THE HAGUE UNIVERSITY OF APPLIED SCIENCES × TEAM IMP

HYPER PARAMETER TUNING

Using genetic algorithm

SUMMARY

Genetic algorithms

Hyper-parameters tuning

Limitations (+ solutions)

Implementation

Some results

GLOSSARY

Genes

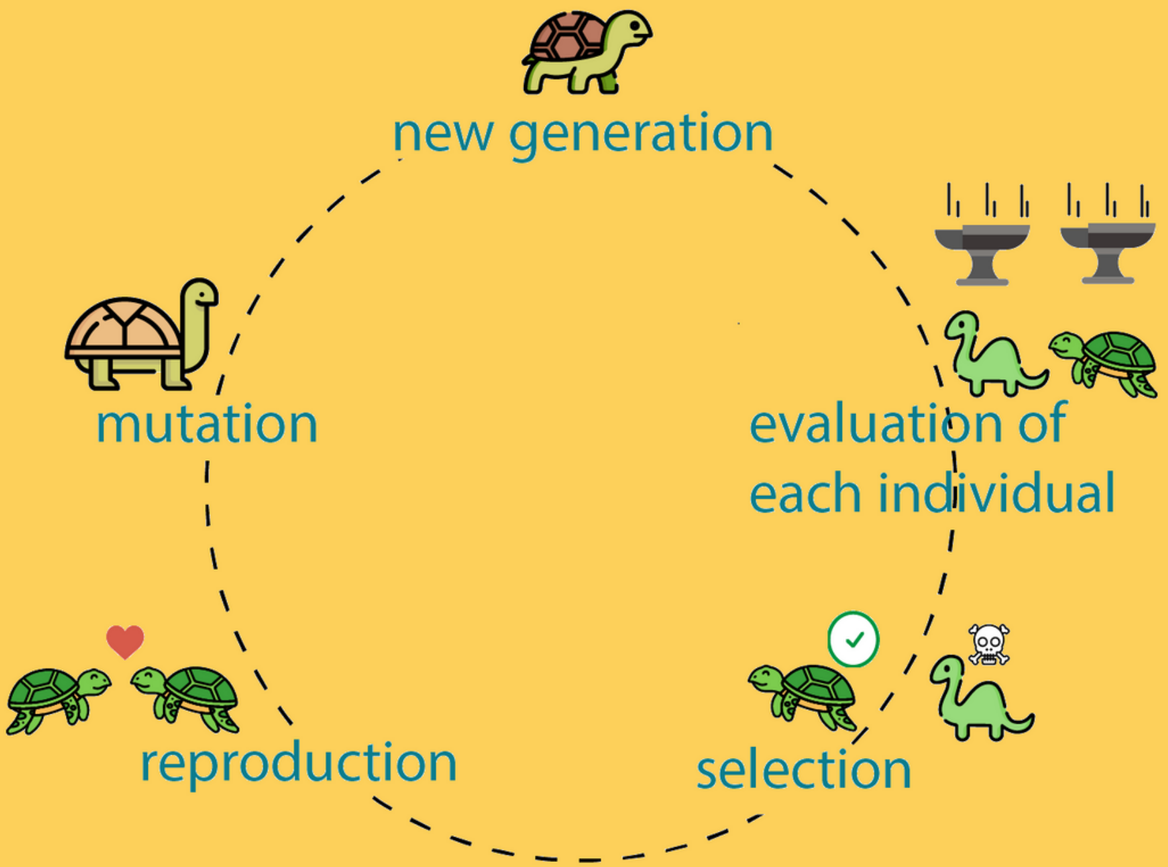
Genomes

Population

Generations

Fitness

GENETIC ALGORITHM



GENETIC OPERATIONS

FULL MUTATION

Creates a fully random new genome

PARTIAL MUTATION

Copies a genome from the population and changes randomly one of his genes

CROSSOVER

Performs a uniform crossover between 2 parents: picks random genes from parent 1 and 2

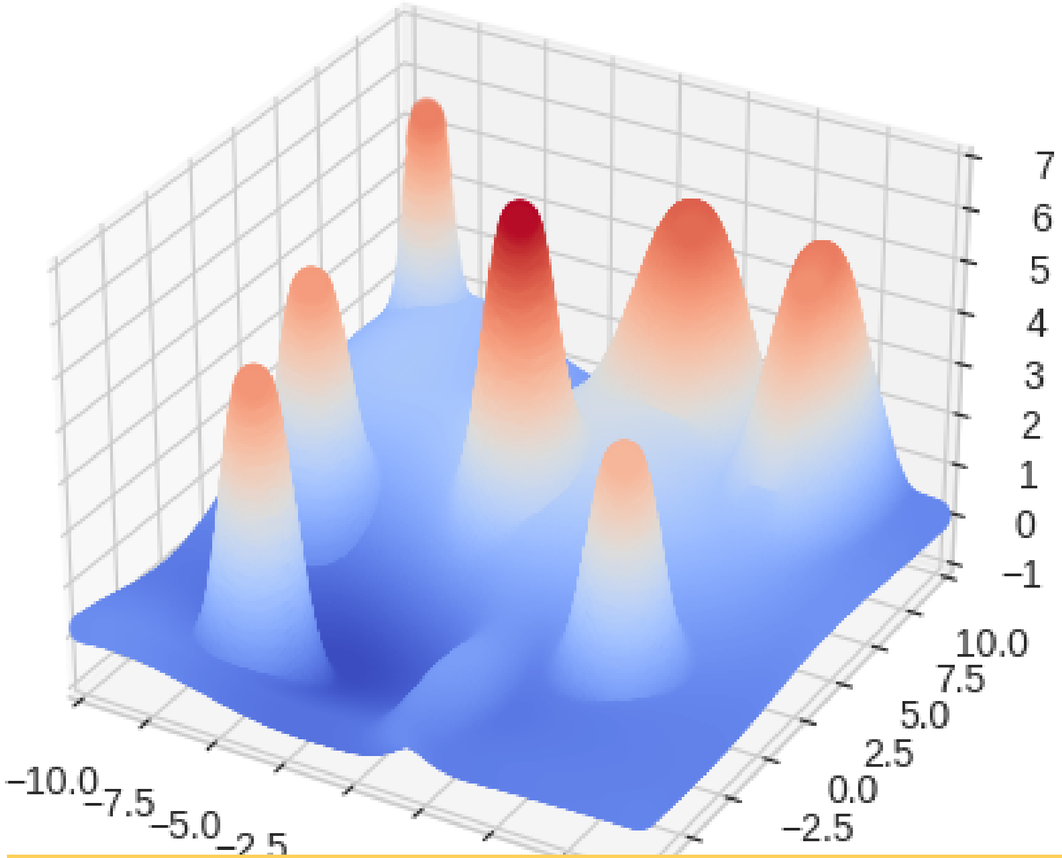
HYPER-PARAMETERS OPTIMIZATION

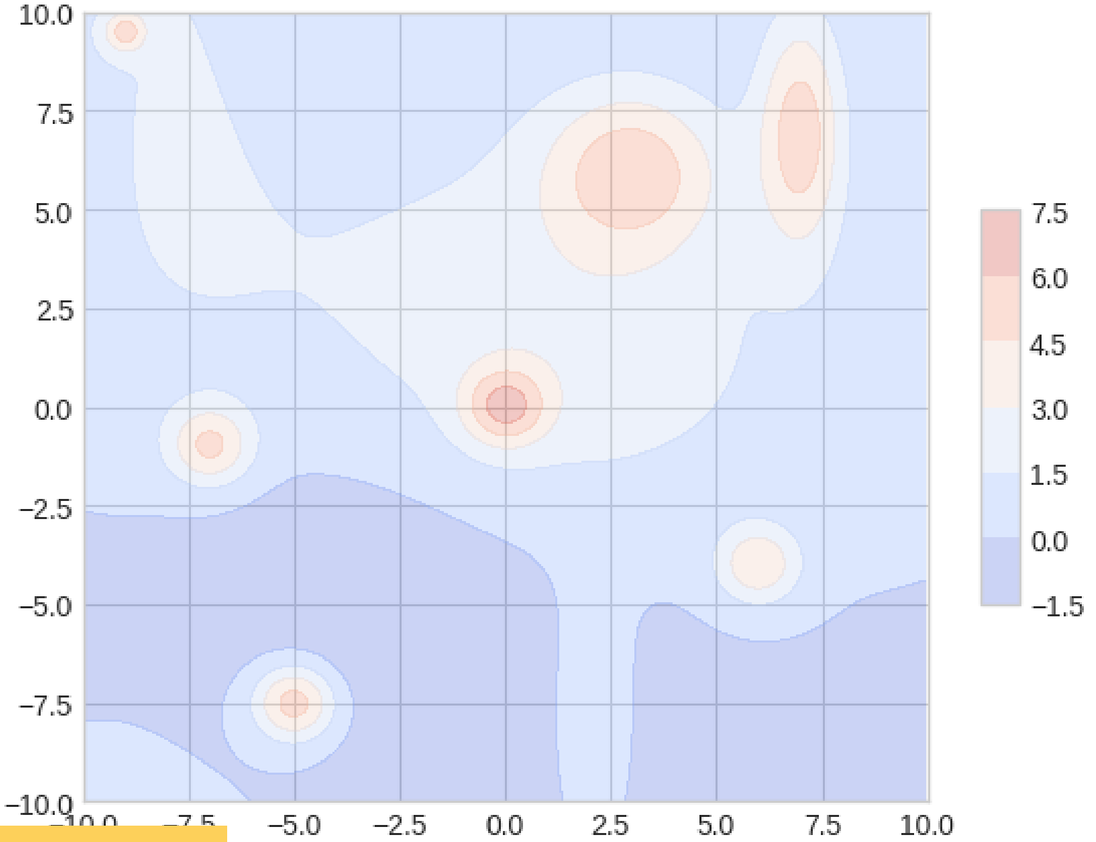
GENE = HYPER-PARAMETER

GENOME = HYPER-PARAMETERS CONFIGURATION

FITNESS FUNCTION = TRAIN AND EVALUATE THE MODEL WITH THE HYPER-PARAMETERS CONFIGURATION

RUN THE GA TO FIND THE BEST-FITTING CONFIGURATION

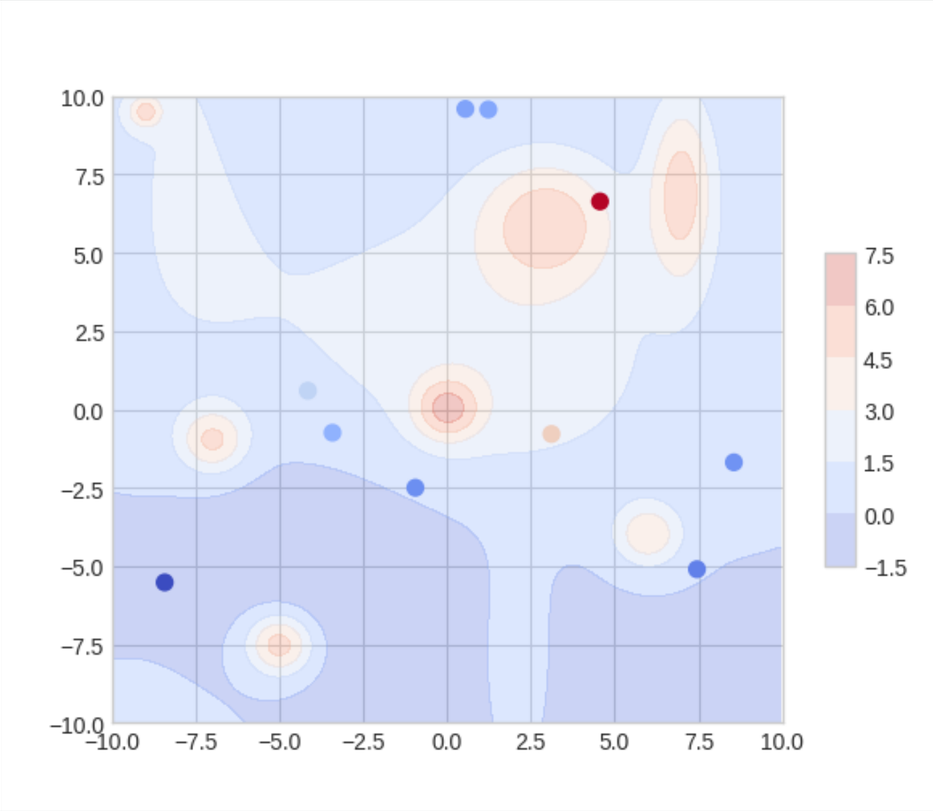




DEMO VISUALIZATIONS

LIMITATION

INITIAL SPACE EXPLORATION



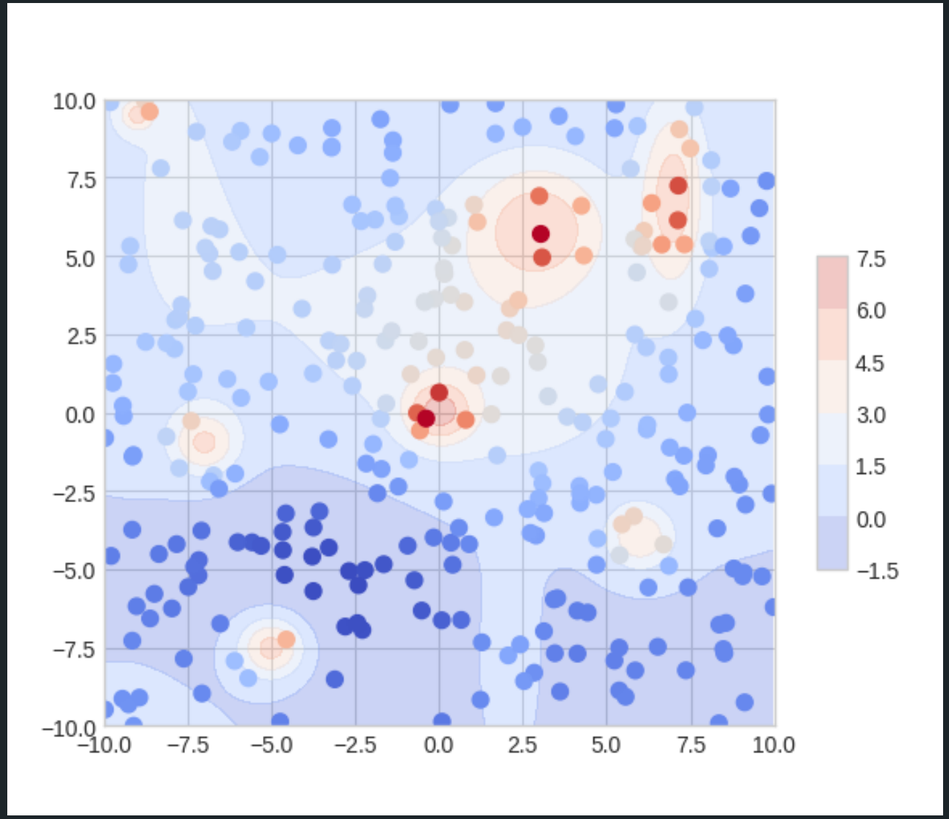
unsufficiently explored space

POSSIBLE CAUSES

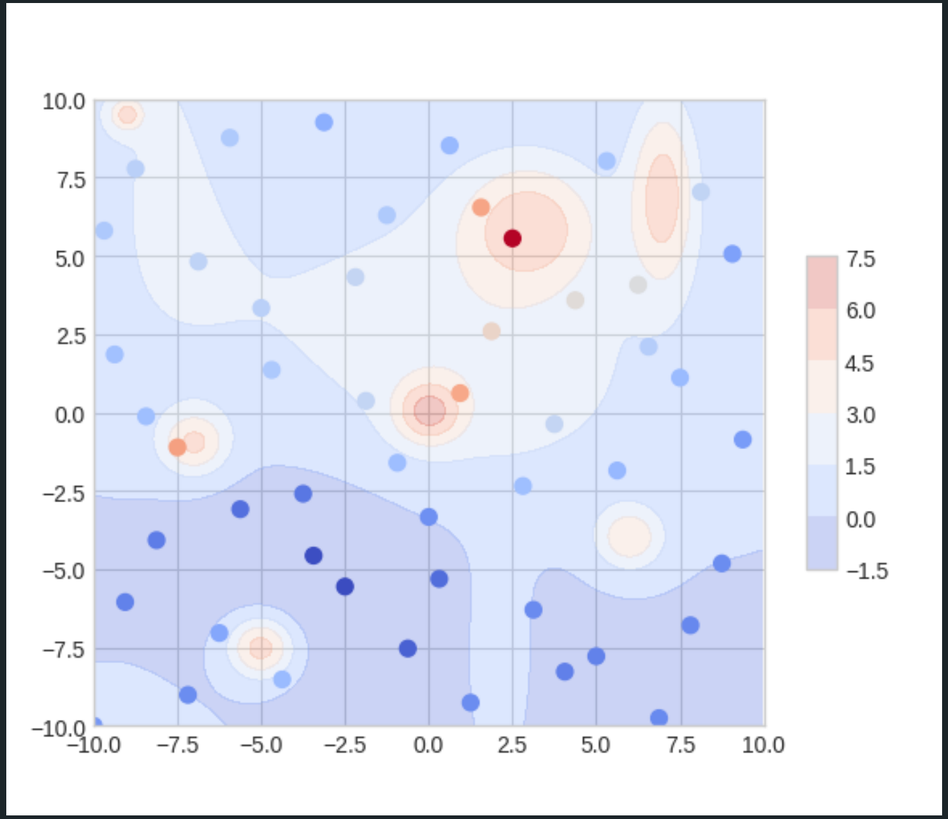
- not enough genomes
- too large bounds
- too many dimensions

SOLUTION

INITIAL SPACE EXPLORATION



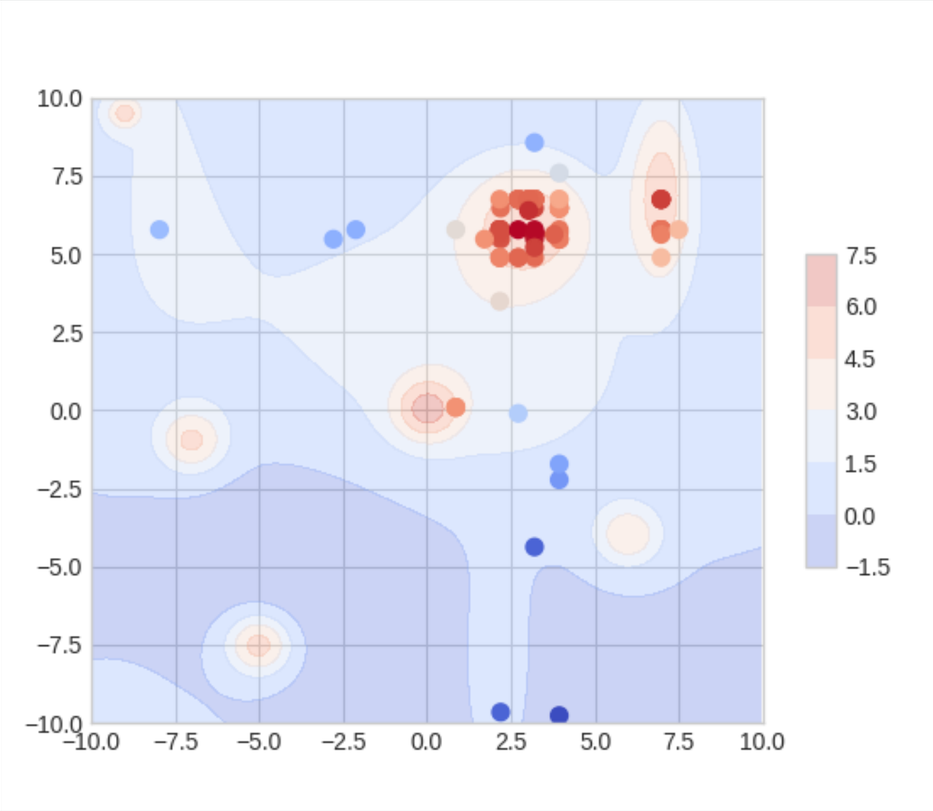
well explored space: numerous genomes



well explored space: low discrepancy sequence (Halton sequence here)

LIMITATION

CONVERGENCE TOWARDS A LOCAL OPTIMUM



genomes converging towards a local optimum

POSSIBLE CAUSES

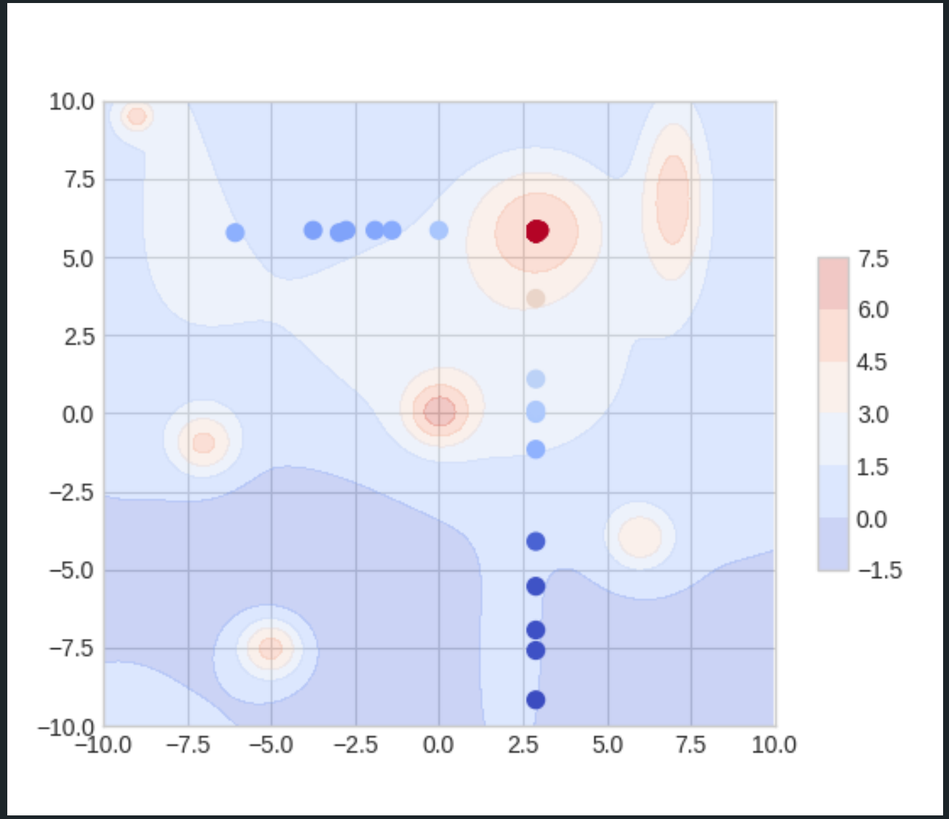
- not enough genomes
- not enough mutation

POSSIBLE SOLUTIONS

- same as previous
- add mutation (full and partial)
- penalize values too close to each other

LIMITATION

NO CLEAR STOP CRITERION MOST OF THE TIME



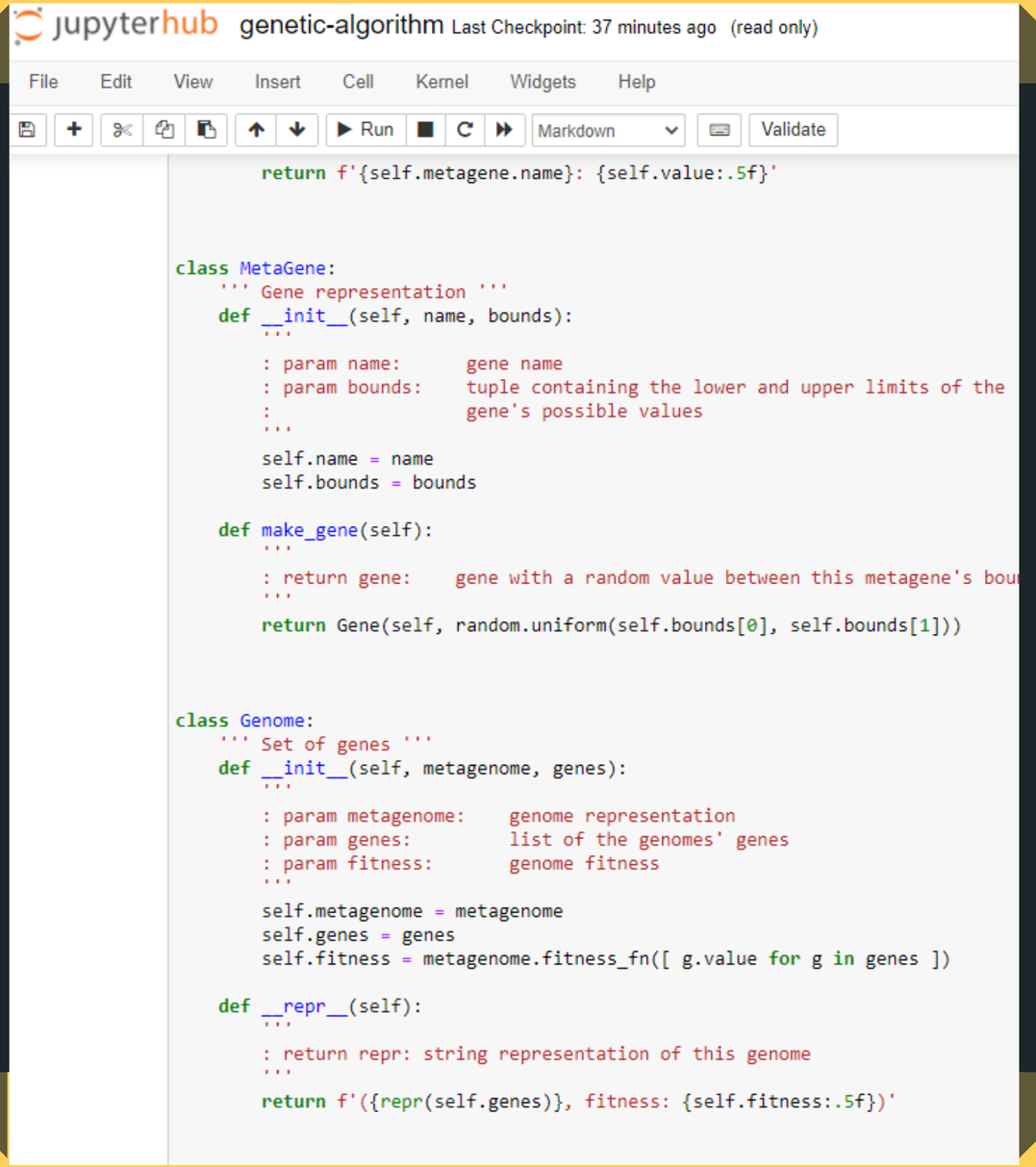
global optimum not reached

POSSIBLE SOLUTIONS

- variance of the best genomes

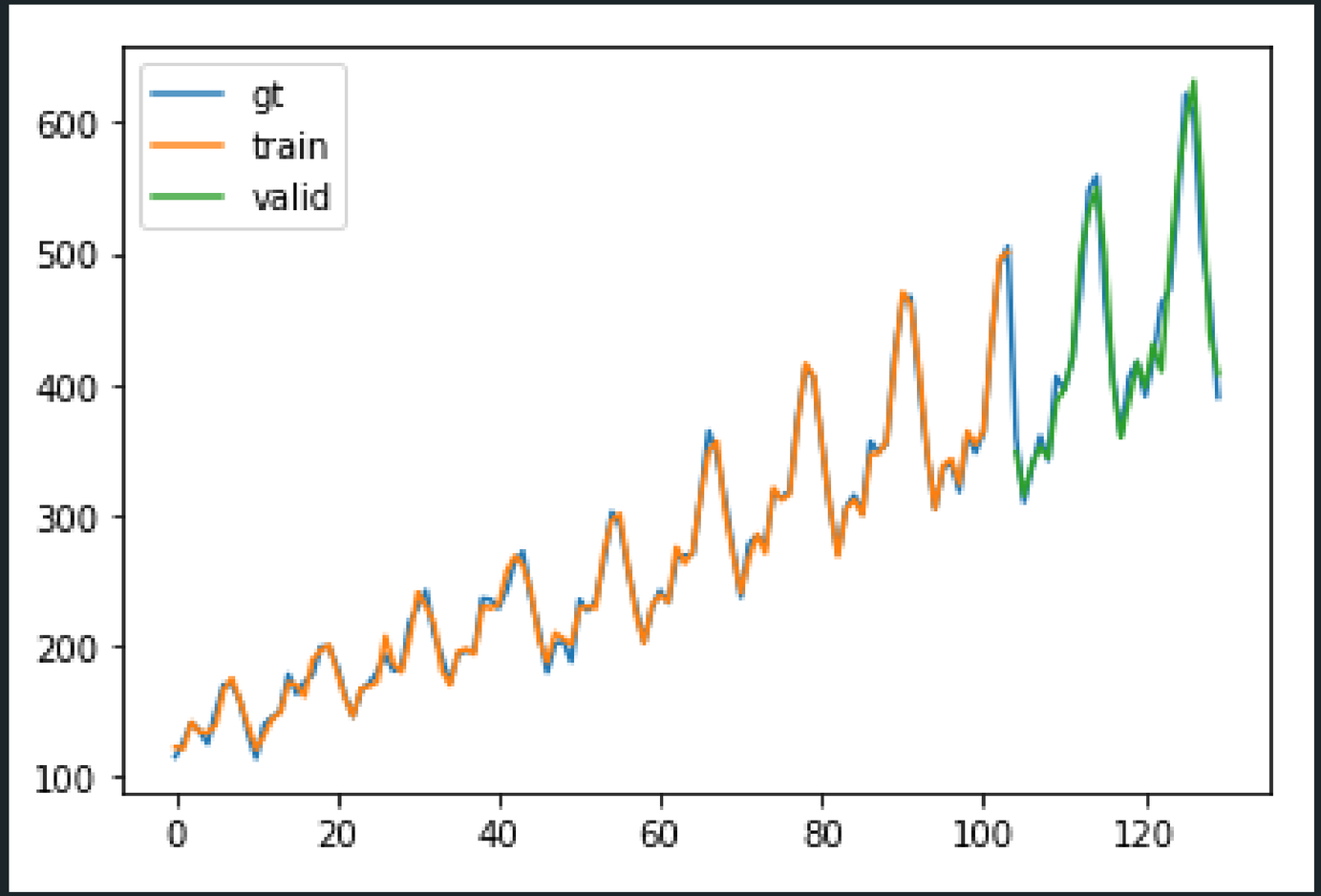
- not always applicable, and never certain

JUPYTER NOTEBOOK



LECTURE EXAMPLE - L6.3 RNN

RESULTS



OUR RESULTS

Batch size	32
Hidden layers size	100
Loss function	MSE
Number of hidden layers	1
Random state	?
RNN architecture	LSTM
Window size	12
Best R2 score	0.9399

RESULTS WITHOUT HYPER PAREMETER TUNING

Batch size	8
Hidden layers size	80
Loss function	Huber
Number of hidden layers	2
Random state	15
RNN architecture	GRU
Window size	12
Best R2 score	0.9636
Generations	40

RESULTS WITH HYPER PAREMETER TUNING

REFERENCES

LOW-DISCREPANCY SEQUENCES (HALTON SEQUENCE)

http://extremelearning.com.au/unreasonable-effectiveness-of-quasirandom-sequences/

VARIANCE AS A STOPPING CRITERION FOR GENETIC ALGORITHMS

https://www.isical.ac.in/~sankar/paper/Bhandari-2012.pdf

QUESTIONS ?

THANKS FOR YOUR ATTENTION

GITHUB REPOSITORY

https://github.com/thuas-imp-2021/Learning-Lab

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