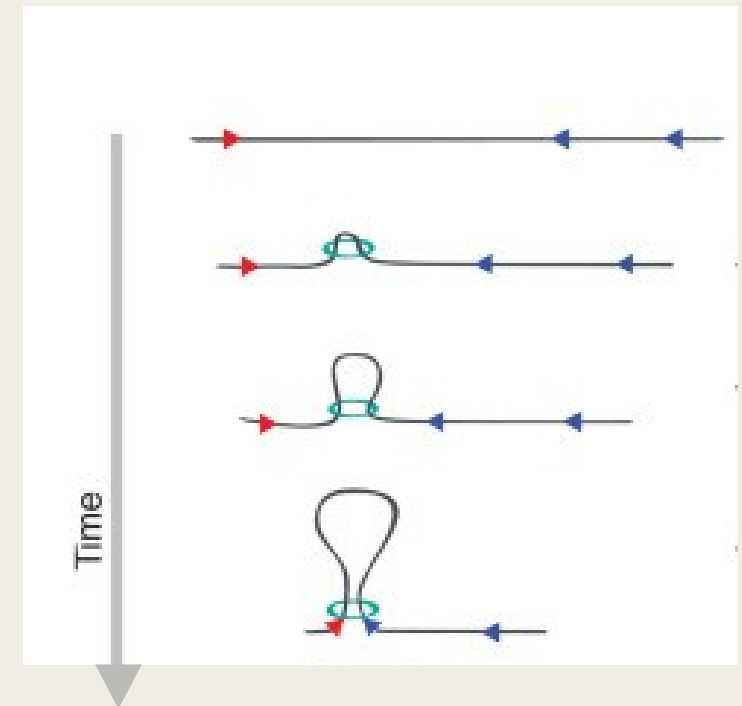# LOOP CALLERS

*Relating chromatin loops to GWAS studies in CLL*

CARLOS MADARIAGA ARAMENDI
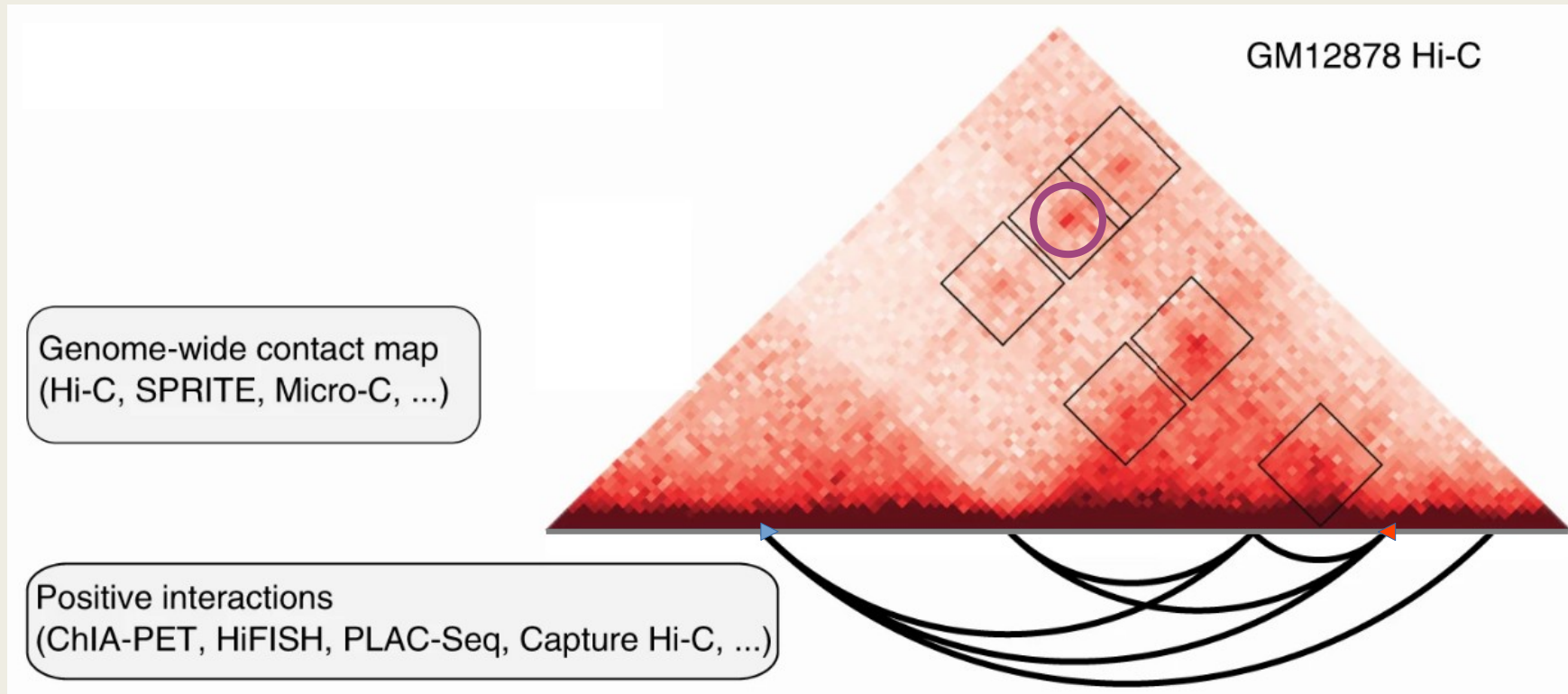
François Serra – Alba Lepore – Jon Sánchez

# Chromatin loops

- What are they?
- How they occur?
- What is it function?
- When they happen?
- Types of looped structures



*The Cohesin Release Factor WAPL Restricts Chromatin Loop Extension*

# Chromatin loops

# Definition and purpose

Tools that implement an algorithm
which detects chromatin loops

This is made using Hi-C data; protocol derived
from Chromosome Conformation Capture (3C)
and its successors (4C & 5C), that allows to study
the 3D structure of genomes

Using Hi-C data we can create an interaction map
of the chromatin ,so we can infer the chromatin
loops reflecting interactions of promoters & enhancers,
gene loops, etc.
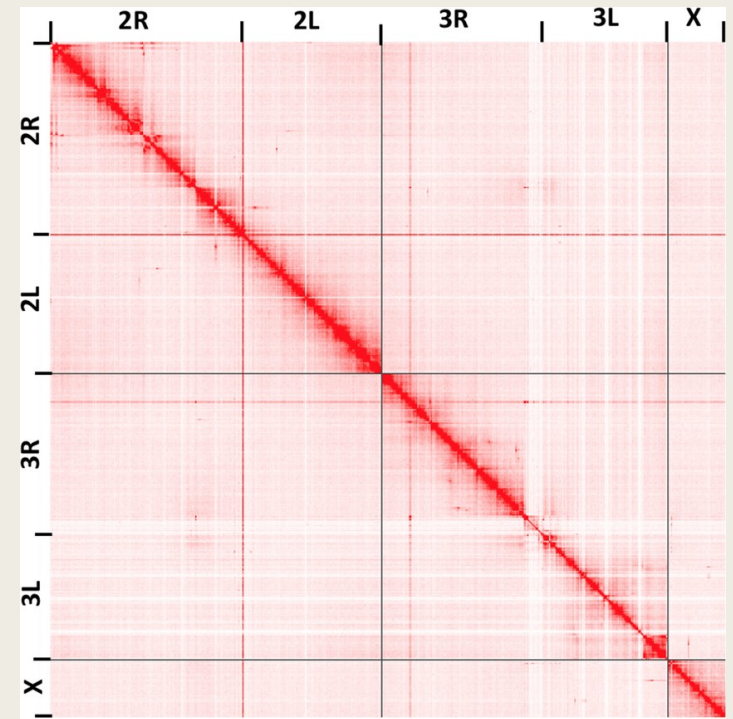


*Hi-C interaction map for assembled A. Funestus scaffolds generated using the Juicebox Hi-C visualization program*

# Different Tools Available

- The different tools detect different loops

- Also the number of loops detected is different

- More accuracy analyzing the intersecting loops



HiCCUPS HiCExplorer
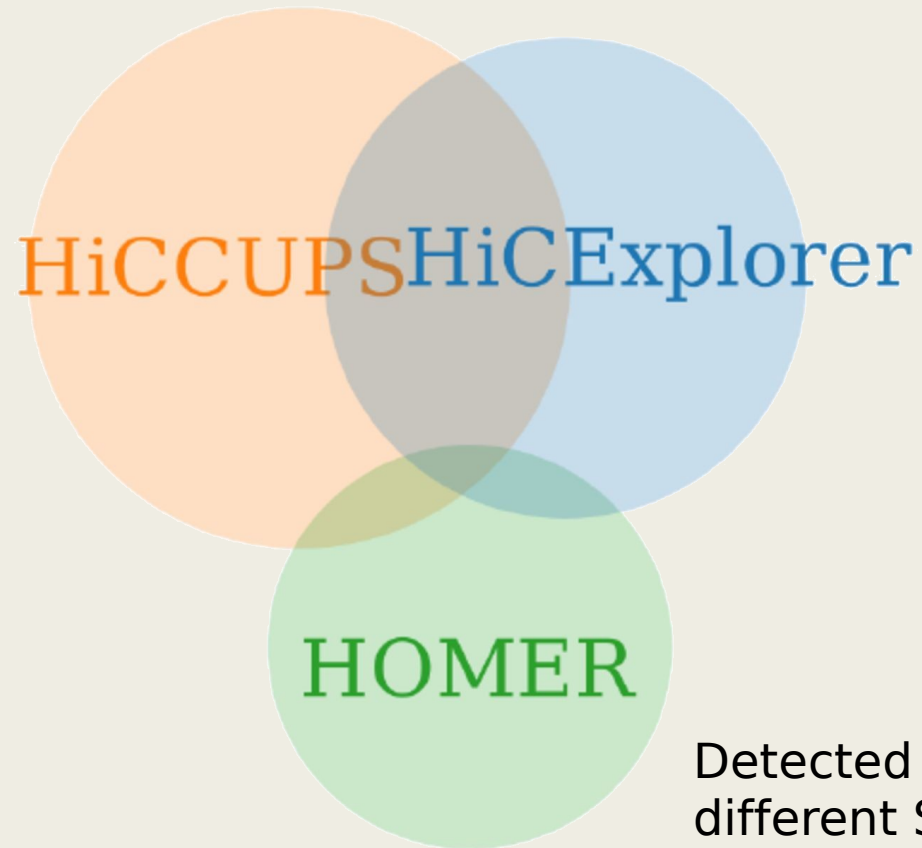
HOMER

Detected Loops by different Software tools

# HOMER

■ **H**ypergeometric **O**ptimization of **M**otif **E**n**R**ichment

■ Set of Motif Discovery and next-gen sequencing analysis too

■ Analyze ChIP-Seq, GRO-Seq, RNA-Seq, DNase-Seq and Hi-C

■ Installation: Using perl by command line

■ Procedure: Trim FASTQ files, align them to the reference genome and

assembly them into a HOMER-style tag directory. After that, the analysis

is carried out to find the loops and regions of our interest.

■ We can also use Hi-C Summary files (tab-delimired text files)

# HiCCUPS

- Juicer tool that implements an algorithm for finding chromatin loops

- Juicer: one-click pipeline for processing Hi-C datasets

- Installation: It requires Juicer, which also requires some

dependencies, as GNU, BWA or CUDA and NVIDIA GPU

- Usage: You need to specify the matrix size, the chromoso

the resolution(s), the Hi-C file to analyze and the output dire

- It outputs several files; the 'merged_loops' file is what we
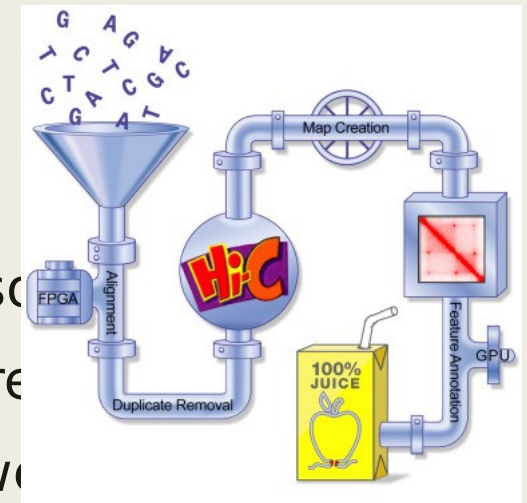
# MUSTACHE

- Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation

- Tool for multi-scale detection of chromatin loops from Hi-C and Micro-C contact maps in high resolutions

- Several ways to install it: Conda (recommended), Docker, PIP or Github.

- Input: Text format, Juicer .hic files, Cooler .cool and .mcool files. Output: TSV format

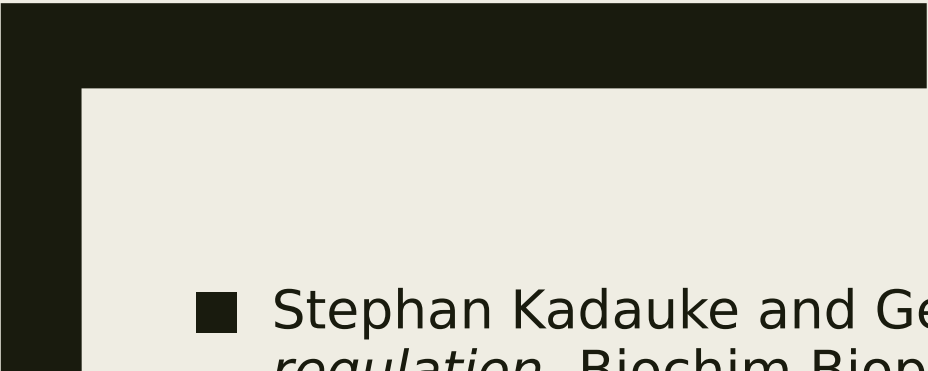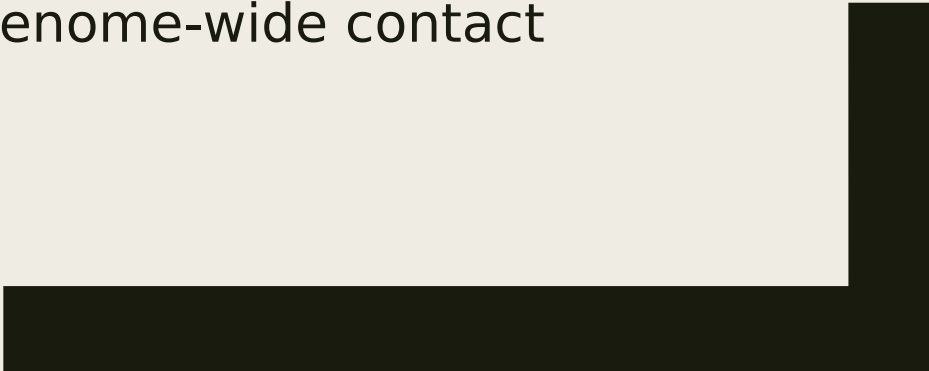- Subject chromosome and resultion also need it to run the tool.

# PEAKACHU

- Unveil Hi-C Anchors and Peaks

- Takes genome-wide contact data as input and returns coordinates of likely interactions such as chromatin loops.

- ML framework based on sklearn to generate random forest models

trained on example interactions predicted by an arbitrary experiment

- Designed to accept any genome-wide contact map (Micro-C…)

- Requires several packages. Conda recommended to install

- Input: .cool or .hic files. Also .bedpe text file with training data.

- It can work as a regular loop caller with the 'score_genome' function
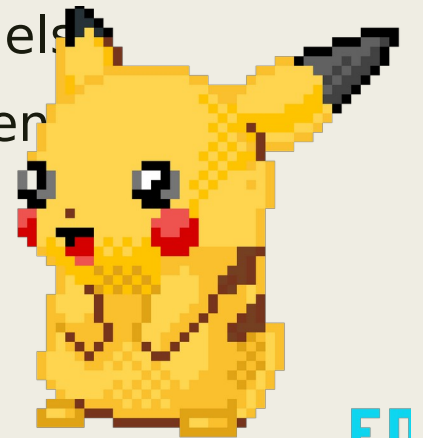
# Traditional vs Modern Loop Callers
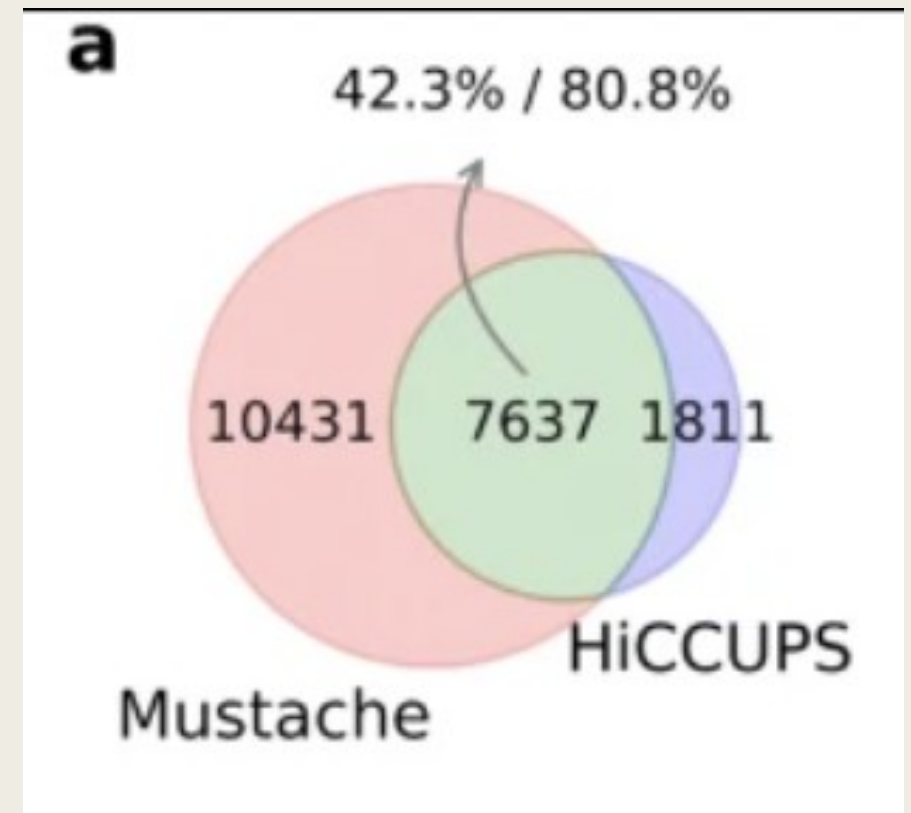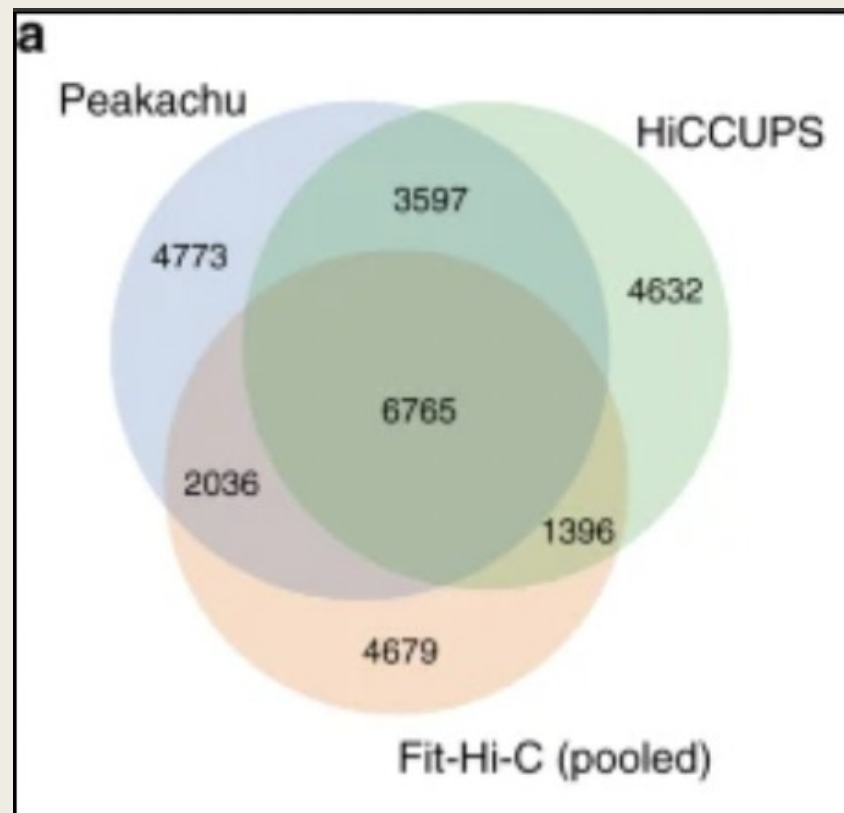
- Stephan Kadauke and Gerd A. Blobel. *Chromatin loops in gene regulation* Biochim Biophys Acta. 17–25 (2008)

- Joachim Wolff, Rolf Backofen, Björn Grüning. *Loop detection using Hi-C data with HiCExplorer*. bioRxiv. (2020)

- Salameh, T.J., Wang, X., Song, F. et al. A supervised learning framework for chromatin loop detection in genome-wide contact maps. Nat Commun 11, 3428 (2020)

# References

THANK YOU FOR YOUR ATTENTION! ANY QUESTIONS?