

ДОДАТОК А

Використані протоколи

Протокол для опису типу проекту

code of project type

1st digit - is code of task

1 - classification, 2 - clasterisation, 3 - regression

2nd digit - is a code for project input data type

0 - audio, 1 - text, 2 - image, 3 - video, 4 - table, 5 - timesteps

3rd digit - is a code for type of project

0 - custom, 1 - applied, 2 - optimising

4th digit - type of optimising algorithm

0 - without, 1 - genetic, 2 - immune

5-6th digit - type of aplied models project

00 - without, 01 - ResNet50V2

7th digit - is additional

-if not optimising && image, 0 - simple convolutional, 1 - perceptron,

For example 1221000 is a code of project which use c2d_gui window:

<i>task:</i>	<i>(1)classification</i>
<i>input type:</i>	<i>(2)image</i>
<i>project type:</i>	<i>(2)optimising</i>
<i>optimising algorithm:</i>	<i>(1)genetic</i>
<i>applied:</i>	<i>(0)</i>
	<i>(0)without</i>
<i>additional:</i>	<i>(0)simple convolutional</i>

Лістинг – Протокол мережевої взаємодії

```
def send_remaster(target: str, data: Any, socket):
    data = {"target": target, "data": data}
    data = json.dumps(data)
    data += "&"
    socket.send(bytes(data, encoding="utf-8"))
```

Протокол визначення набору елементів для відображення як список проектів

"name" - name of project: QLabel

"type" - type of project: QLabel

"play_pause" - play/pause button: QToolButton

"archive" - archive button: QToolButton

"sett" - settings of project button: QToolButton

"stop" - stop button: QToolButton

"progbar" - progress bar: QProgressBar

"toQueue" - toQueue button: QToolButton

"plot" - show plots button: QToolButton

...

ДОДАТОК Б

Реалізація основного циклу генетичного пошуку

```

def c2dEvolve(self):
    self.population.clear()
    ##### Initialise population #####
    send_remaster("gen_epoch", 0, self.pc_sock)
    for i in range(self.project_params.popSize):
        self.population.append(C2dChromosome(self.project_params))
        self.population[i].name = str(i + 1)
        print(self.population[-1].getNetConfig(0))
        send_remaster("chr_config", self.population[-1].getNetConfig(0),
                      self.pc_sock)
        self.calculate_c2d(self.population[-1], self.project_params,
                           self.net_port, self.opt_sock)
        data = json.loads(self.listener.buffer)
        self.listener.buffer = ""
        paramsCount = data.get("data")[0]
        report = data.get("data")[1]
        self.tempMetrics.append([paramsCount, report])
        self.population[i].paramsCount = paramsCount
        self.population[i].report = report
        send_remaster("interim_est",
                      [paramsCount, report.get("accuracy")], self.pc_sock)

    self.setAssessment(1, self.tempMetrics)
    self.population.sort(key=lambda x: x.assessment, reverse=True)
    send_remaster("accuracy", self.getAccuracy(0), self.pc_sock)
    send_remaster("assesment", self.getAssessment(1, 0), self.pc_sock)
    send_remaster("params", self.getParams(0), self.pc_sock)
    send_remaster("assesment_str", self.getAssessment(0, 0), self.pc_sock)

    #####

    ##### Main cycle with genetic operators #####
    select = selection(len(self.population), self.project_params.selection)
    for epoch in range(self.project_params.genEpoch):
        self.tempMetrics.clear()
        send_remaster("gen_epoch", epoch + 1, self.pc_sock)
        for i in range(len(self.population)):

```

```

is_cross = False
is_mutate = False
if i < select[0]:
    self.tempMetrics.append([self.population[i].paramsCount,
                            self.population[i].report])
    continue
elif i < select[0] + select[1]:
    is_cross = self.population[i].mutate(self.project_params.mutateRate)
else:
    is_mutate = self.population[i].mutate(self.project_params.mutateRate)
if is_cross or is_mutate:
    send_remaster("chr_config", self.population[i].getNetConfig(0),
                 self.pc_sock)
    self.calculate_c2d(self.population[i], self.project_params,
                     self.net_port, self.opt_sock)
    data = json.loads(self.listener.buffer)
    self.listener.buffer = ""
    paramsCount = data.get("data")[0]
    report = data.get("data")[1]
    send_remaster("interim_est",
                 [paramsCount, report.get("accuracy")], self.pc_sock)
    self.population[i].paramsCount = paramsCount
    self.population[i].report = report
    self.tempMetrics.append([paramsCount, report])

else:
    self.tempMetrics.append([self.population[i].paramsCount,
                            self.population[i].report])

self.setAssessment(1, self.tempMetrics)
self.population.sort(key=lambda x: x.assessment, reverse=True)
send_remaster("accuracy", self.getAccuracy(epoch + 1), self.pc_sock)
send_remaster("assesment", self.getAssessment(1, epoch + 1), self.pc_sock)
send_remaster("params", self.getParams(epoch + 1), self.pc_sock)
send_remaster("assesment_str", self.getAssessment(0, epoch+1), self.pc_sock)

self.project_controller.is_run = False
self.pc_sock.close()

```

ДОДАТОК В

Перелік графічних матеріалів

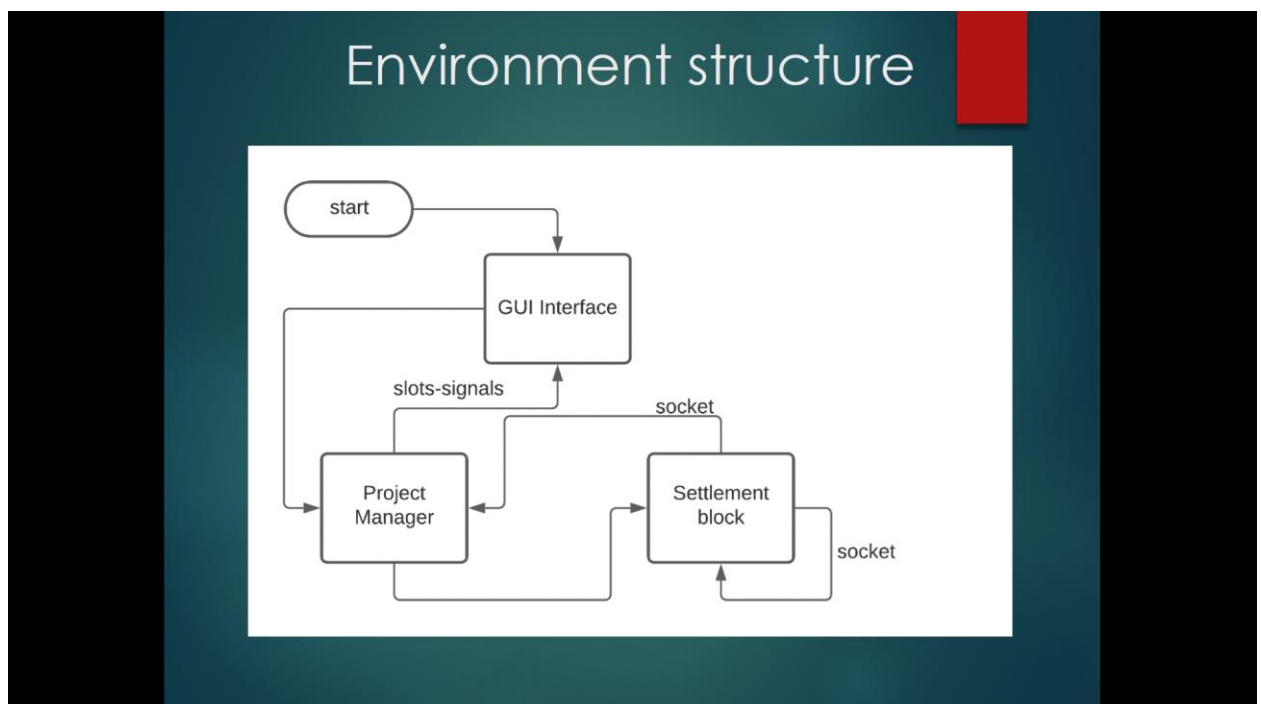

МІНІСТЕРСТВО ОСВІТИ І НАУКИ УКРАЇНИ
ХАРКІВСЬКИЙ НАЦІОНАЛЬНИЙ УНІВЕРСИТЕТ РАДІОЕЛЕКТРОНІКИ
ФАКУЛЬТЕТ КОМП'ЮТЕРНОЇ ІНЖЕНЕРІЇ ТА УПРАВЛІННЯ
КАФЕДРА КІТС

**Інтелектуальна система побудови
неймережевих моделей**

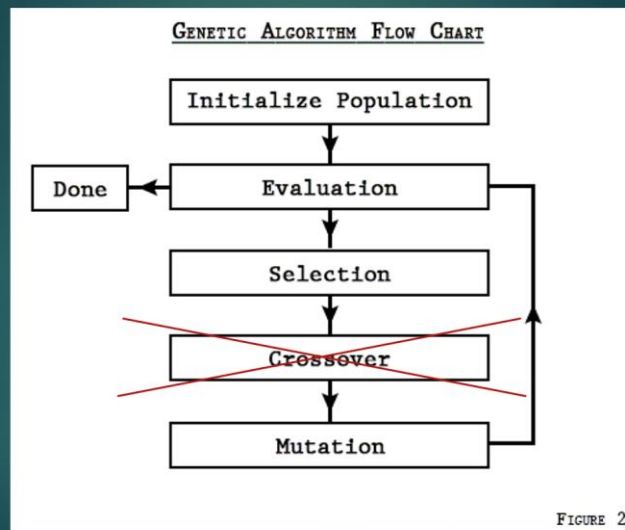
Магістрант гр. КІТм-19-1
Науковий керівник

Васильєв С.О.
проф. Безсонов О.О.

Харків 2020



Genetic algorithm



Hyperparameters

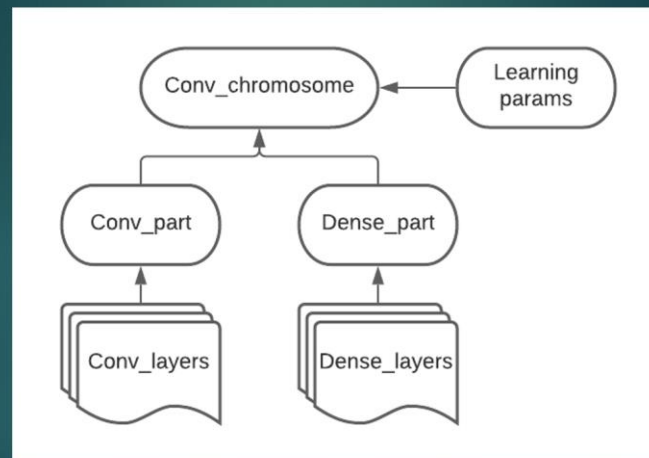
Structure

- Numb and type of layers
- Activation function
- Layer params

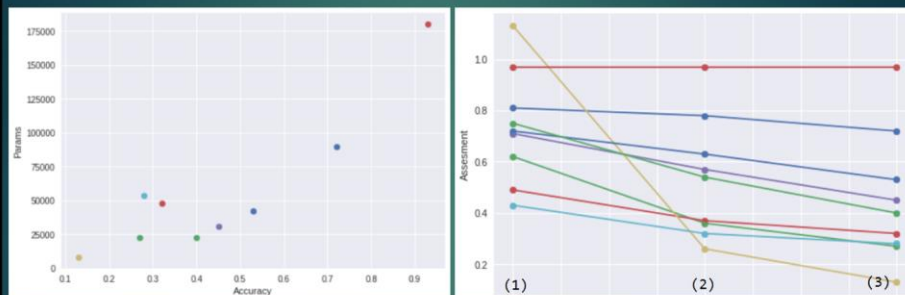
Fitting

- Optimizer
- Loss function
- Init LR
- Epoch

Structure of chromosome



Fitness Function

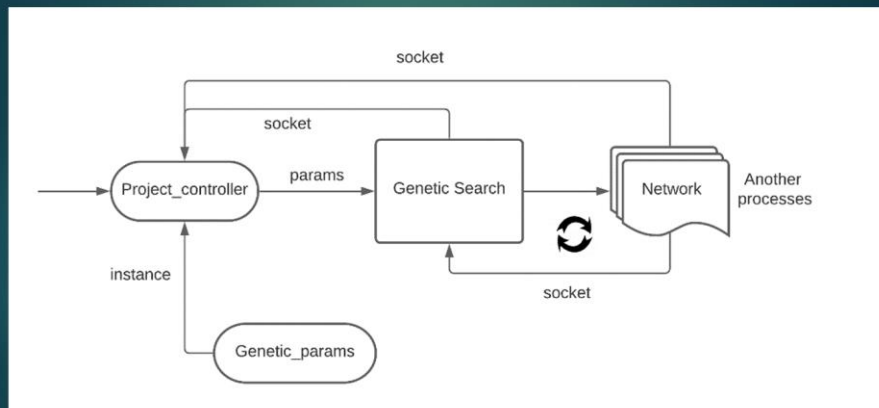


$$A_i = \alpha_i + \frac{p_{\min}}{p_i} \quad (1)$$

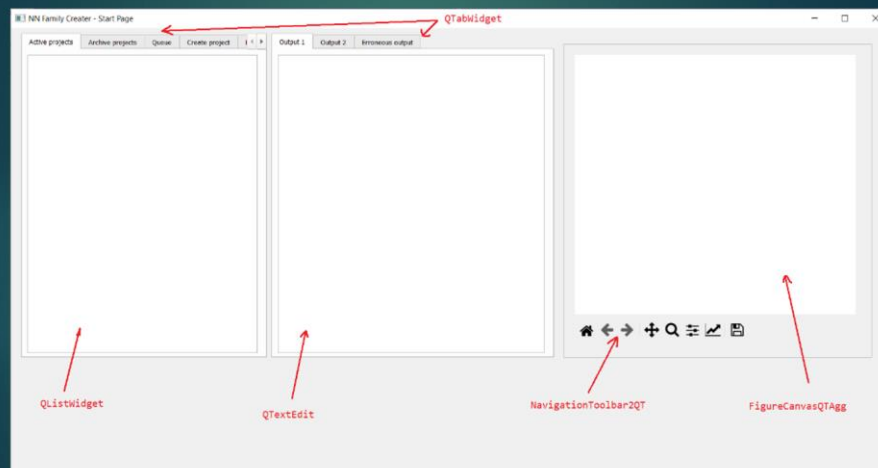
$$A_i = \alpha_i + \alpha_i \cdot \frac{p_{\min}}{p_i} \quad (2)$$

$$\begin{cases} A_i = \alpha_i + \alpha_i \cdot \frac{p_{\min}}{p_i}, & \text{if } \alpha_i > t \\ A_i = \alpha_i, & \text{if } \alpha_i < t \end{cases} \quad (3)$$

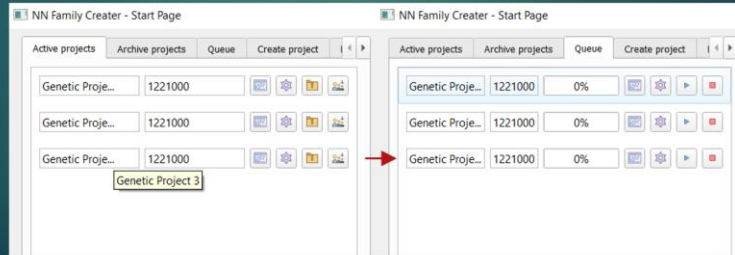
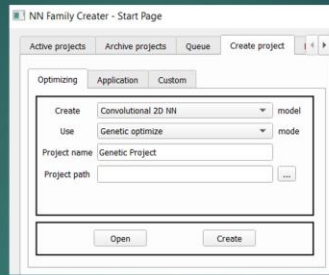
Genetic fitting



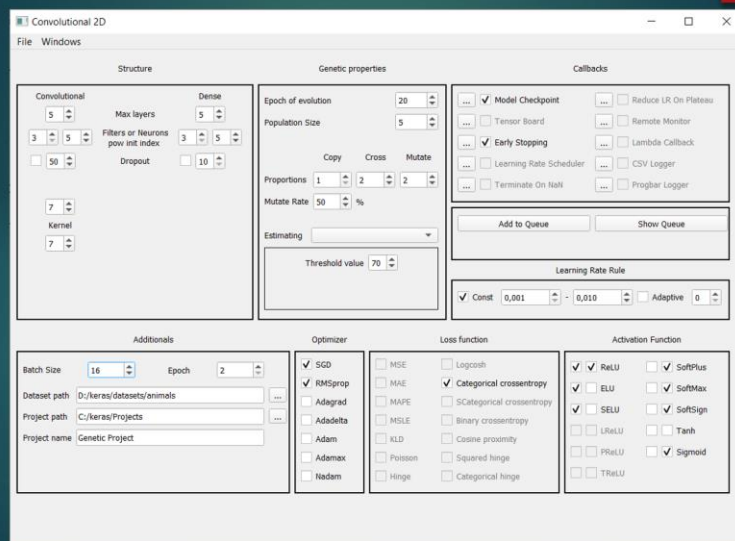
Start page



Getting start



Convolutional project settings



Different Plots

