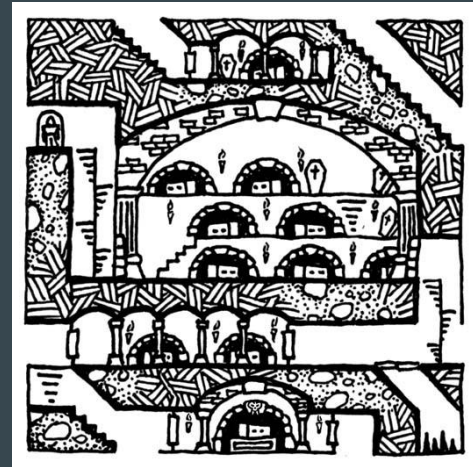
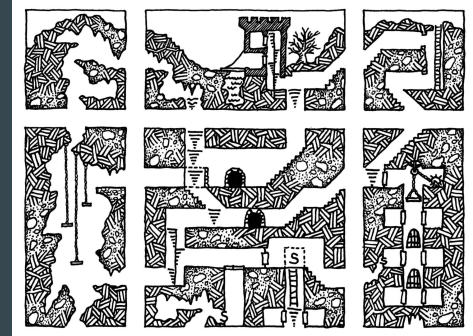
- Used to be more painful with Microsats
- Easier now with RAD-Seq (RAD, GBS...)
- Maps have much higher density
- Creating linkage maps is complex
- Different map making software
- How do we validate maps?



# Validating Maps

- Hard and done by hand
  - Identical markers (~microsatellites)
  - Comparing few maps
  - Fails for different GBS libraries
- 
- Incomplete assembled genomes
  - Cannot be used to validate a single map
  - Why not compare lots of maps together?

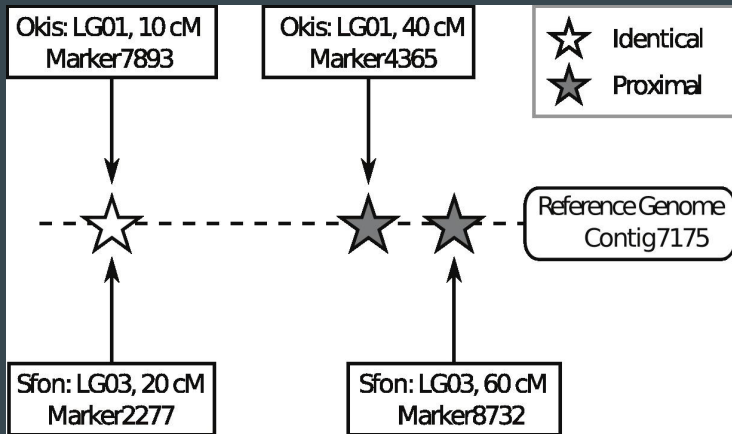
# The Story behind MapComp



# Comparing Maps

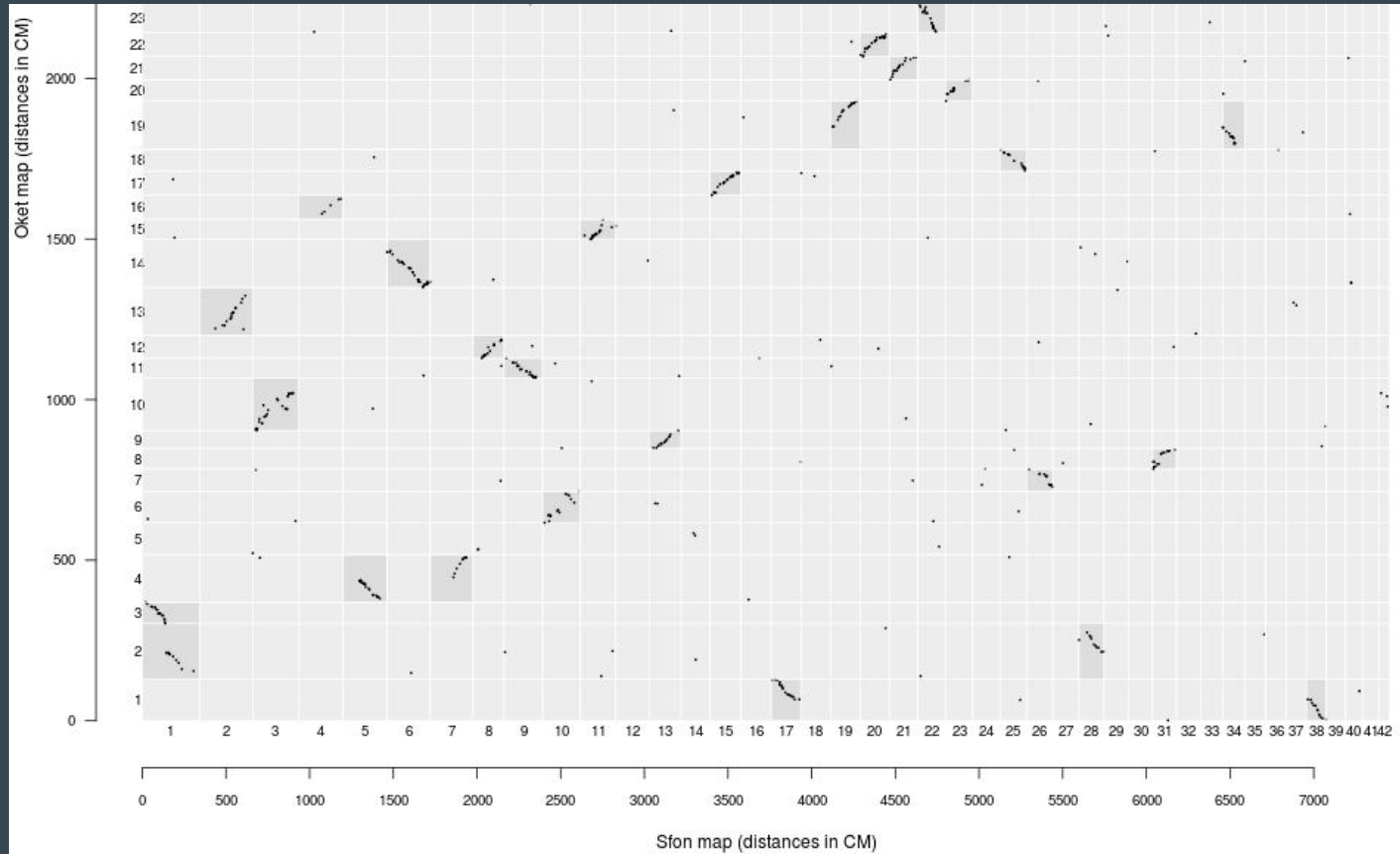
# The Story behind MapComp

- How do we compare 10 maps?
- Developed **MapComp** to solve this problem
- Use a reference genome
- Align all markers from all maps to it
- Find the best marker pairs per species pairs



# Comparing Maps

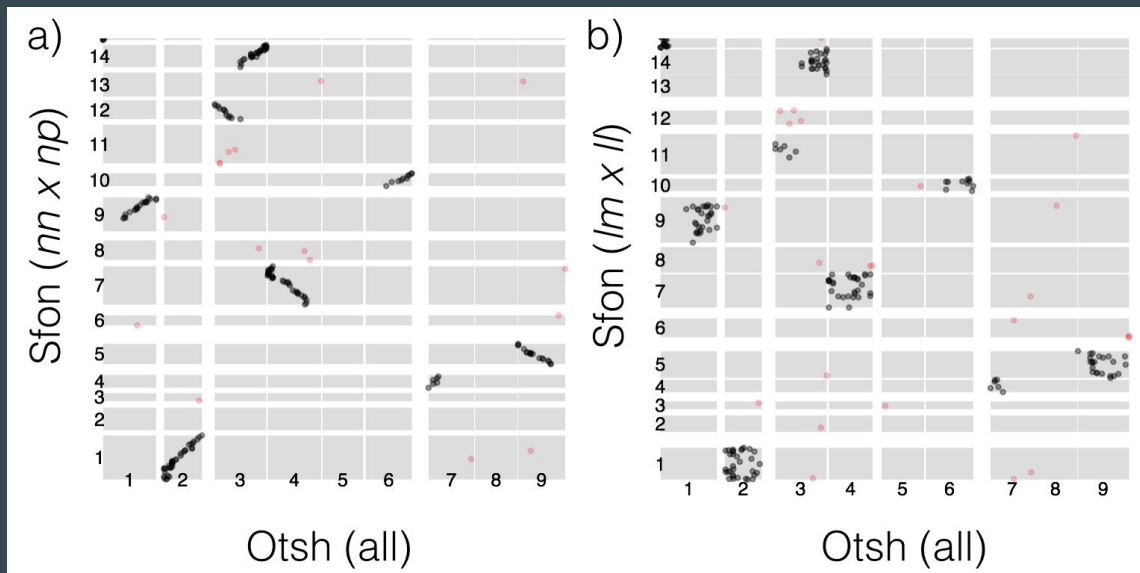
# The Story behind MapComp



# Comparing Maps

# The Story behind MapComp

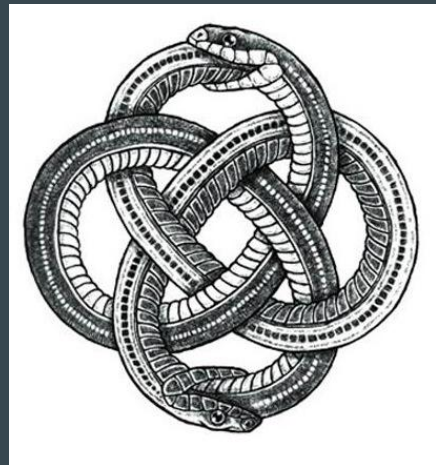
- Marker type validation



# Prerequisites

- Linux or MacOS
  - Python 2.7
  - numpy
  - bwa
  - samtools
  - R language
- 
- Hosted on Github

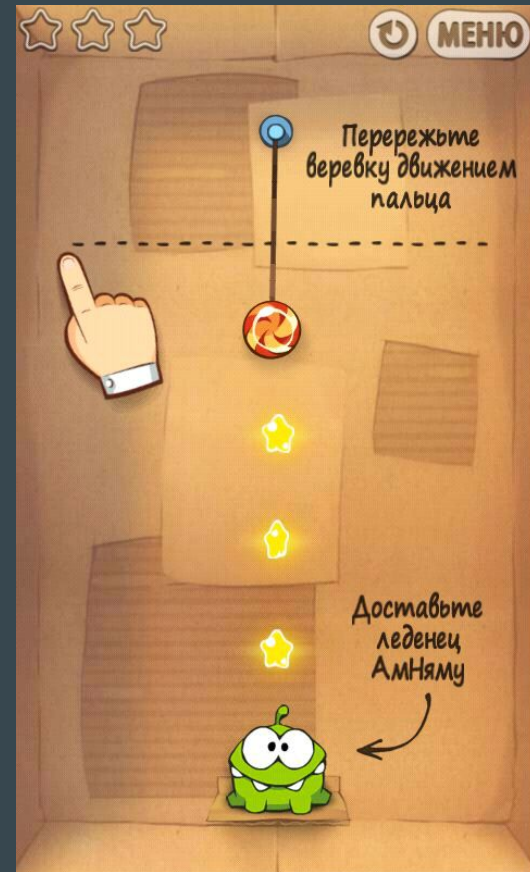
# Using MapComp



# Tutorial

- In [README.md](#)
- Renaming + indexing tutorial genome
- Tutorial input file (.csv)
- Creating fasta file
- Running MapComp
  - Mapping the reads
  - Identifying good loci
  - Extracting good loci
  - Creating best marker pairs
  - Generating figures

# Using MapComp

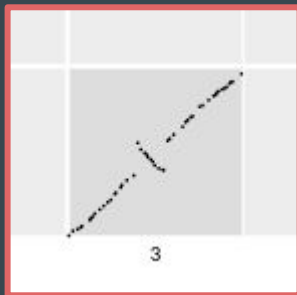




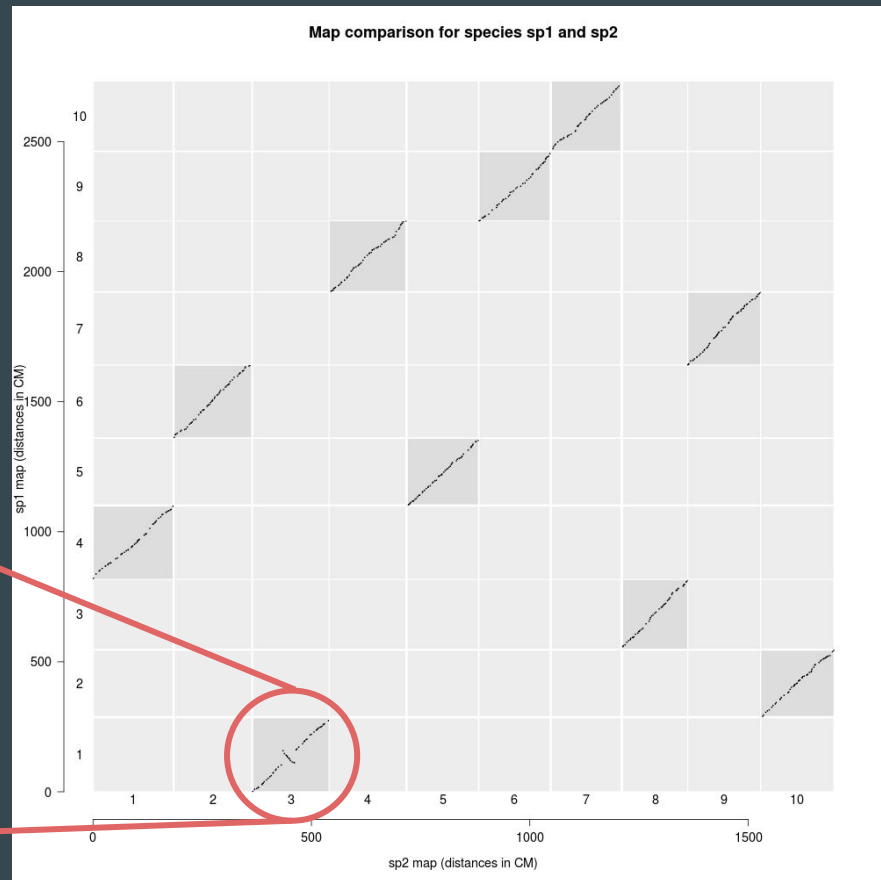
# Looking at the output

- Map comparison figures
- Corresponding LGs
- Intermediate files
- Is this for real?

Species1	LG	Species2	LG
sp1	1	sp2	3
sp1	2	sp2	10
sp1	3	sp2	8
sp1	4	sp2	1
sp1	5	sp2	5
sp1	6	sp2	2
sp1	7	sp2	9
sp1	8	sp2	4
sp1	9	sp2	6
sp1	10	sp2	7



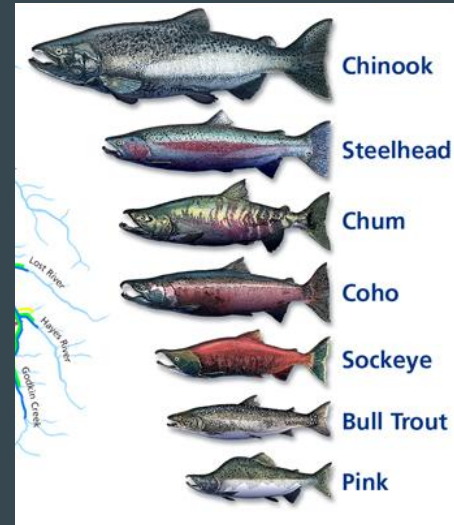
# Using MapComp



# Using with Real Data

- Brook char (*Salvelinus fontinalis*) data from:  
Sutherland BJC, Gosselin T, Normandeau E, Lamothe M, Isabel N, Bernatchez L. Novel method for comparing RADseq linkage maps reveals chromosome evolution in salmonids. bioRxiv. 2016: 1-44. doi:10.1101/039164  
<http://biorxiv.org/content/early/2016/02/09/039164>
- Map data of other salmonids (cited papers)
- Fragmented genome (works if big scaffolds)

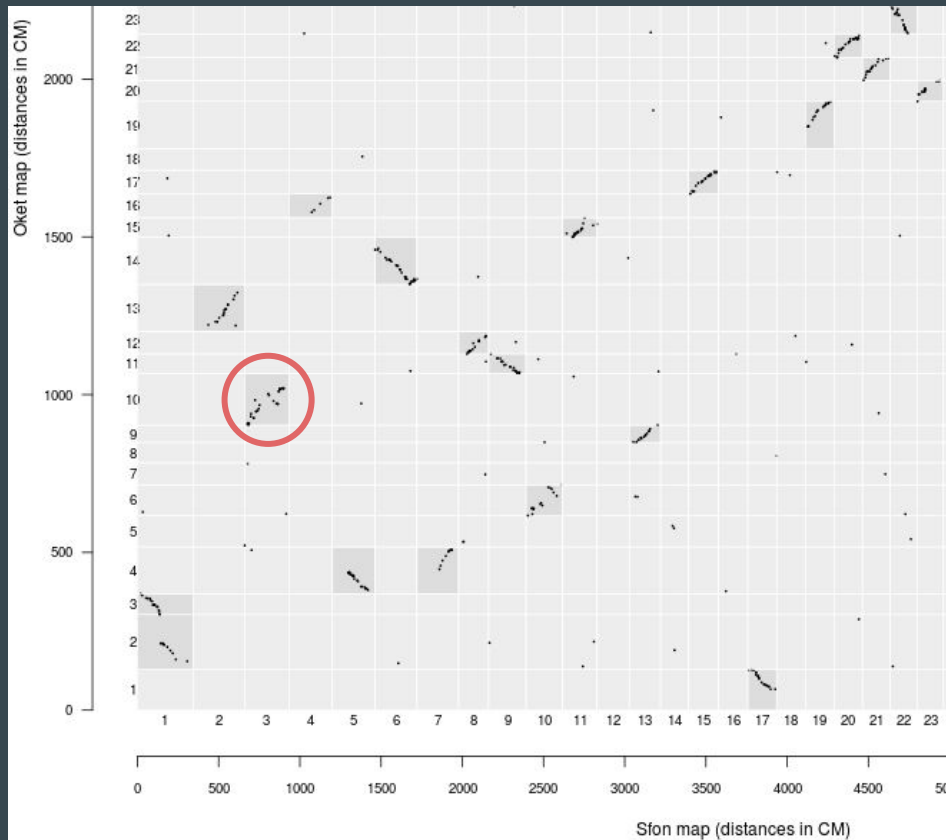
# Using MapComp



# Comparing all the maps

- All maps correlate well
- *Salvelinus fontinalis* = good
- Inversions
- Corresponding LGs
- Fusions and fissions

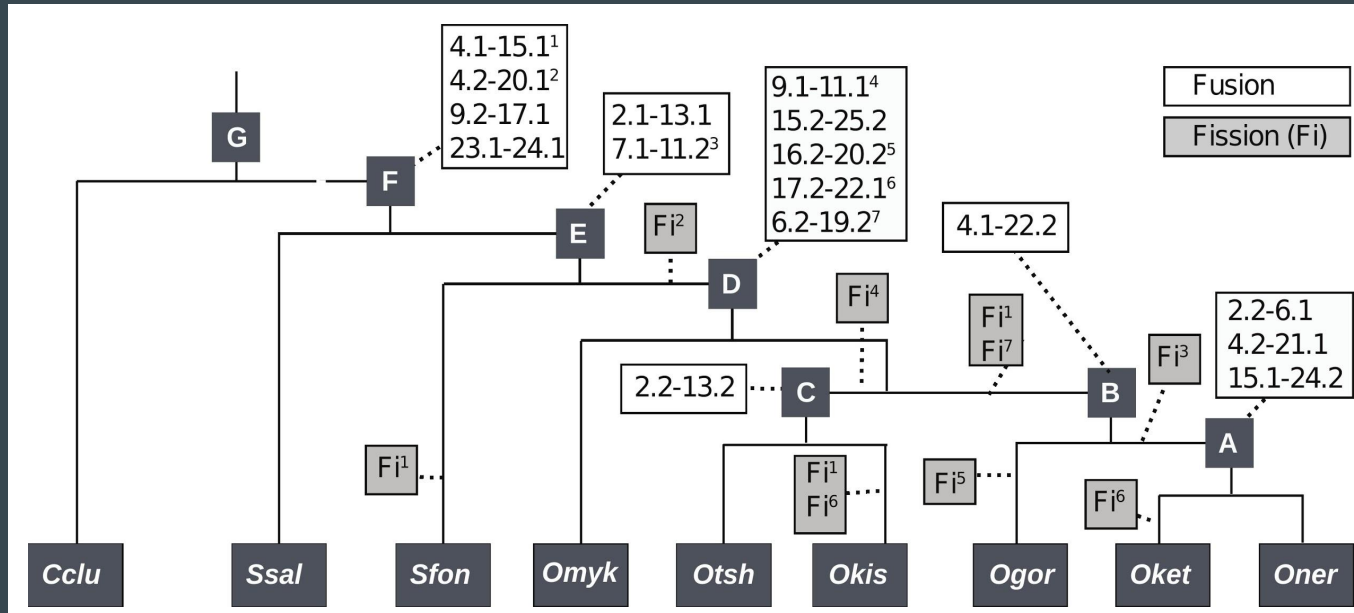
# Using MapComp



# Chromosome Evolution

# Using MapComp

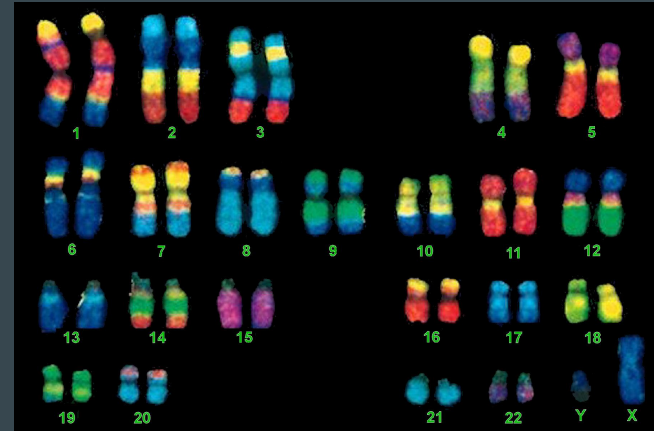
- Detailed portrait of chromosome evolution in salmonids
- Reconstructing / validating phylogeny
- Orthology of chromosome arms for ALL species



# Finding Chromosomes

## Other Uses

- SNPs linked to a trait (eg: sex)
- What LG do they belong to?
- Use MapComp with a good map
- Add your markers
- Find markers in .info file
- Link corresponding linkage groups



# Transferring Positions

## Other Uses

- Anonymous markers
- Can we order them based on another map?
- Again, use MapComp with a good map
- Add your markers
- Find markers in `.info` file
- Transfer corresponding marker positions
- Should be used with caution



# Get creative!

# Other Uses

- Test it on your favorite species!
- There are probably other use cases



# Famous Last Words

# Conclusion

- I am not afraid to die. *Charles Darwin*
- They couldn't hit an elephant at this distance. *John Sedgwick*
- I wish I'd drunk more champagne. *John Maynard Keynes*

- You can find MapComp here:  
[github.com/enormandeu/mapcomp](https://github.com/enormandeu/mapcomp)
- And the article here:  
<http://biorxiv.org/content/early/2016/02/09/039164>

