

EGU22-8122

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# A Genetic Algorithm Approach to Infer Jupiter's Rossby Wave Structure from JunoCam Images

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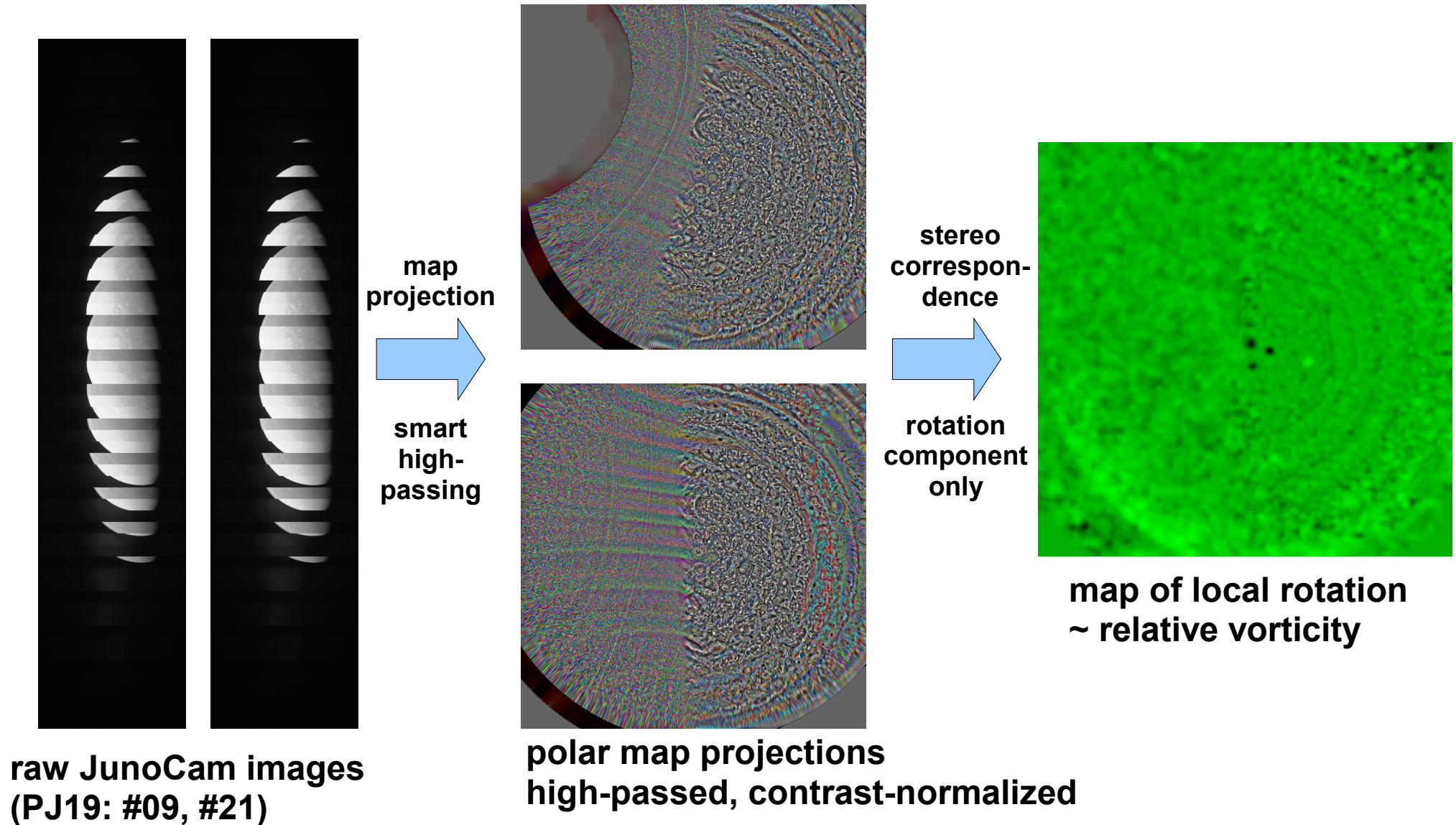
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<sup>2</sup>Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA, USA

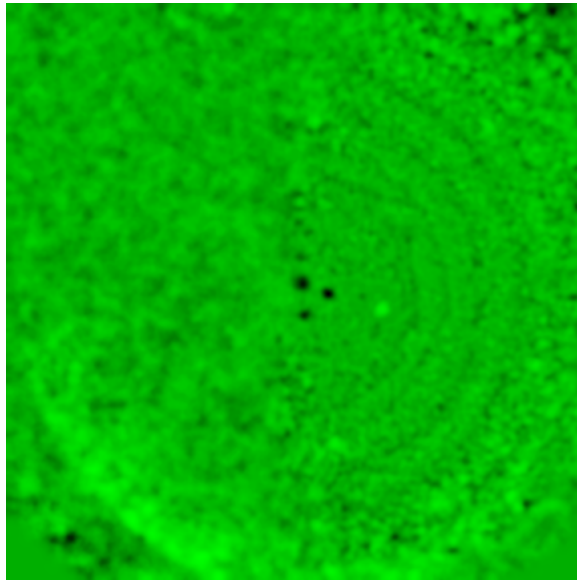
<sup>3</sup>Planetary Science Institute, Tucson, AZ, USA

# We derive a vorticity map from a pair of raw JunoCam images.

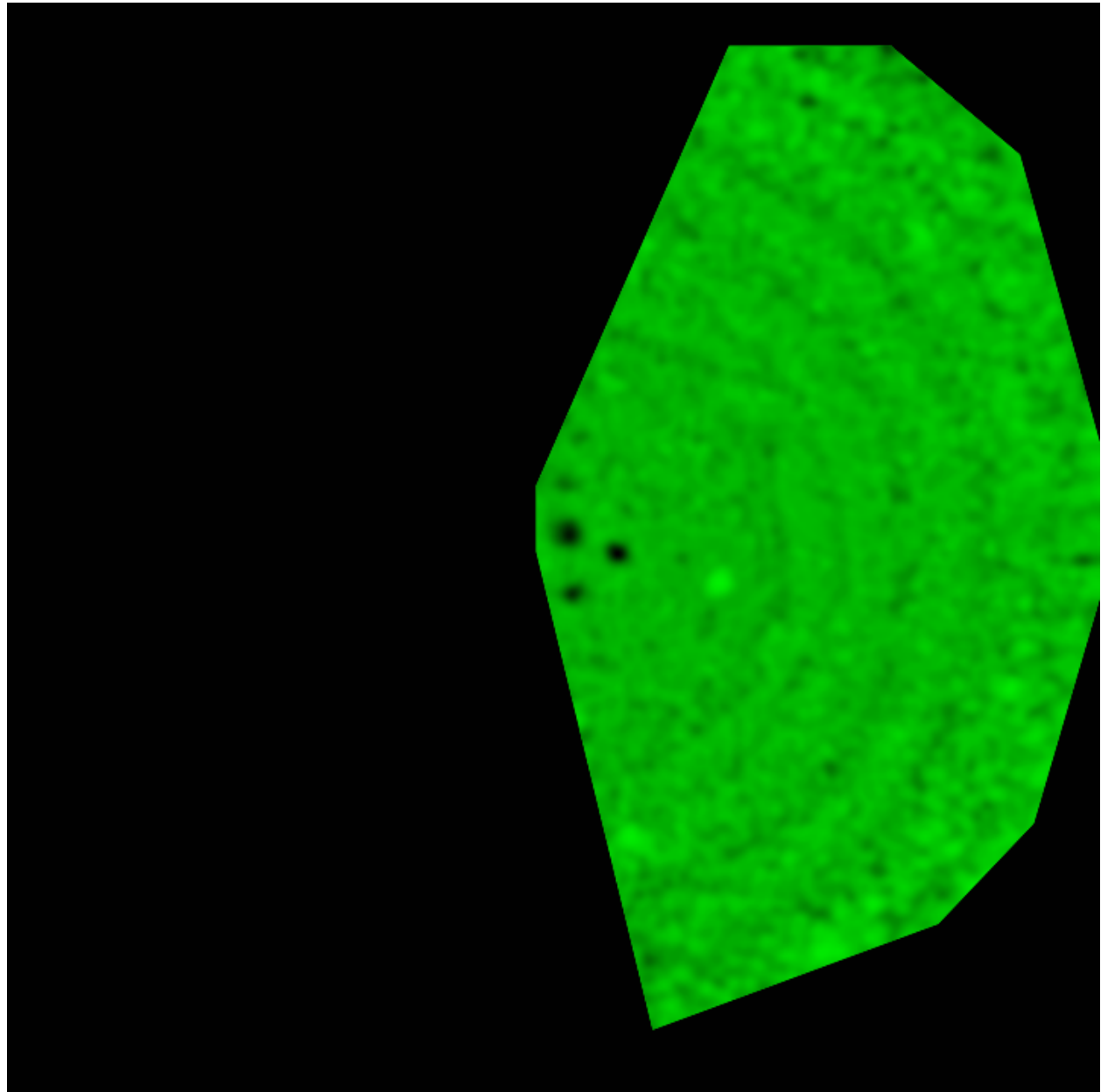
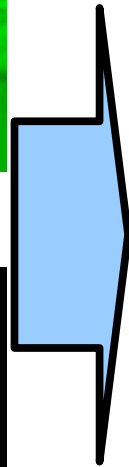
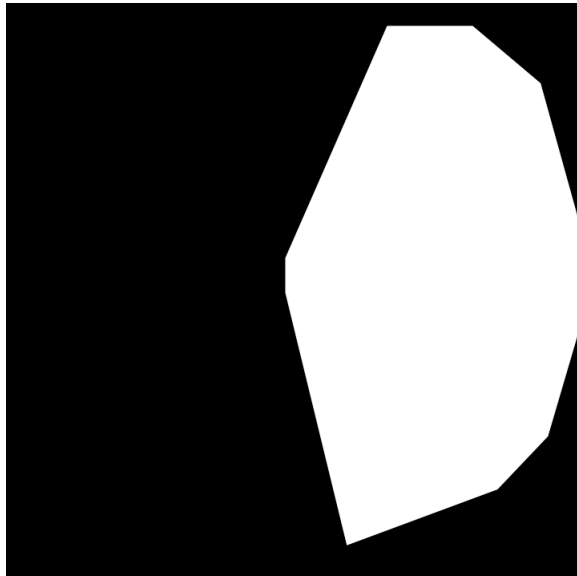
Method: Map projection followed by stereo correspondence.



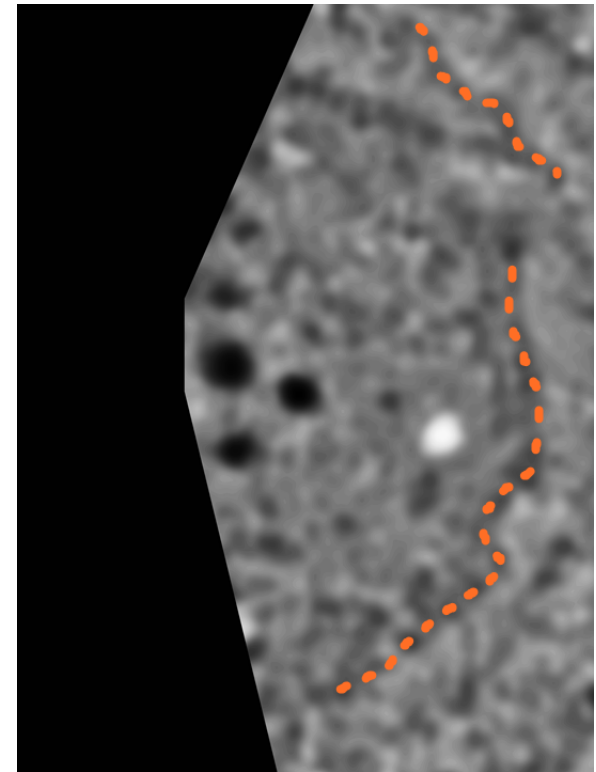
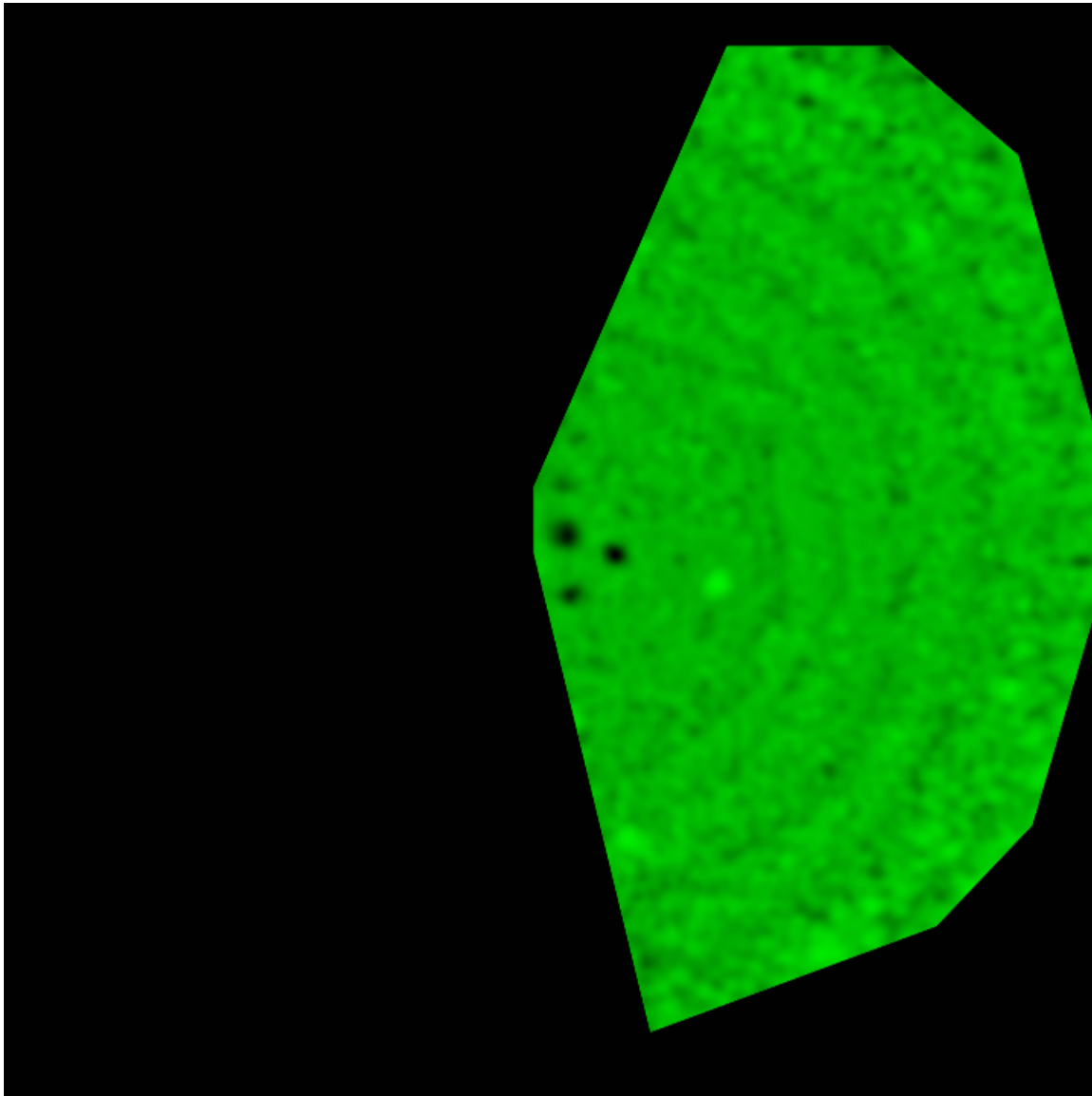
# Clip vorticity data to valid area



clip with mask



**If I could ask a computer about Rossby waves  
in this vorticity map,  
what would be its answer?**



**?**



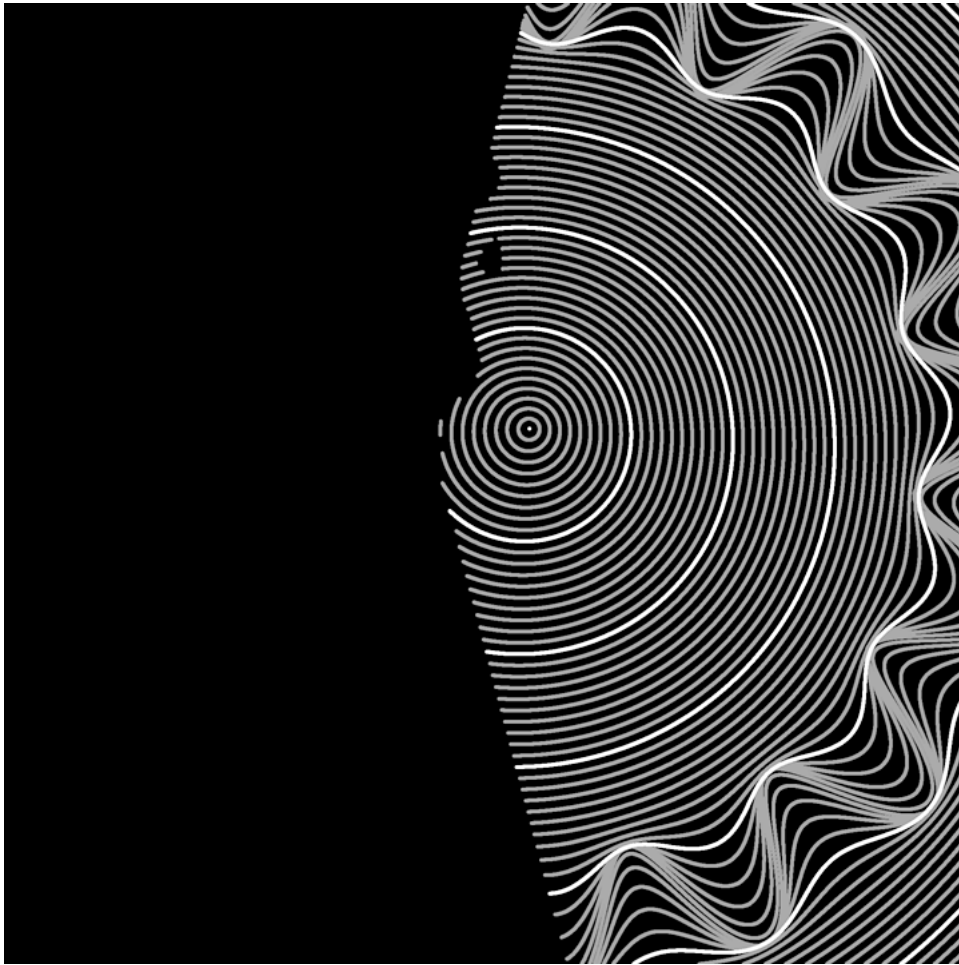
**If I could ask a computer about Rossby waves  
in this vorticity map,  
what would be its answer?**

**Ok, let's find it out!**

**If I could ask a computer about Rossby waves  
in this vorticity map,  
what would be its answer?**

**Approach:  
Genetic algorithm  
after pre-conditioning**

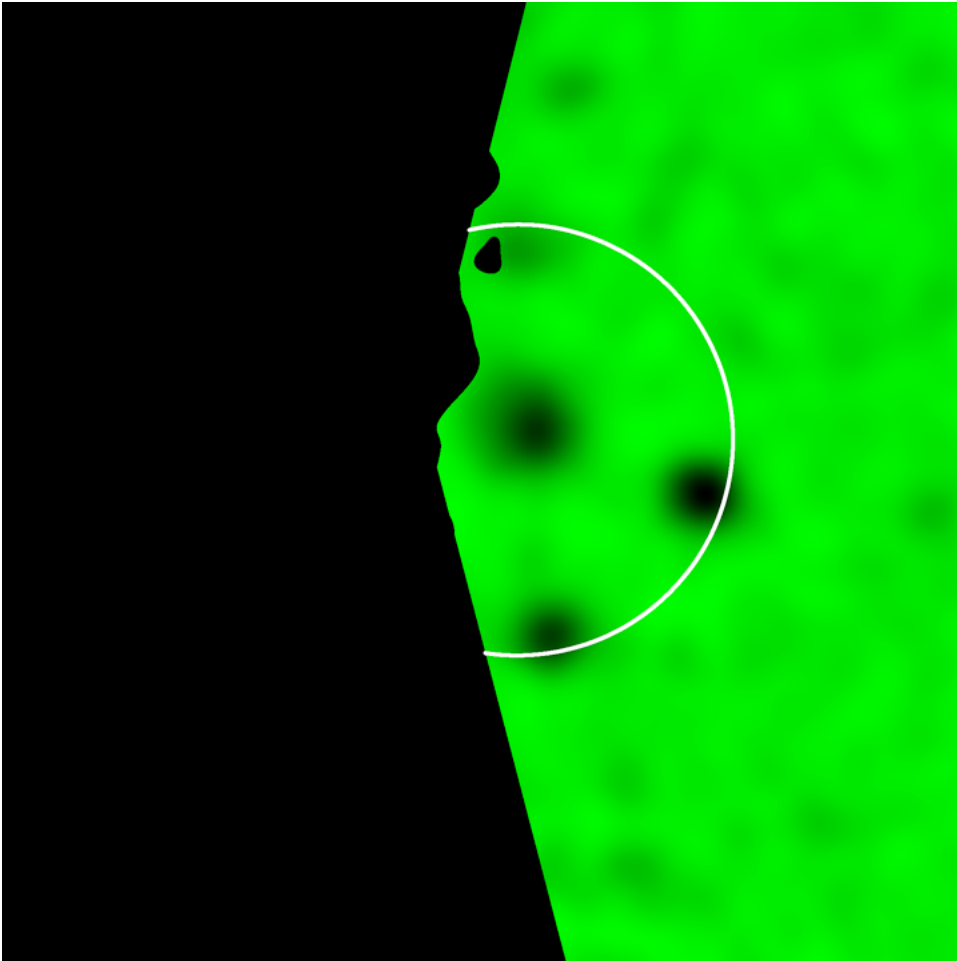
**A description by Fourier terms would be nice.  
Gauss-weighted around a given latitude.  
something like this one**



**A description by Fourier terms would be nice.  
Gauss-weighted around a given latitude.  
or that one**



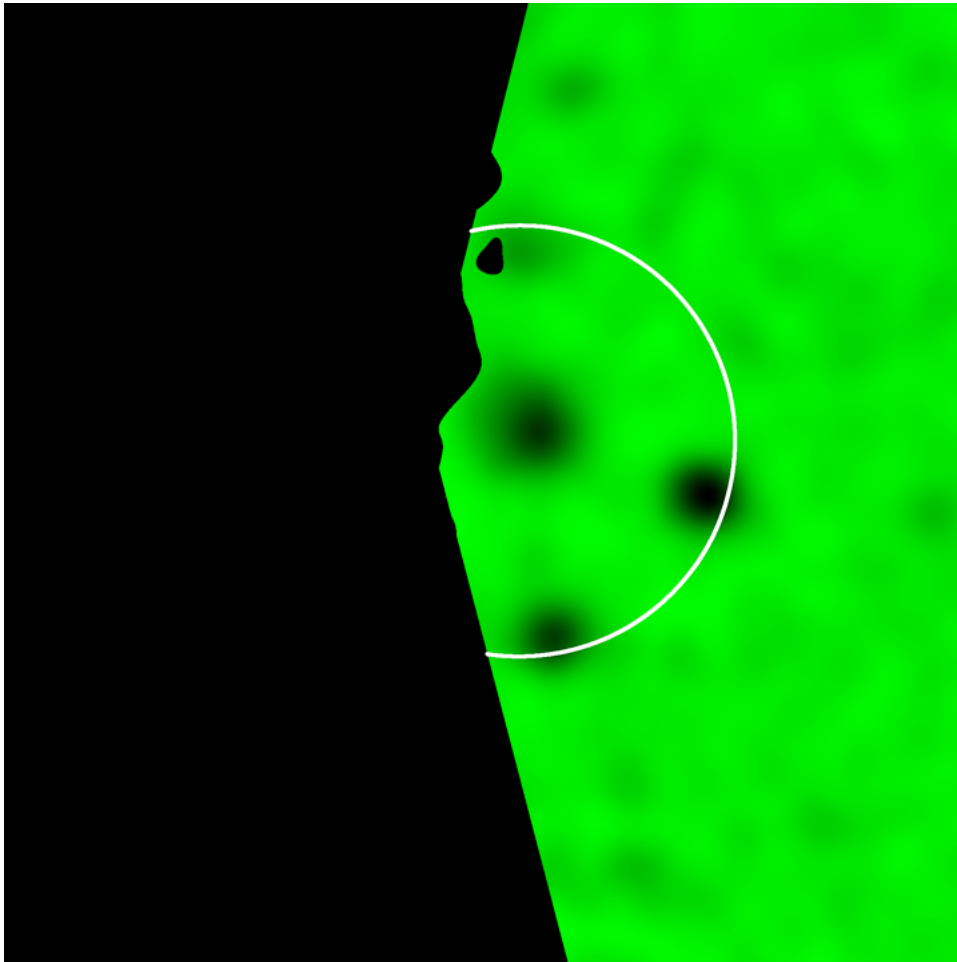
**So, let's start with a single latitude**



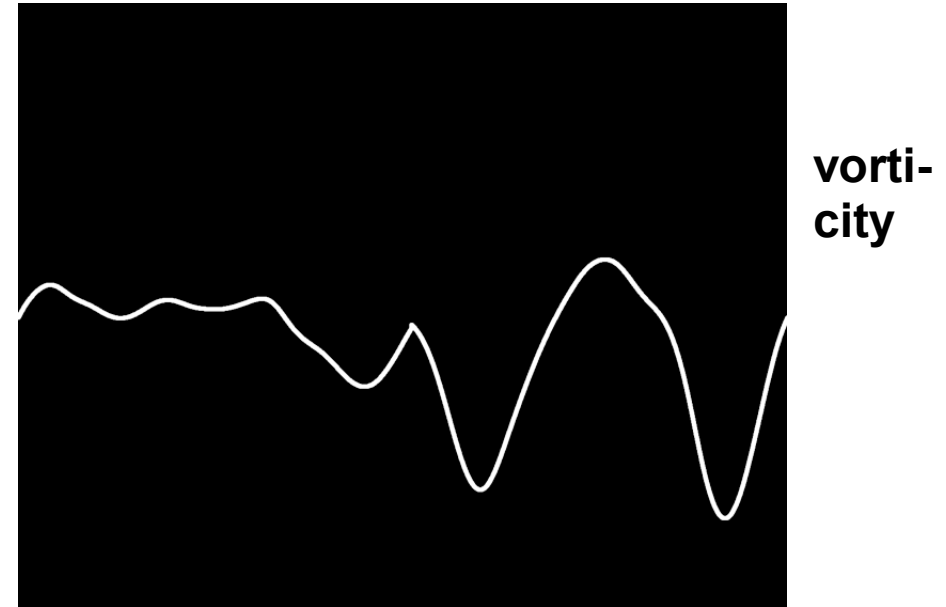
**select one single fiber**



**The standard deviation of vorticities  
along our distorted circle of latitude  
will provide us with  
a fitness measure.**



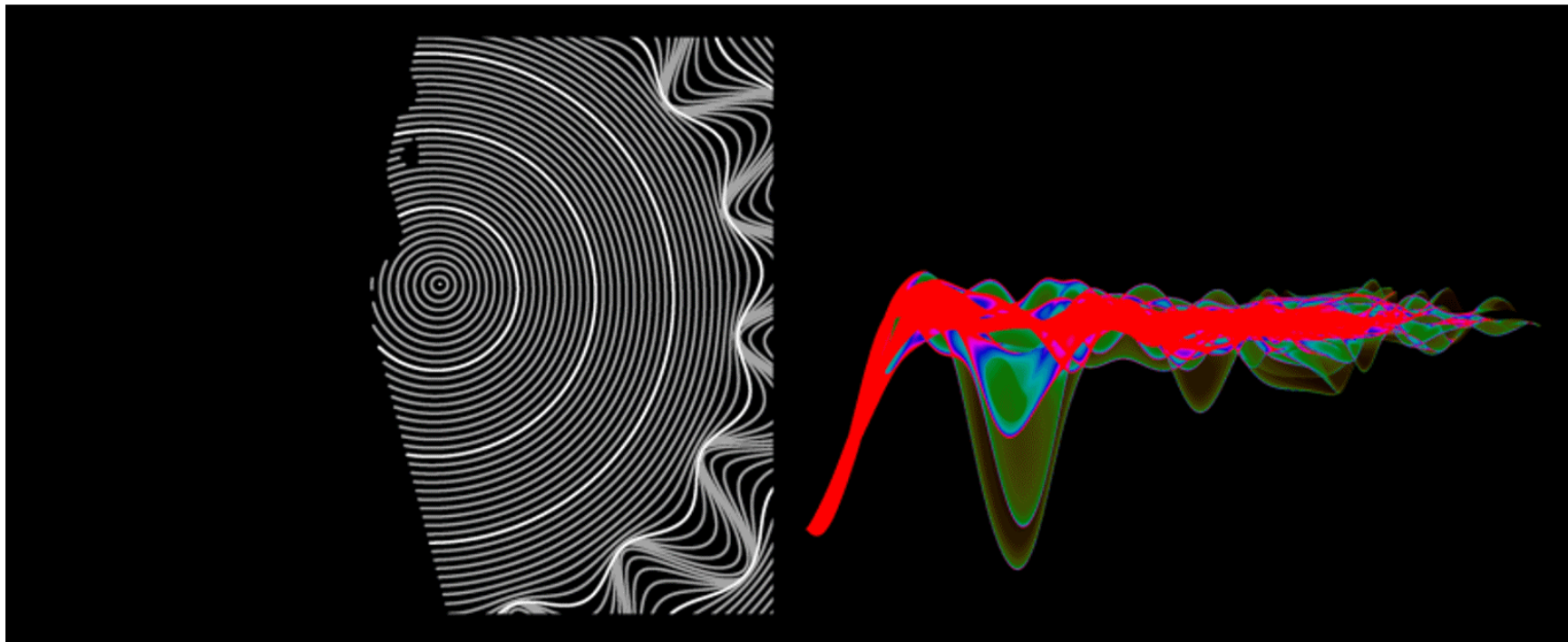
**selected fiber**



**length parameter of valid arc**

**vorticity value as  
a function of arc length  
along the valid portion  
of the fiber**

**Note: Fourier terms have effect on statistics,  
including the standard deviation  
of the vorticity values sampled  
along a fiber (distorted circle of latitude).**



**vorticity**

**fibraton  
(set of fibers,  
fiber means distorted  
circles of latitude)**

**generalized latitude parameter  
heat map of vorticity  
probability density function;  
fiber corresponds to a column.**

**Back to a single given latitude:  
run over  
zonal wave numbers,  
meridional amplitudes,  
and phase shifts,  
in order to find a good candidate  
for that specific latitude.  
A Monte-Carlo search will do the job.**

# Encode each Fourier term as a bit string, and call it a gene.

## Example Fourier term parameters for colatitude $11.5^\circ$ :

00000000000000000000000100010000000010	Param 0: zonal wave number = 3
01000001101111011100100010010111	Param 1: amplitude = $2.054416939^\circ$
00011000100010001000100010001000	Param 2: colatitude $\mu = 11.5^\circ$
00000001011011000001011011000001	Param 3: (co)latitude $\sigma = 0.5^\circ$
00111011010001011101110010000010	Param 4: rotation phase = 0.308713

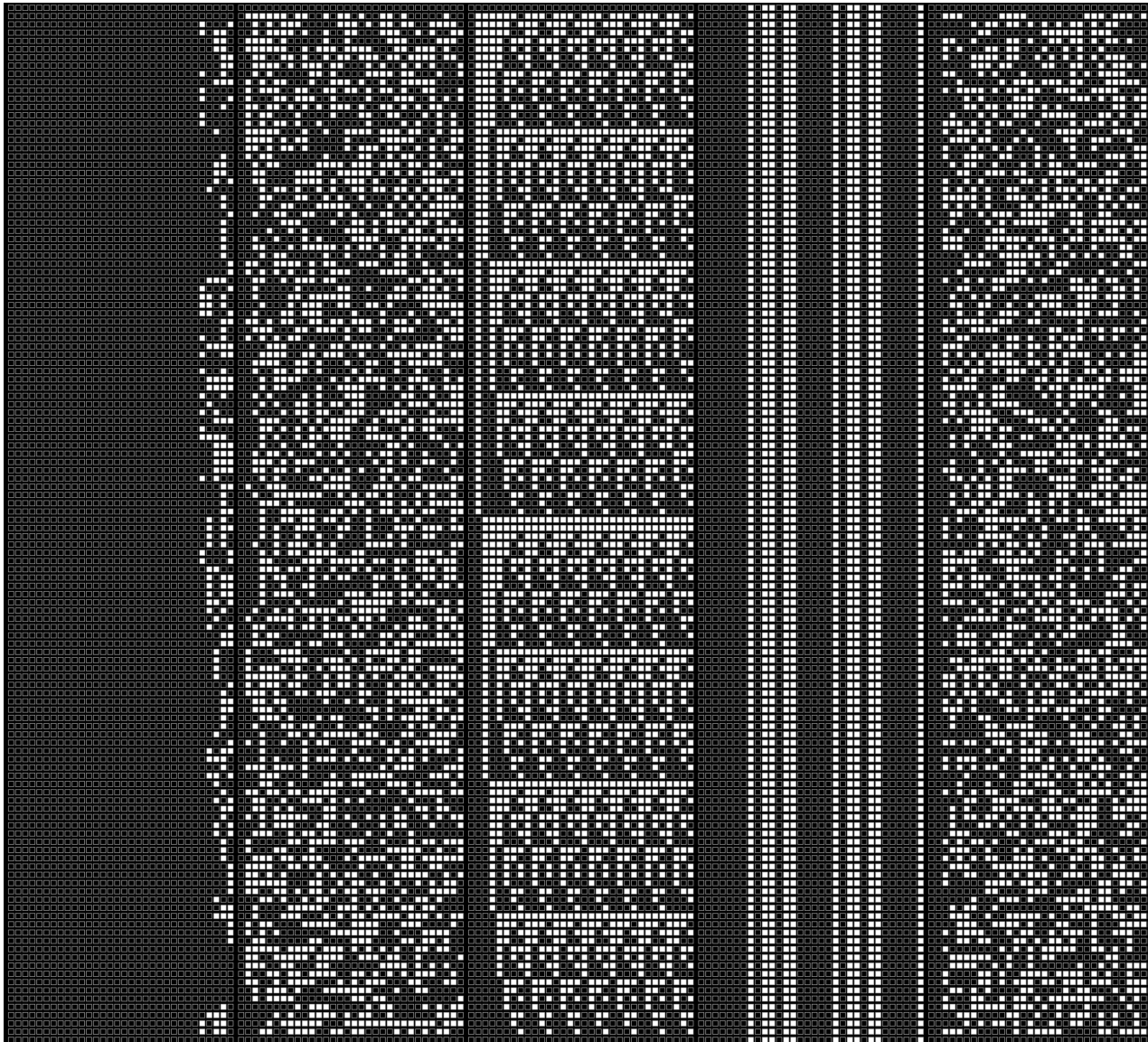
## graphical plot of bit string:



**Repeat this task for all considered latitudes  
within the latitude range of interest  
in sufficiently small latitude steps.**



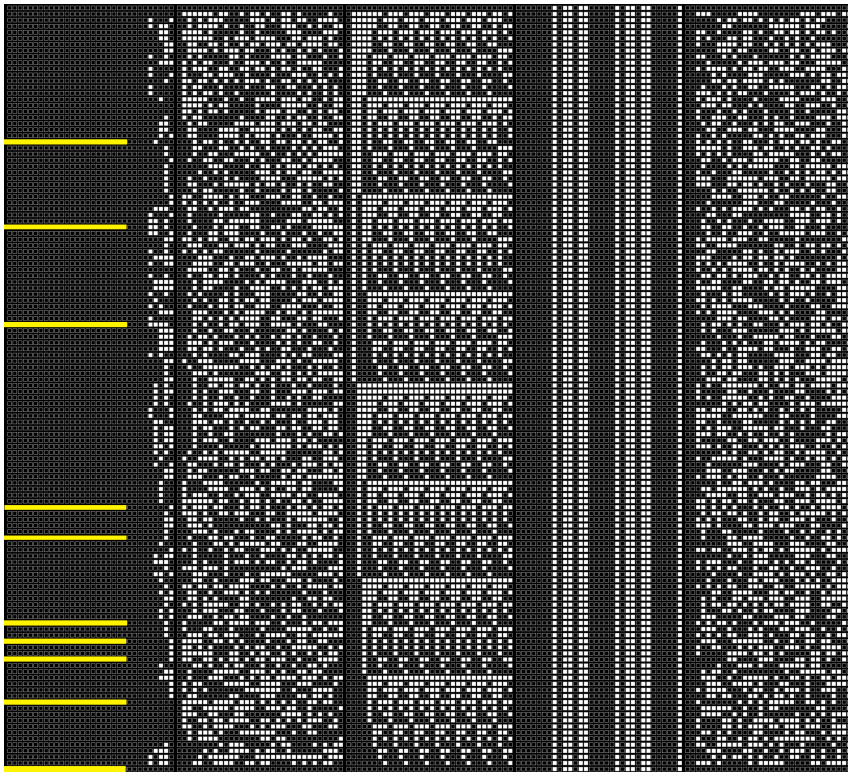
**The results will provide us  
with a gene pool of initial values  
to seed the search for a global solution.**



**Each row  
encodes  
a gene.**

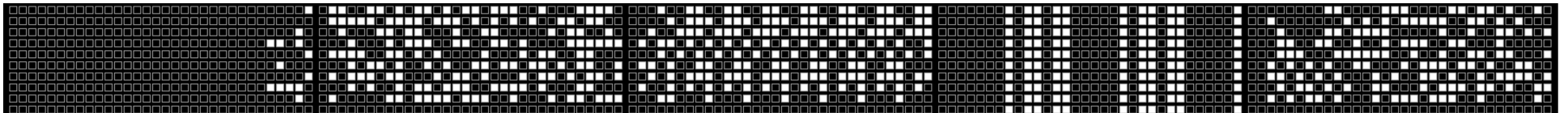
**Provide each  
gene with  
the encoding of  
a reasonable  
sigma for the  
meridional  
Gauss weight,  
e.g.  $0.5^\circ$   
latitude.**

**Call a set of genes a genome.  
A genome shall be of the complexity  
of the global solution we aim at.  
Assemble a genome by choosing genes  
randomly from the gene pool.**



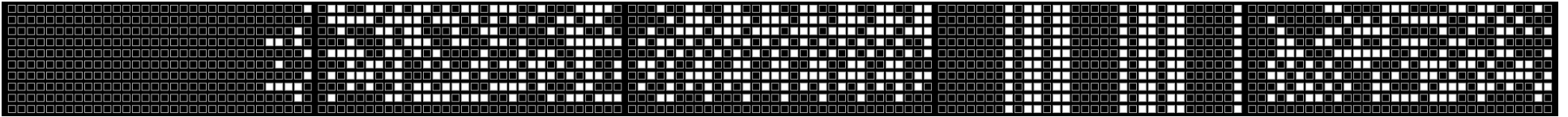
**Gene pool:  
Randomly selected genes are  
marked with yellow bars.**

**Genome assembled from  
randomly chosen genes**

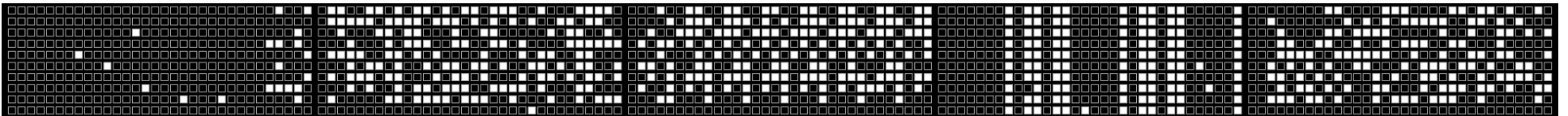


# Allow for point mutations on the selected genome.

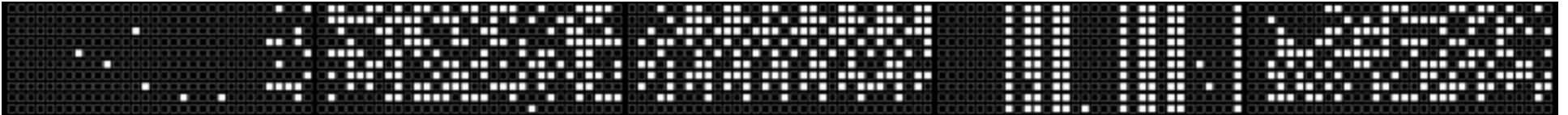
before point mutation



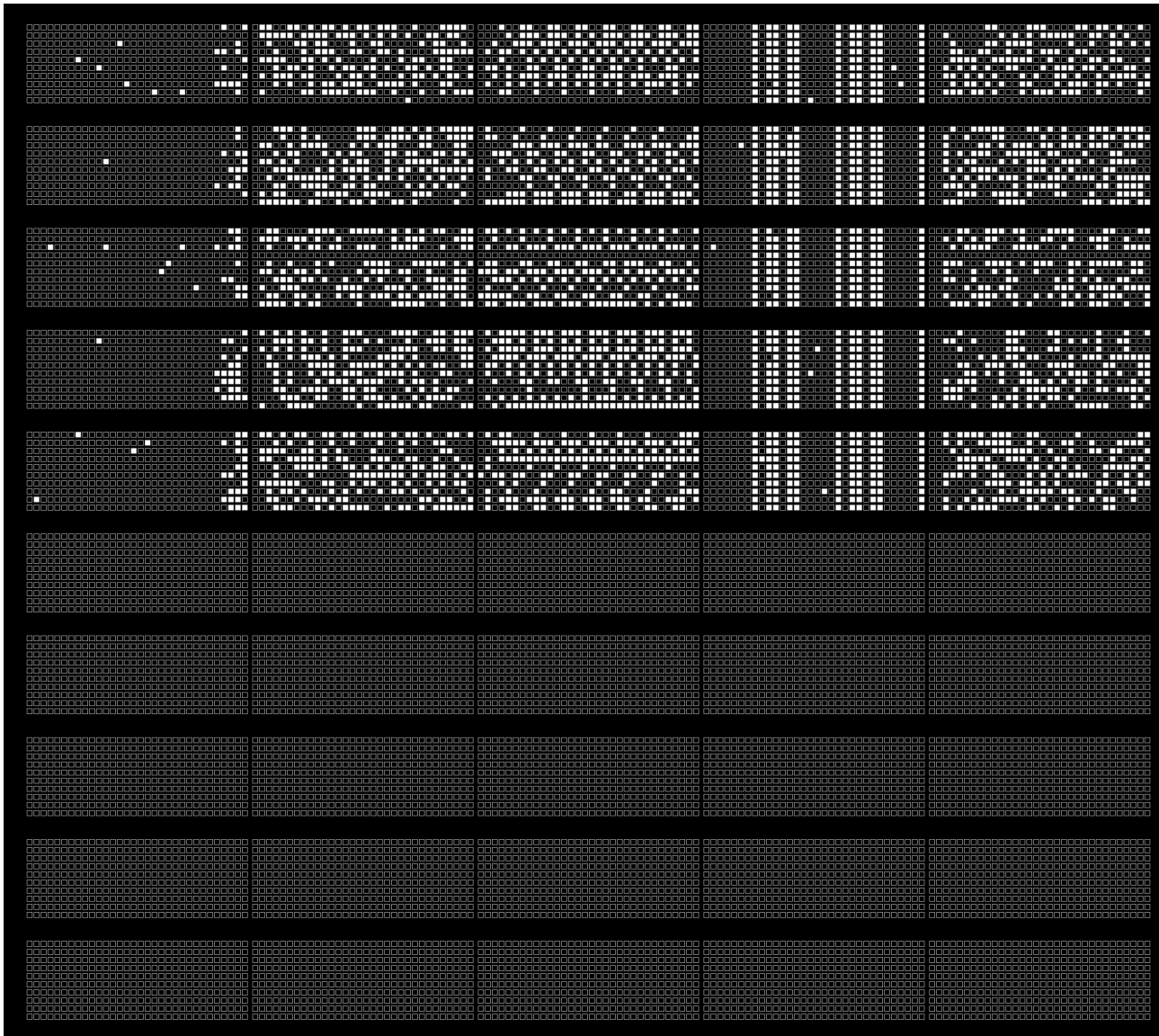
after point mutation



blink before/after point mutation

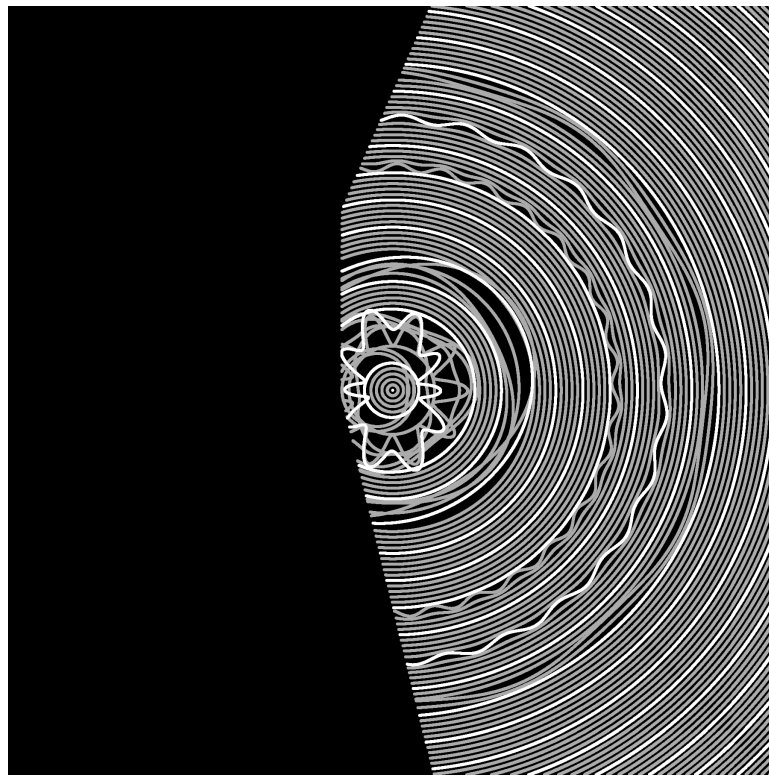


**Repeat this selection process  
in order to  
seed half of a population of genomes.**



**population of  
10 genomes,  
5 genomes  
valid.**

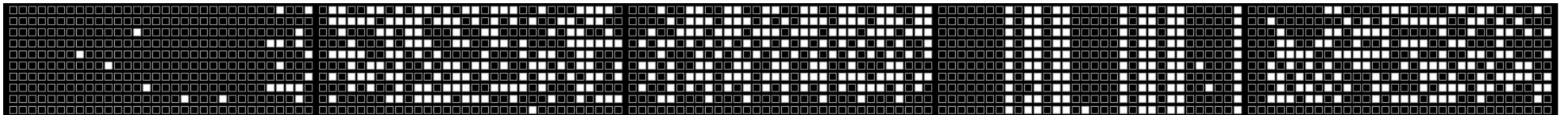
**A genome is considered a genotype,  
while its translation into  
a sum of meridionally Gauss weighted  
Fourier terms  
is considered its phenotype.**



**phenotype:  
circles of latitude  
meridionally distorted by  
meridionally Gauss-weighted  
Fourier terms (fibers)**

**translate**

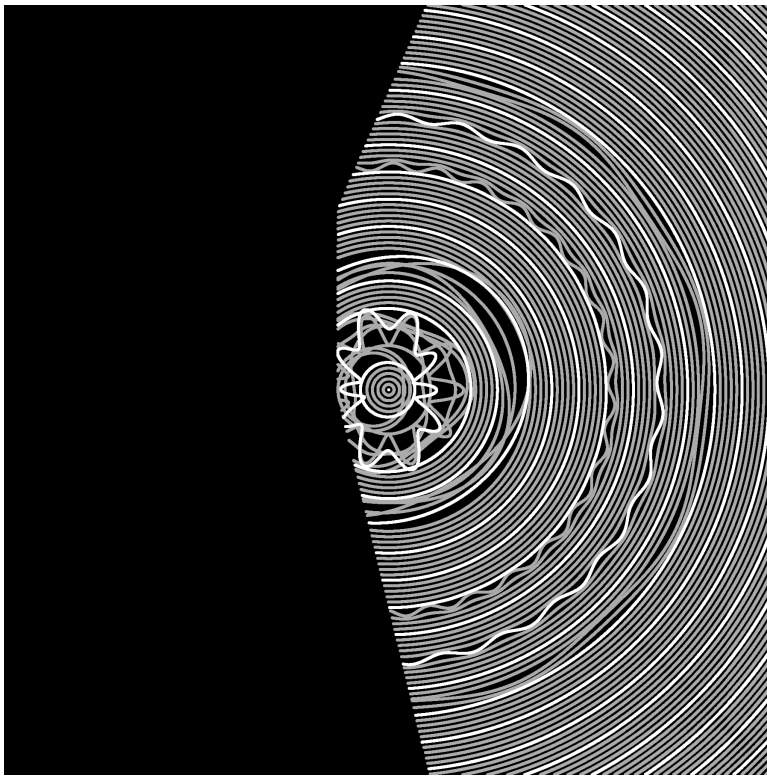
**genotype: string of bits**



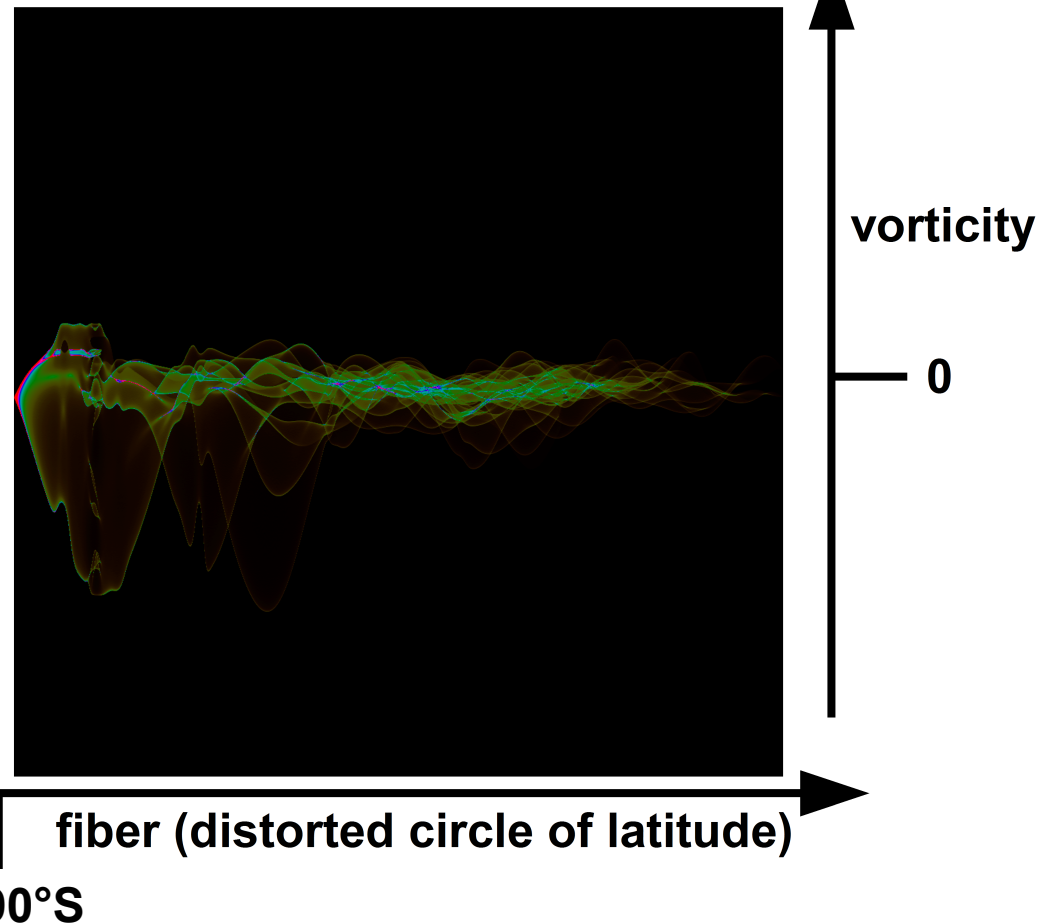


**The fitness of a phenotype  
can be defined by the mean  
of all standard deviations of vorticities  
along respective distorted circles of latitude.**

**phenotype**

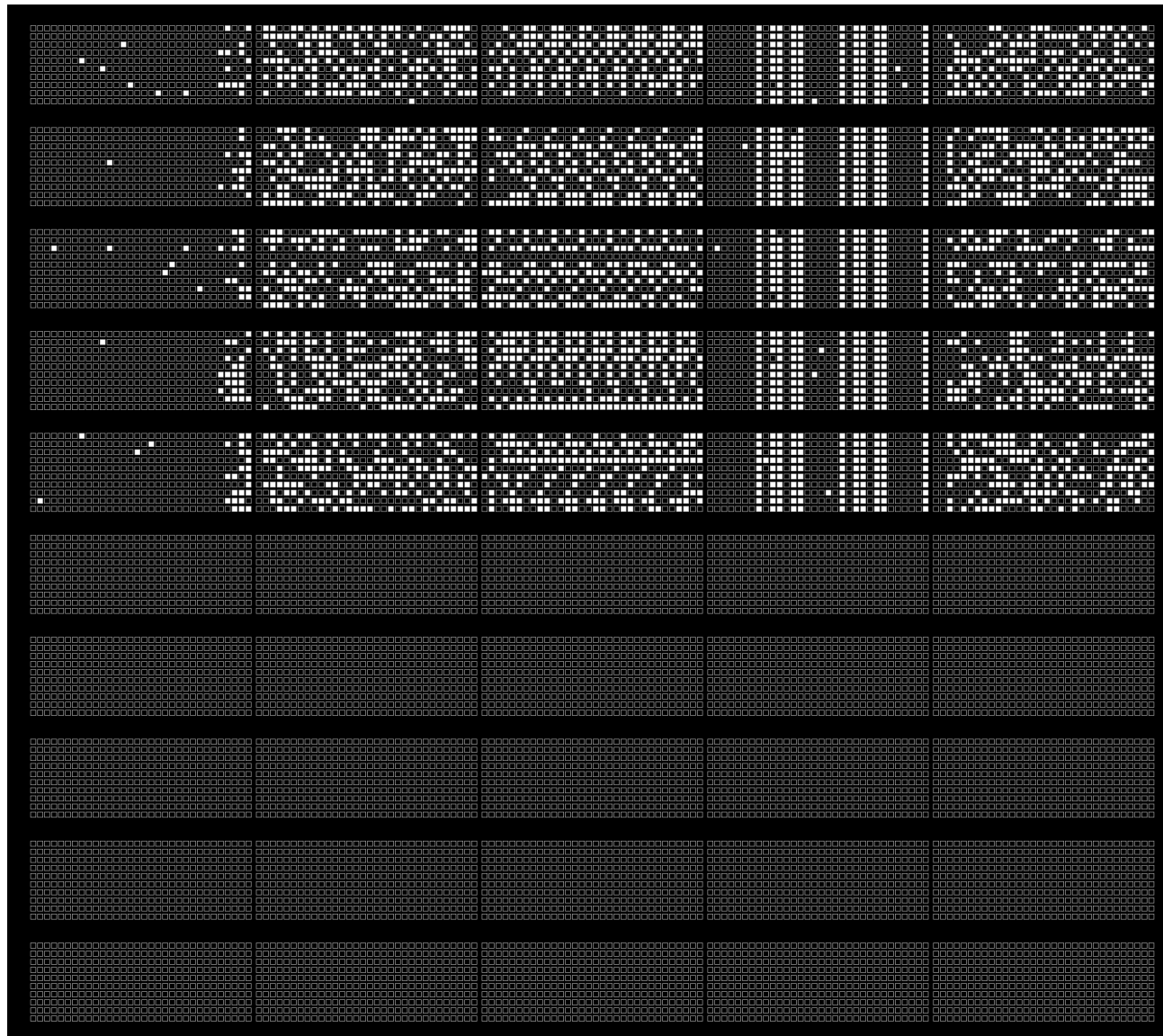


**vorticity statistics**



**fitness := mean of standard deviation of vorticity on fiber = 0.000009703286**

**This way, each valid genome of our population  
is attributed with  
a measure of its fitness.**



**0.000009579028927**

**0.000009549332881**

**0.000009807979462**

**0.000009869549860**

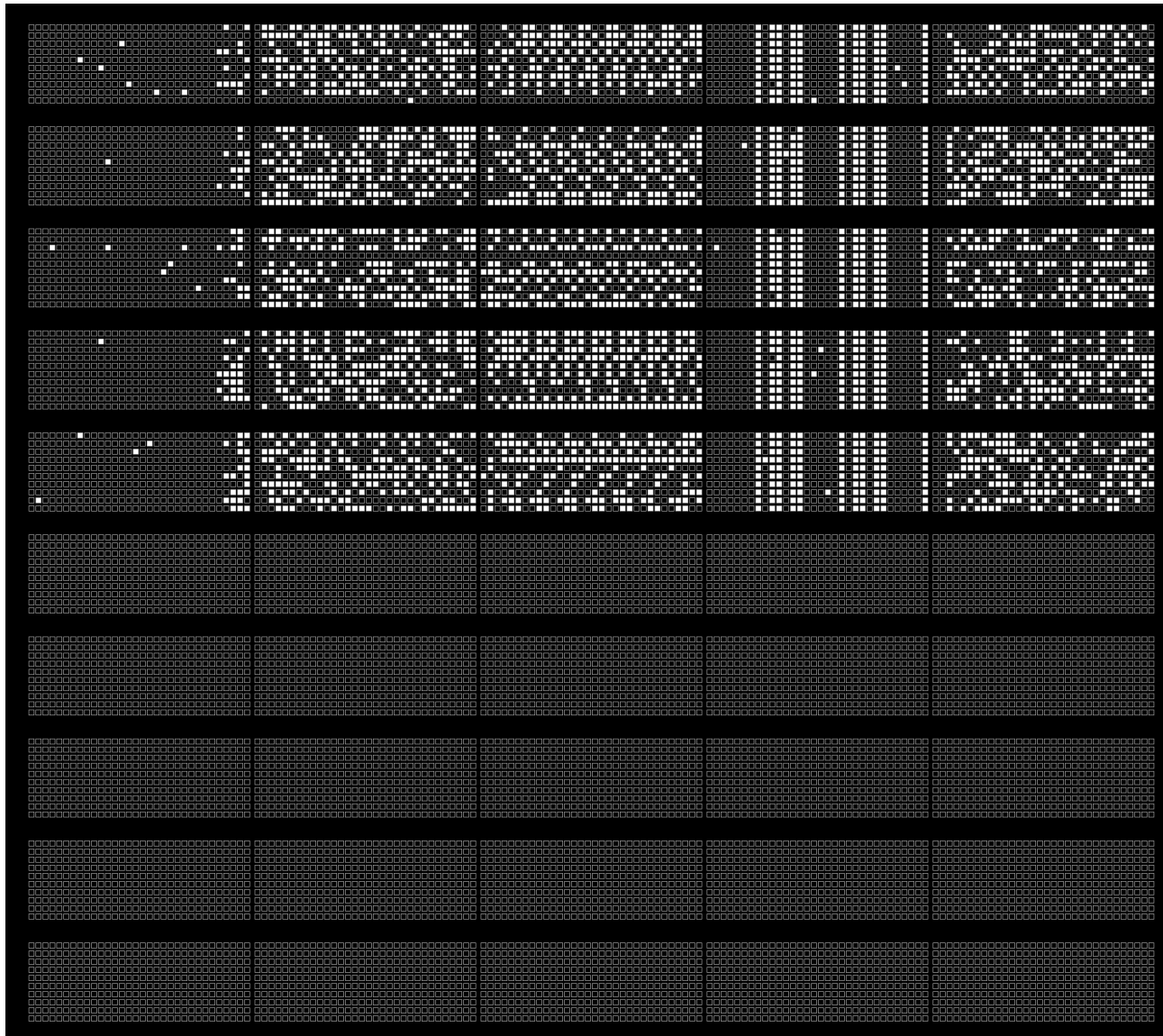
**0.000009767088421**

**n/a**

**fitness value  
of each valid  
genome of the  
population**

# Evolve the population by looping over the following steps:

**fitness**



**0.000009579028927**

**0.000009549332881**

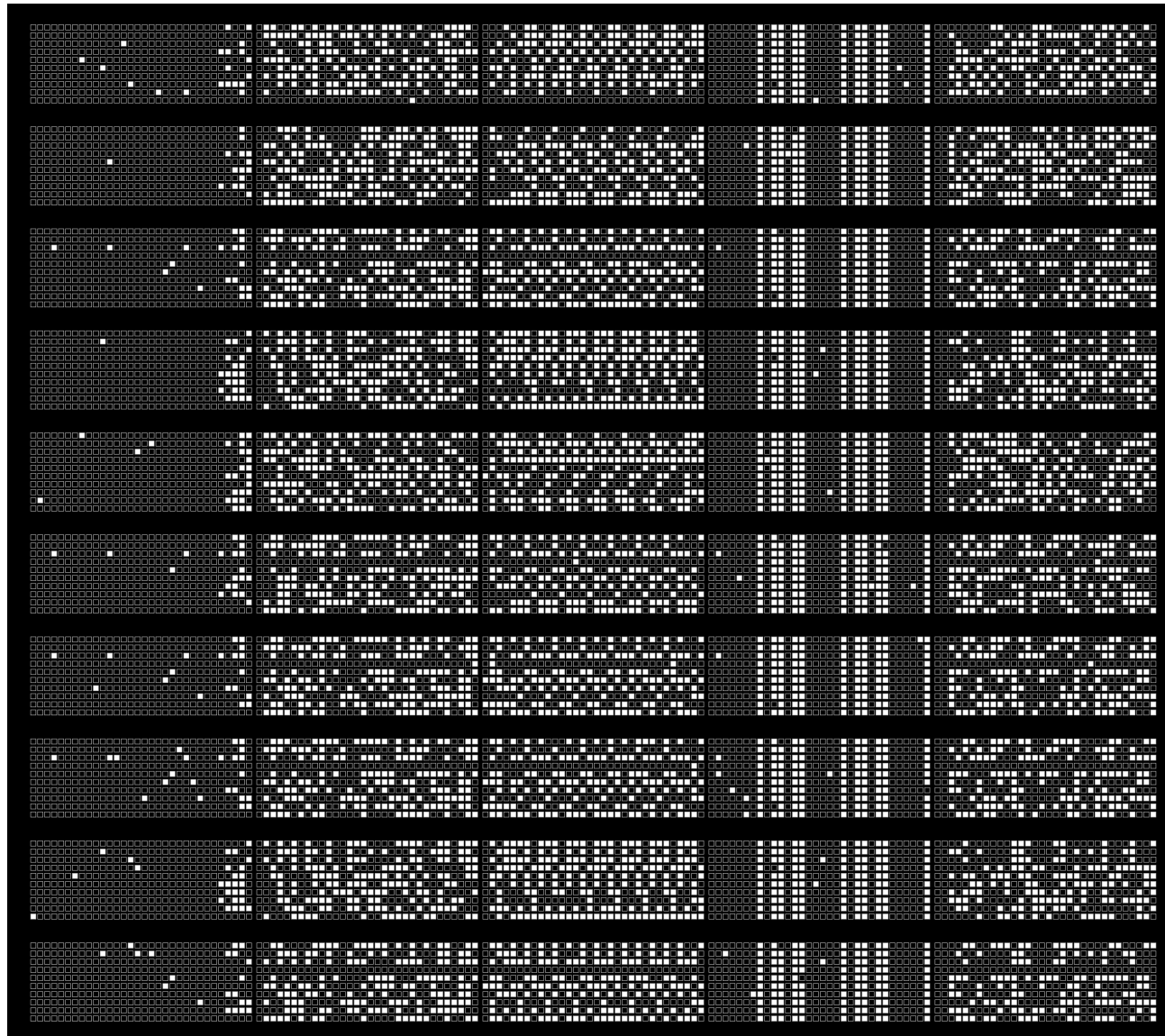
**0.000009807979462**

**0.000009869549860**

**0.000009767088421**

# Evolve the population by looping over the following steps:

Replenish the population with new genomes.



0.000009579028927

0.000009549332881

0.000009807979462

0.000009869549860

0.000009767088421

0.000009869170102

0.000009997889944

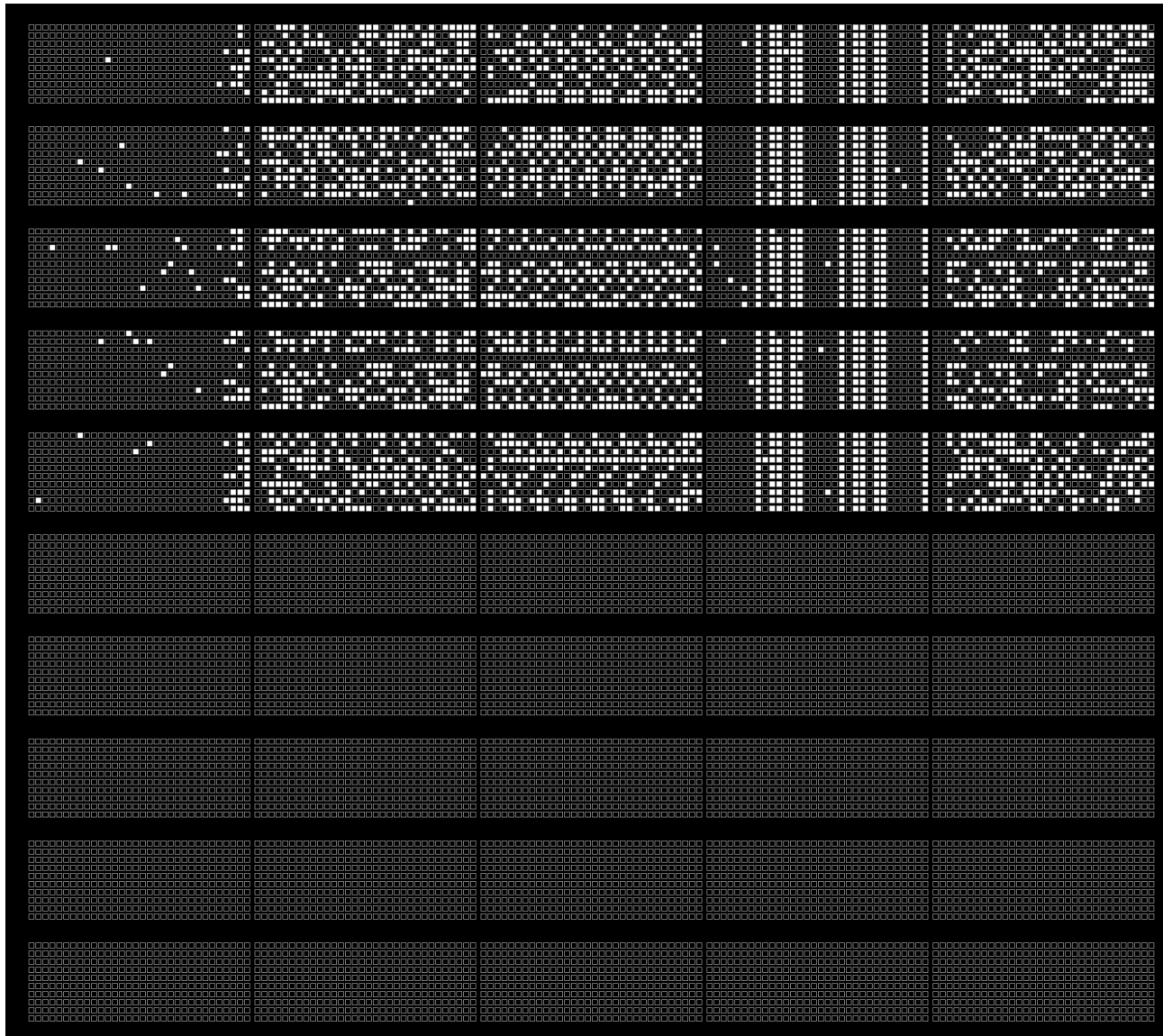
0.000009690615493

0.000009847701584

0.000009708270703

# Evolve the population by looping over the following steps:

Sort the genomes of the population by their fitness,



0.000009549332881

0.000009579028927

0.000009690615493

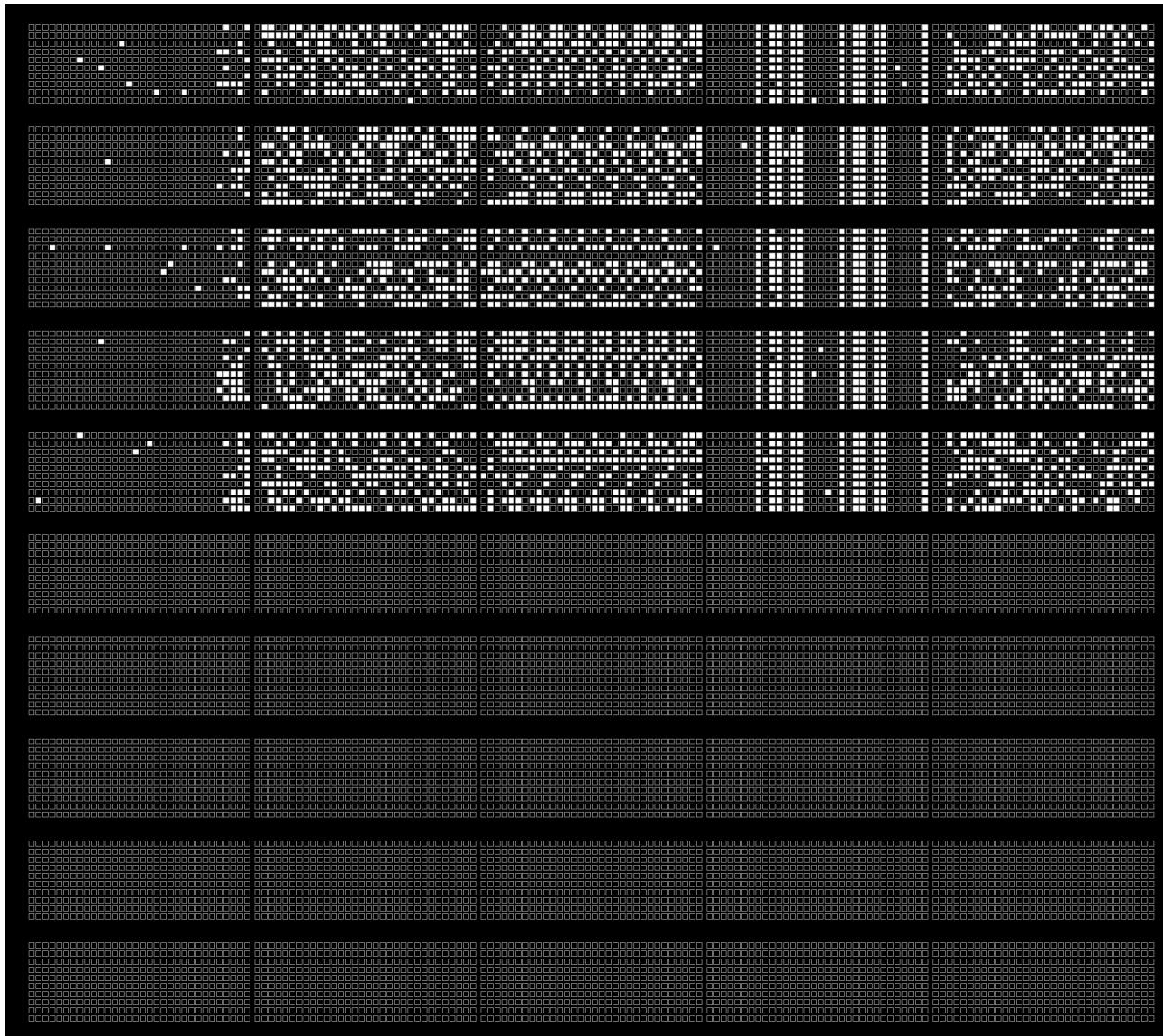
0.000009708270703

0.000009767088421

and invalidate  
the least fit half  
of the population.

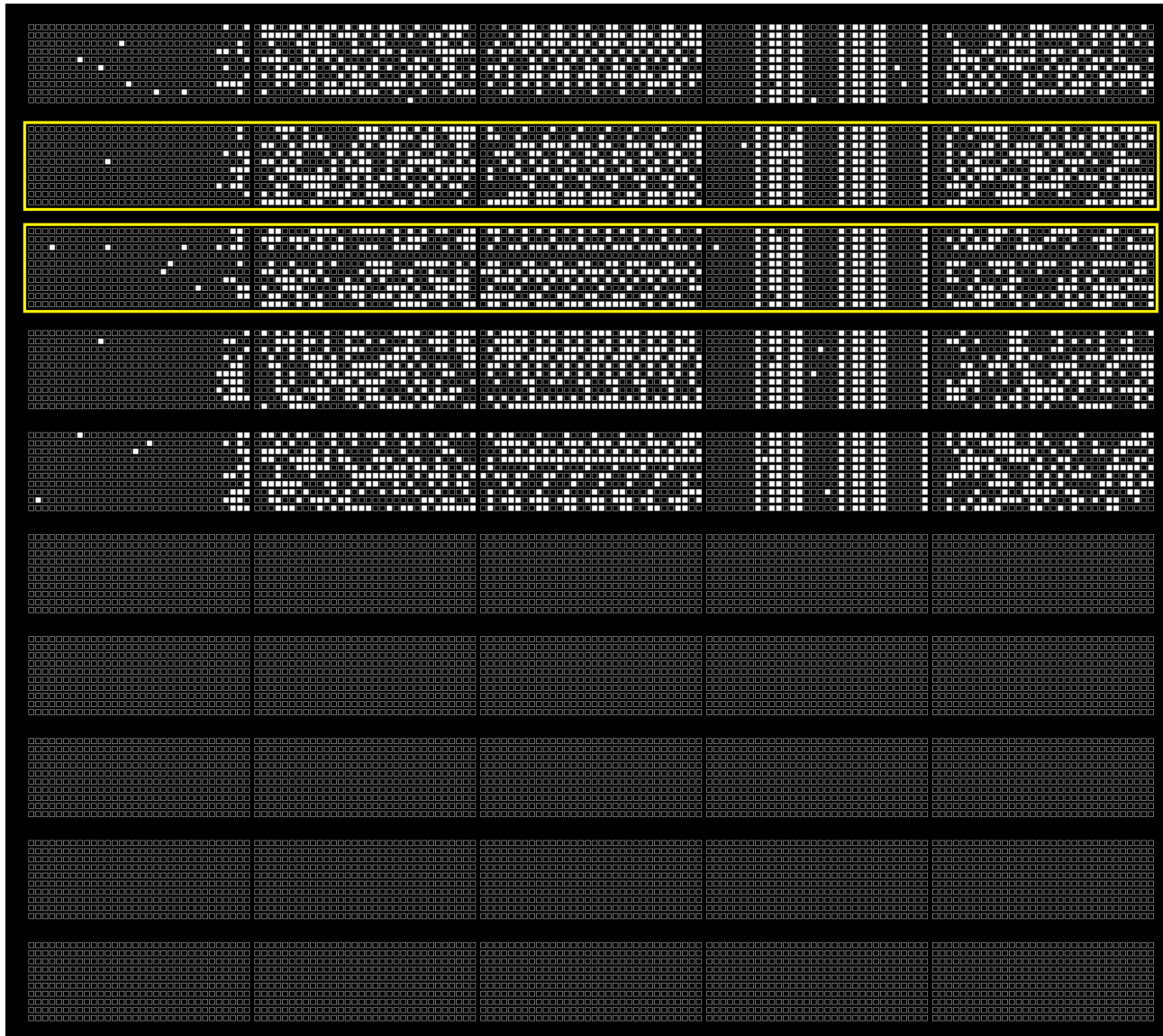


# A new genome is derived from the population the following way:



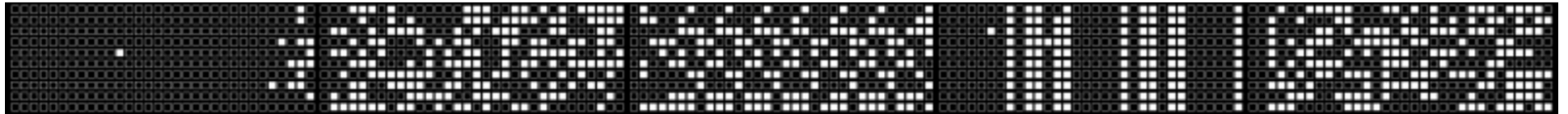
# A new genome is derived from the population the following way:

Randomly choose two genomes of the population.

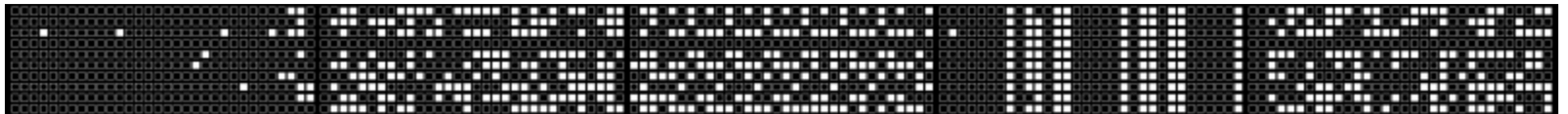


# A new genome is derived from the population the following way:

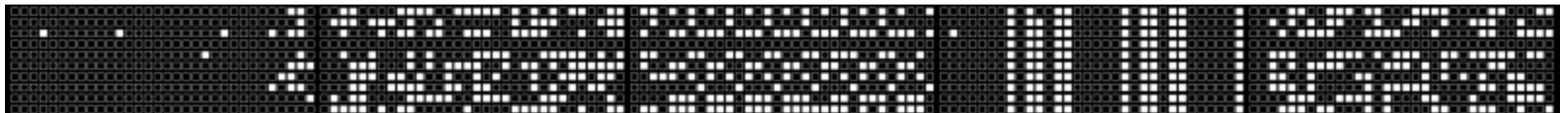
Recombine the two randomly chosen genomes by  
randomly choosing about half of the genes from each of  
the two chosen genomes.



**X**



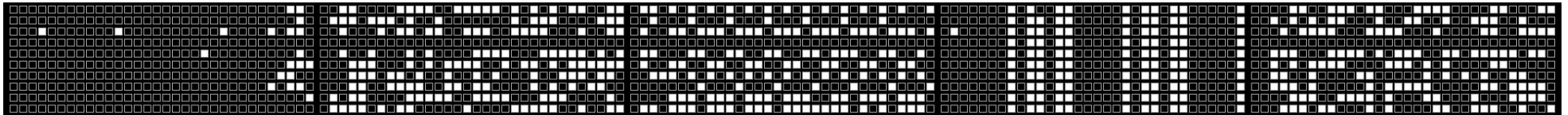
**=**



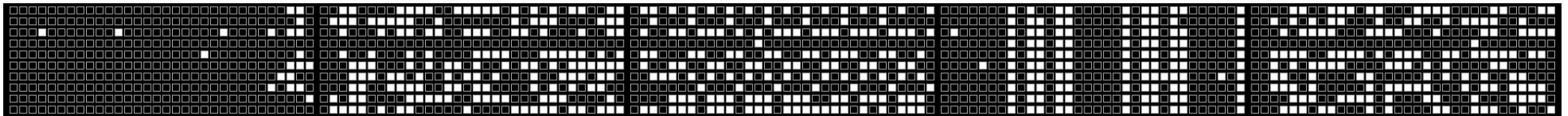
# A new genome is derived from the population the following way:

Add random point mutations to the recombined genome.

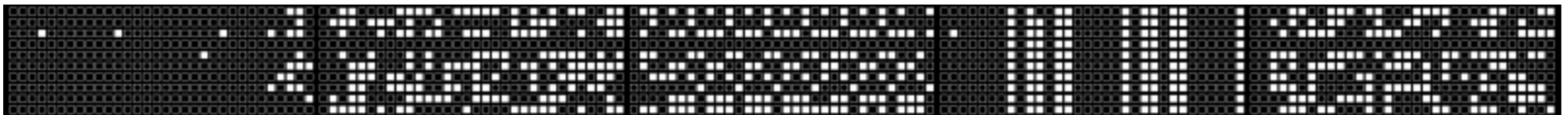
before point mutation:



after point mutation:



blink before / after point mutation:



# Preliminary results

- Runs with several random populations tend to return unique results where Rossby wave structures look evident.
- They tend to return ambiguities where structures look less evident.
- Alternative solutions can be attributed with an objective measure of fitness.

## Conclusion

When observing the development of Rossby wave structures over time, we should be prepared to deal with ambiguities. Those may become part of a best objective description.

**This was a little too fast?**

**Take a look at the copy of  
these presentation slides  
in the EGU2022 abstract section.**

**Thank you!**

# Backup slides

# Why is a genetic algorithm approach used?

## Selected traditional approaches to fit a set of parameters:

### Hill climbing or gradient methods:

Infinite-dimensional parameter space with many local stationary points expected. Method family unlikely to return a solution close to a global optimum.

### Fourier analysis:

No time series available.

### Neural networks:

No training database available.

### Genetic algorithm, ingredients:

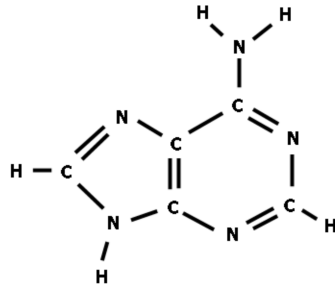
- genotype to encode phenotype,
- fitness assessment of phenotype.

**Both ingredients are available!**



# Genotype

Inspired by biology:  
mRNA contains  
sequence of  
nucleobases  
(simplified)



**adenine**

reduced  
to  
letter

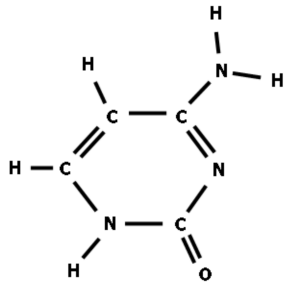
**A**

reduced  
to  
digits  
0 - 4

**0**

reduced  
to two  
binary  
digits

**00**

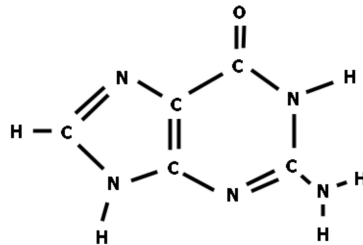


**cytosine**

**C**

**1**

**01**

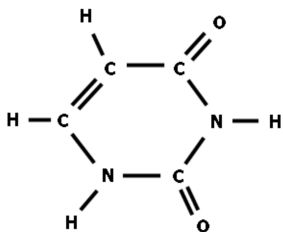


**guanine**

**G**

**2**

**10**



**uracil**

**U**

**3**

**11**

# **Genotype encodes phenotype, phenotype maps to fitness.**

**Biology (much simplified)**

**Each sequence of 3 nucleobases (mRNA)  
encodes one amino acid.  
sequence of amino acids = peptide.**

binary representation	101011 000000 100111 101100 010111
mRNA (genotype)	GGU AAA GCU CUA CCU

**encodes**

peptides (phenotype)	Gly – Lys – Ala – Leu – Pro
----------------------	-----------------------------

**determine**

**fitness**

**(of organism within a given environment)**

# Rossby wave encoding

**Genome consists of genes.**

**Each gene encodes a Fourier term.**

**Fourier term has parameter set.**

**Each parameter encoded as 32 bit integer.**

# **What's the underlying motivation to search for the Rossby wave structure?**

- Retrieve a sharper and more „natural“ way to describe zonal vorticity profiles by reducing the standard deviation along fibers, here along distorted circles of latitude.**
- Find a zonal dynamical pattern that can be used as a context for local fluid dynamical simulations.**
- Find an objective and reproducible way to describe Rossby waves, including ambiguities, if they cannot be resolved.**