

Data structure

	Part 1															Part 2	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
	Hidden Size			Stacked Layers			Learning Rate		Batch Size			Epochs				Split	
Chromosome 1																	
Chromosome 2																	

Part 1

- *Hidden size* = number of memory cells.
- *Stacked layers* = number of layers inside LSTM.
- *Learning rate* = step rate for optimizing the gradients during the backpropagation.
- *Batch size* = number of samples used in one iteration of training.
- *Epochs* = number of training iterations.

Part 2

- *Split* = Dataset partitions splitted in training and test datasets.

ICAN (inter and intra-chromosome crossover)

Phase 1: inter crossover

	Part 1															Part 2	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
	Hidden Size			Stacked Layers			Learning Rate		Batch Size			Epochs			Split		
Chromosome 1																	
Chromosome 2																	
Offspring 1																	
Offspring 2																	

During inter crossover 2 chromosomes exchanges genes to generate 2 new offsprings for the next generation(**Single-point crossover or multiple-points crossover etc. can be used for inter *crossover phase*.**

Phase 2: intra-chromosome crossover

	Part 1															Part 2	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
	Hidden Size			Stacked Layers			Learning Rate		Batch Size			Epochs				Split	
Chromosome 1																	
Chromosome 2																	
Offspring 1																	
Offspring 2																	

During intra crossover, genes are exchanged within chromosomes to generate new offsprings for the next generation(*This is done to introduce additional variability*).

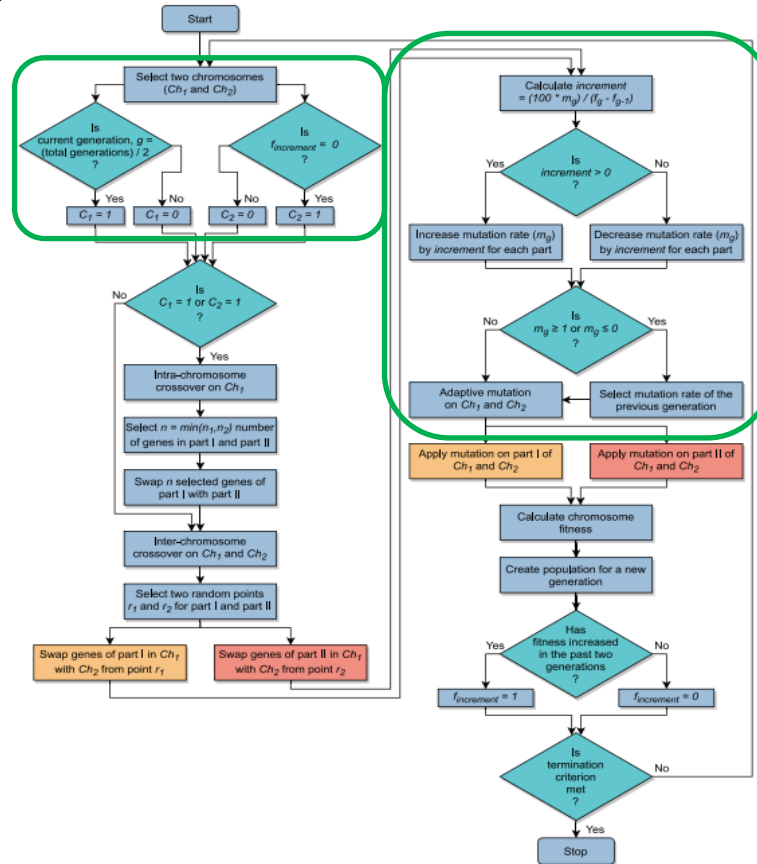
Phase 3: Adaptive bit-flip mutation

	Part 1															Part 2	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
	Hidden Size			Stacked Layers			Learning Rate		Batch Size			Epochs			Split		
Chromosome 1																	
Chromosome 2																	
After mutation																	
Offspring 1																	
Offspring 2																	

$$MSE = \frac{1}{N} \cdot \sum_{i=1}^N (Y_i - \hat{Y}_i)^2$$

This process of selection, inter-chromosome crossover, and adaptive mutation are repeated until the defined criterion is met.

GA flow chart



$$\text{increment} = \frac{100 \times m_g}{f_g - f_{g-1}}$$

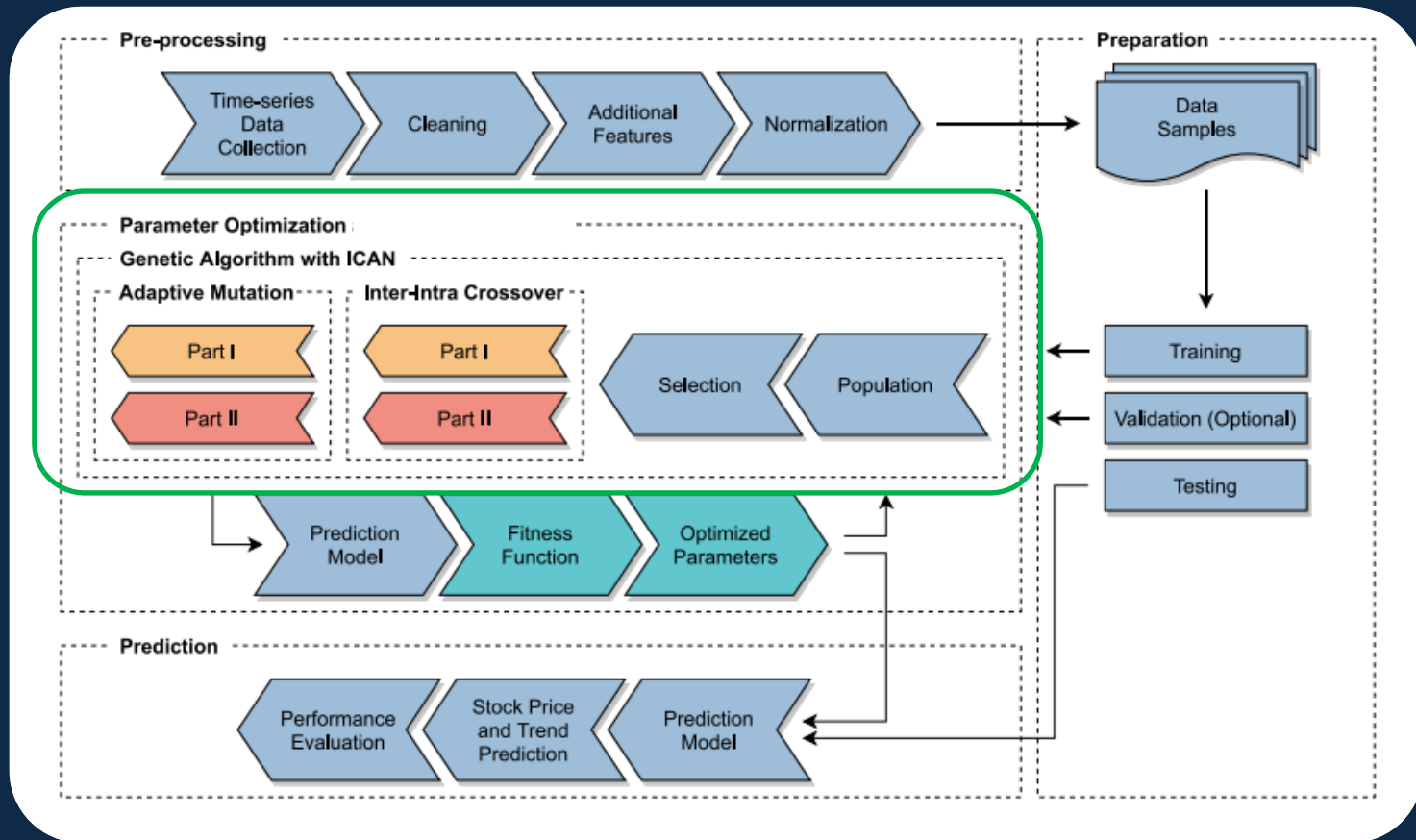
Where :

mg = mutation rate

fg = fitness value in actual generation

fg -1 = fitness value in previous generation

Model flow chart



Results

