

Thesis

# Chromatin Compartments and Selection on X

Søren Jørgensen

2024-11-28





# Chromatin Compartments and Selection on X

How Edges of Active Chromatin Align with Selection Regions in  
Primates

Søren Jørgensen



2024-11-28

Submitted in fulfillment of the requirements of the degree of

“ 3-dimensional structure of chromatin brings light onto the mystery of selfish genes.

- Søren Jørgensen //

# Table of contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
1.1	Sexual reproduction (spermatogenesis, meiosis) . . . . .	1
1.2	Selfish genes (and randomness) . . . . .	1
1.3	High-Throughput Chromosome Conformation Capture (Hi-C) . . . . .	2
<b>2</b>	<b>Methods</b>	<b>3</b>
2.1	Downloading Data and Project Structure . . . . .	3
2.2	Handling coolers (Or: preparing coolers) . . . . .	5
<b>3</b>	<b>Results</b>	<b>7</b>
<b>4</b>	<b>Discussion</b>	<b>9</b>
	<b>Bibliography</b>	<b>11</b>



# 1 Introduction

## 1.1 Sexual reproduction (spermatogenesis, meiosis)

The production of gametes in a sexually reproducing organism is a highly complex process that involves numerous elements. Spermatogenesis, the process of forming male gametes, involves four stages of differentiation from a germ cell through *spermatogonia*, *pachytene spermatocyte*, and *round spermatids* to *spermatozoa*, or *sperm* (Wang et al. 2019), and it is the very basis of male reproduction. The specialized cell division of meiosis neatly handles the pairing, recombination, and segregation of homologous chromosomes, thereby ensuring proper genetic distribution. Deeply understanding the steps of molecular steps of reproduction and how our genetic material is inherited is essential in biology, bringing insight to areas such as speciation, population diversity, and (male) infertility.

## 1.2 Selfish genes (and randomness)

The conventional story of meiosis in gametogenesis is one of random segregation of the sex chromosomes. They split into haploid gametes, where each chromosome has an equal chance of being passed on to a gamete. That seems like a fair game, but what if some genes are cheating the system by making others less viable. A meiotic driver is a selfish gene element that modulates meiosis and preferentially transmits its own allele through meiosis, regardless of the downstream fitness effects it may have (good or bad) on the organism it is part of. This phenomenon challenges the traditional understanding of selection, extending its scope beyond the fitness effects on an organism to include selective pressures at the molecular level. For example, if some genes on the X chromosome create a disadvantage for gametes that *do not* contain those genes, making sure the Y chromosome is not as viable as the X, resulting in a sex imbalance and possibly numerous other downstream effects. That is exactly what is coined *sex chromosome meiotic drive* (Jaenike 2001), a result of selfish genetic elements.

Motivated by previous results in the Munch Research group (Munch 2024) on hybrid incompatibility and extended common haplotypes (Skov et al. 2023; Sørensen et al. 2023) that could be explained by meiotic drive, we wanted to investigate how these patterns correlate with chromatin compartments.

## 1 Introduction

### 1.3 High-Throughput Chromosome Conformation Capture (Hi-C)

Our DNA can be divided into different orders of structure. 3C focus on identifying the highest orders of organization inside the nucleus, that is, when the 30 nm thick coil of chromatin fibers folds into loops, Topologically Associating Domains (TADs), and chromatin compartments. Here, we narrow our focus on the largest of the structures, *compartments*, that is known to determine availability to transcription factors, thus making an *A* compartment *active*—and the *B* compartment *inactive*. The introduction of the Hi-C (high-throughput 3C) method (Lieberman-Aiden et al. 2009) opened new possibilities for exploring the three-dimensional organization of the genome.

## 2 Methods

In this project, we formulate two objectives:

**A**: Reproduce the Hi-C interaction maps and eigendecomposition from (Wang et al. 2019), with some modifications. We briefly use *HiCExplorer*, but change the analyses to use the *Open2C Ecosystem* (Open Chromosome Collective 2024) which have a Python API as well as command-line functions, which can be paired very well with Jupyter Notebooks. The majority of the data analysis was run with a *gwf* workflow, and the commands that were visually inspected were run in Jupyter Notebooks.

**B** Compare with regions of selection that are found in *papio anubis*, and maybe in *human* too. Investigate the biological meaning of the results.

All computations were performed on GenomeDK (GDK) [ref], an HPC cluster located on Aarhus University, and most of the processing of the data was nested into a *gwf* workflow [ref], a workflow manager developed at GDK. I would like to thank GDK and Aarhus University for providing computational resources and support that contributed to these research results.

The whole of this project is carried out with reproducibility in mind, so an effort (and quite a significant amount of time) has been put into documenting code and organizing the project for readability and transparency through a Quarto project [ref]. Therefore, all code, virtual environments and text is made available as a Quarto book, rendered directly from the GitHub repository with GitHub Pages []. To make this possible, the Quarto documentation has been extensively studied and discussed with *KMT* [ref, acknowledge].

### 2.1 Downloading Data and Project Structure

To reproduce the results from (Wang et al. 2019), I chose to use their raw data directly from the SRA portal [ref]. I filtered the data to contain all their paired-end Hi-C reads, and included only macaque samples. The data set also contains RNAseq data, and the same tissues for both macaque and mouse. The meta data for the data set was extracted into a runtable `SRA-runtable.tsv`. To get an overview of the data accessions used in this analysis, we will first summarize the runtable that contains the accession numbers and some metadata for each sample (Table 2.1). It adds up to ~1Tb of compressed `fastq` files, holding ~9.5 billion reads, roughly evenly spread on the 5 tissue types.

## 2 Methods

Table 2.1: The most relevant columns of the `SRA-runtable.tsv` file

Table 2.1

	source_name	BioSample	Run	GB	Bases	Reads
16	fibroblast	SAMN08375237	SRR6502335	29.771059	73,201,141,800	244,003,806
17	fibroblast	SAMN08375237	SRR6502336	22.755361	65,119,970,100	217,066,567
18	fibroblast	SAMN08375236	SRR6502337	21.434722	52,769,196,300	175,897,321
19	fibroblast	SAMN08375236	SRR6502338	21.420030	52,378,949,100	174,596,497
20	fibroblast	SAMN08375236	SRR6502339	10.207410	28,885,941,600	96,286,472
9	fibroblast	SAMN08375237	SRR7349189	52.729173	139,604,854,200	465,349,514
10	fibroblast	SAMN08375236	SRR7349190	53.085520	142,008,353,400	473,361,178
21	pachytene spermatocyte	SAMN08375234	SRR6502342	60.258880	150,370,993,500	501,236,645
22	pachytene spermatocyte	SAMN08375234	SRR6502344	27.146048	65,697,684,300	218,992,281
23	pachytene spermatocyte	SAMN08375234	SRR6502345	26.202707	63,490,538,700	211,635,129
0	pachytene spermatocyte	SAMN09427370	SRR7345458	55.970557	153,281,577,900	510,938,593
1	pachytene spermatocyte	SAMN09427370	SRR7345459	53.982492	144,993,841,200	483,312,804
11	pachytene spermatocyte	SAMN08375235	SRR7349191	51.274476	137,821,979,100	459,406,597
24	round spermatid	SAMN08375232	SRR6502351	20.924497	55,095,075,300	183,650,251
25	round spermatid	SAMN08375232	SRR6502352	41.133960	115,578,475,800	385,261,586
26	round spermatid	SAMN08375232	SRR6502353	36.444117	96,195,161,400	320,650,538
2	round spermatid	SAMN09427369	SRR7345460	38.244654	104,105,827,200	347,019,424
3	round spermatid	SAMN09427369	SRR7345461	53.996261	144,532,309,500	481,774,365
12	round spermatid	SAMN08375232	SRR7349192	52.384556	140,431,608,000	468,105,360
29	sperm	SAMN08375229	SRR6502360	26.653940	64,752,370,800	215,841,236
30	sperm	SAMN08375228	SRR6502362	23.973440	58,369,232,700	194,564,109
13	sperm	SAMN08375229	SRR7349193	52.806276	141,148,572,300	470,495,241
14	sperm	SAMN08375229	SRR7349195	22.444378	60,523,788,600	201,745,962
15	sperm	SAMN08375229	SRR7349196	38.253606	104,119,671,000	347,065,570
27	spermatogonia	SAMN08375231	SRR6502356	22.845286	58,909,579,800	196,365,266
28	spermatogonia	SAMN08375231	SRR6502357	17.947471	46,888,332,900	156,294,443
4	spermatogonia	SAMN09427379	SRR7345462	18.686342	52,032,780,000	173,442,600
5	spermatogonia	SAMN09427379	SRR7345463	29.956561	82,384,836,000	274,616,120
6	spermatogonia	SAMN09427379	SRR7345464	39.145759	105,153,716,100	350,512,387
7	spermatogonia	SAMN09427378	SRR7345465	35.816184	96,048,594,600	320,161,982
8	spermatogonia	SAMN09427378	SRR7345467	28.396816	77,248,140,900	257,493,803

## 2.2 Handling coolers (Or: preparing coolers)

[A flowchart showing the pipeline from .fastq to .mcool. The first 6 steps were done with a Probably BioRender or Inkscape.]

Figure 2.1

## 2.2 Handling coolers (Or: preparing coolers)

### 2.2.1 The gwf workflow targets

A *gwf* workflow was created to handle the first part of the data processing, and each accession number (read pair, mate pair) from the Hi-C sequencing was processed in parallel, so their execution was independent on the other samples.

#### 2.2.1.1 Downloading the reads

The reads were downloaded from NCBI SRA portal [ref] directly to GDK using `sra-downloader` [ref] through docker [ref] as `.fastq.gz` files.

#### 2.2.1.2 Handling the reference

The latest reference genome for rhesus macaque (*macaca mulata*), *rheMac10* (or *Mmul\_10*, UCSC or NCBI naming conventions, respectively) was downloaded to GDK from UCSC web servers with `wget` [ref]. To use `bwa` (Burrow Wheeler's Aligner) [ref] for mapping, *rheMac10* needs to be indexed with both `bwa index` with the `--bwtsw` option and `samtools faidx`, which results in six indexing files for `bwa mem` to use.

#### 2.2.1.3 Mapping paired-end reads

#### 2.2.1.4 Pair and sort the reads

#### 2.2.1.5 Filter (deduplicate) pairs

#### 2.2.1.6 Create interaction matrices (coolers)

#### 2.2.1.7 Pooling samples (Merging coolers)

The strategy to get the best signal was by pooling the interaction matrices. `cooler merge` was used to merge all samples in each sub-folder (cell type) to just one interaction matrix for each cell type. The reason for that is that we choose to trust Wang et al. (2019) when they say that

## *2 Methods*

compartments are highly reproducible between replicates, and by merging all replicates, we will have a more robust signal.

### **2.2.1.8 Create multi-resolution coolers (zoomify)**

### **2.2.1.9 Matrix balancing (Iterative correction)**

### **2.2.1.10 Eigendecomposition**

## **3 Results**

Here are the glorious results



## **4 Discussion**

Here is the discussion



# Bibliography

- Jaenike, John. 2001. "Sex Chromosome Meiotic Drive." *Annual Review of Ecology and Systematics* 32 (1): 25–49. <https://doi.org/10.1146/annurev.ecolsys.32.081501.113958>.
- Lieberman-Aiden, Erez, Nynke L. Van Berkum, Louise Williams, Maxim Imakaev, Tobias Ragoczy, Agnes Telling, Ido Amit, et al. 2009. "Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome." *Science* 326 (5950): 289–93. <https://doi.org/10.1126/science.1181369>.
- Munch, Kasper. 2024. "Munch-Group." <https://munch-group.org/research.html>.
- Open Chromosome Collective. 2024. "Open Chromosome Collective (Open2C)." Resource. *Open2C*. <https://open2c.github.io/>.
- Skov, Laurits, Moisès Coll Macià, Elise Anne Lucotte, Maria Izabel Alves Cavassim, David Castellano, Mikkel Heide Schierup, and Kasper Munch. 2023. "Extraordinary Selection on the Human X Chromosome Associated with Archaic Admixture." *Cell Genomics* 3 (3): 100274. <https://doi.org/10.1016/j.xgen.2023.100274>.
- Sørensen, Erik F., R. Alan Harris, Liye Zhang, Muthuswamy Raveendran, Lukas F. K. Kuderna, Jerilyn A. Walker, Jessica M. Storer, et al. 2023. "Genome-Wide Coancestry Reveals Details of Ancient and Recent Male-Driven Reticulation in Baboons." *Science* 380 (6648): eabn8153. <https://doi.org/10.1126/science.abn8153>.
- Wang, Yao, Hanben Wang, Yu Zhang, Zhenhai Du, Wei Si, Suixing Fan, Dongdong Qin, et al. 2019. "Reprogramming of Meiotic Chromatin Architecture During Spermatogenesis." *Molecular Cell* 73 (3): 547–561.e6. <https://doi.org/10.1016/j.molcel.2018.11.019>.



Bioinformatics Research Centre  
Department of Molecular Biology and Genetics  
Aarhus University  
Universitetsbyen 81  
8000 Aarhus C  
Denmark

