



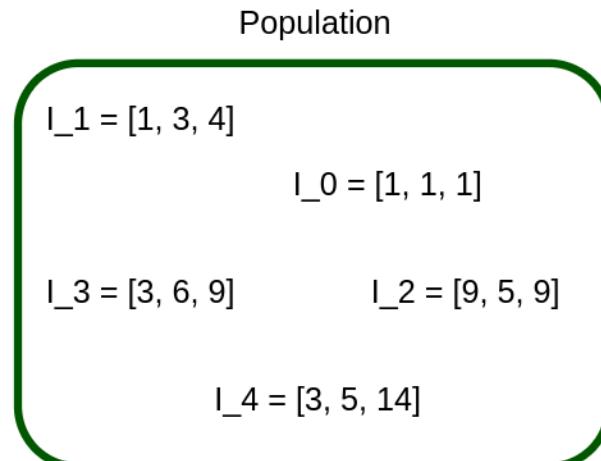
PyGMA : Pythonic Genetic MPI parallelized Algorithm

Agenda

- Genetic Algorithm principles
- PyGMA implementation
- Usage example
- MPI Implementation
- Conclusion

Genetic Algorithm

- GA combines
 - Darwin's theory of evolution
 - Mendel's theory of genetics
- Population
 - Individuals
 - Represent solution
 - Have fitness
 - Evaluation
 - Mutation
 - Recombination



$$Y = w_0 * 3 + w_1 * 1 + w_2 * 2$$

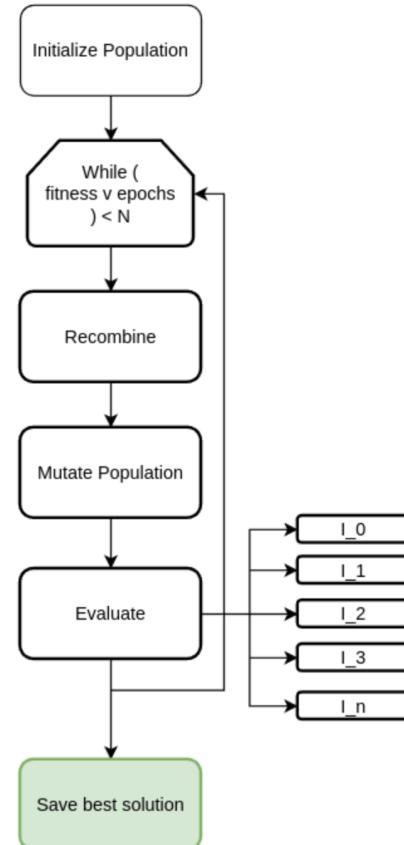
How to choose w_n such that $Y = 42$?

$$I_3 = 3 \times 3 + 6 \times 1 + 9 \times 2 = 33$$

$$\text{error} = | 33 - 42 | = 9$$

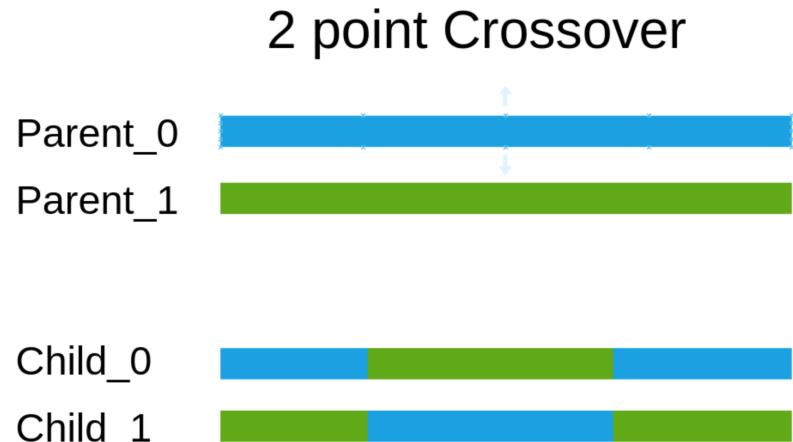
$$\text{fitness} = 1.0 / 9 = 0.111$$

Algorithmic flow



Genetic Operators

- Mutation
 - Random change
 - $1001 \rightarrow 1000$
- Crossover
 - 1, 2, k point
- Bitwise operators
 - AND, OR, XOR
- Chosen Operators depend on the problem



Experiments

- The experiment is the task which the GA should solve

Population

I_1 = [1, 3, 4]

I_0 = [1, 1, 1]

I_3 = [3, 6, 9]

I_2 = [9, 5, 9]

I_4 = [3, 5, 14]

$$Y = w_0 * 3 + w_1 * 1 + w_2 * 2$$

How to choose w_n such that $Y = 42$?

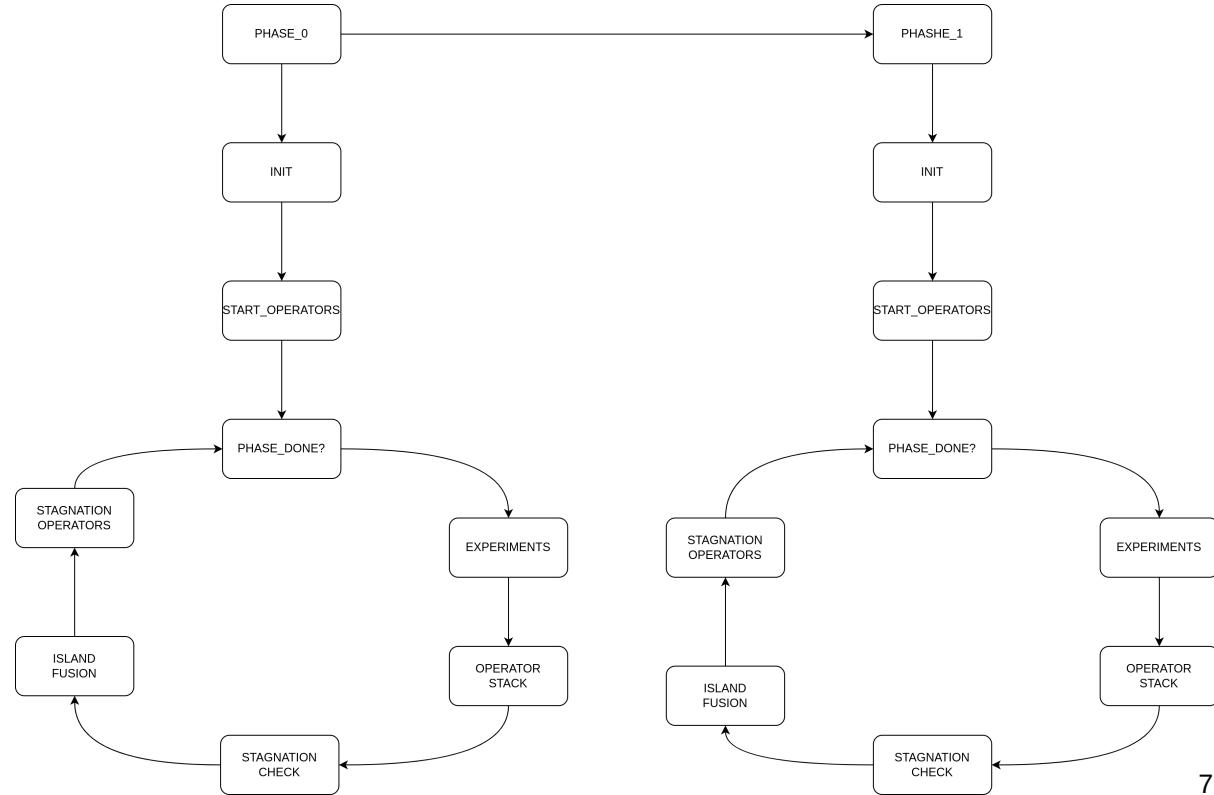
$$I_3 = 3 \times 3 + 6 \times 1 + 9 \times 2 = 33$$

$$\text{error} = | 33 - 42 | = 9$$

$$\text{fitness} = 1.0 / 9 = 0.111$$

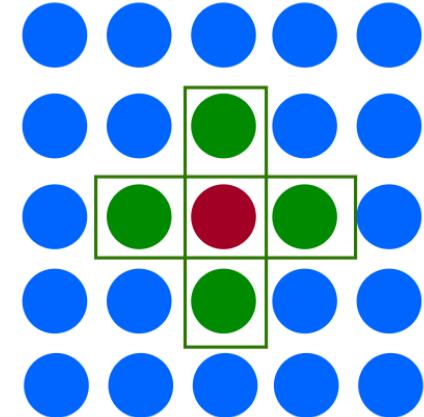
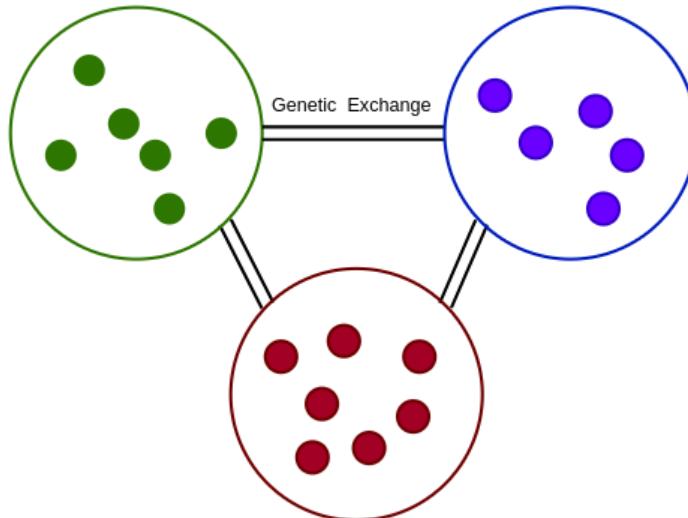
Evolutionary Phase

- Idea:
 - do not solve complex problems directly
 - Solve a simple version first
 - Then a more complex one
 - ...



Evolution Models

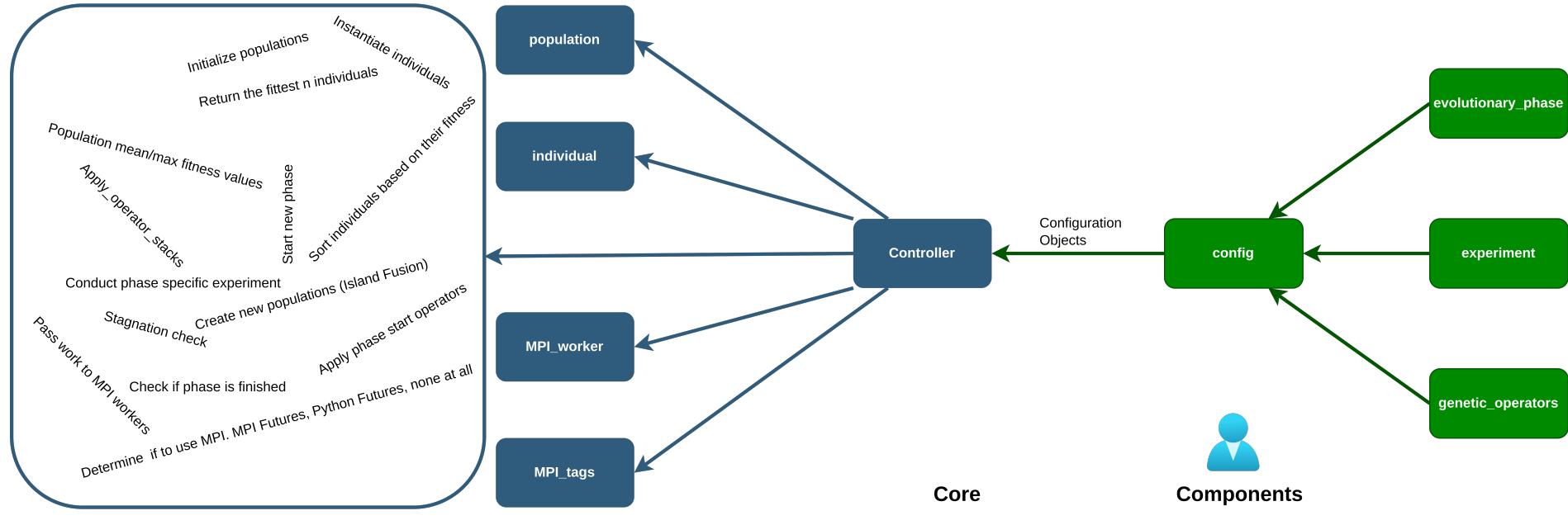
- Island's
 - Island fusion
- Cellular
- Hybrid
 - <Island, Cellular>





PyGMA

- Pythonic Genetic MPI parallelize'd Algorithm
 - Handles the important GA parts
- User interaction
 - Class interfaces
 - Genetic Operators
 - Experiments
 - Evolutionary Phases
 - Config



Usage Example

- Function optimisation
 - $F = x^2 + y^3 + z$
 - How to choose x,y,z such that $F = 424242$?
- Steps
 - Define experiment
 - Define evolutionary phase (optional)
 - Define genetic operators (optional)
 - Create configuration
 - Run PyGMA

Define Experiment

```
class Function_optimisation_experiment(Experiment):
    """
    Find values for the function such that it matches a certain output
    """

    def f(self, x, y, z):
        return x*2 + y*3 + z

    def conduct(self, gene) -> float:
        # split gene into blocks that are binary representation
        # of the numbers
        numbers = np.split(gene, 3)
        # convert the numbers to ints
        x = bool2int(numbers[0])
        y = bool2int(numbers[1])
        z = bool2int(numbers[2])

        # define the objective output for our function
        output = 424242

        # calculate the output
        r = self.f(x, y, z)

        # calc error and fitness
        error = abs(r-output)

        # if error is small fitness is high
        # make sure that if error can not be 0 :)
        fitness = 1.0/(error + 0.0000000000000001)

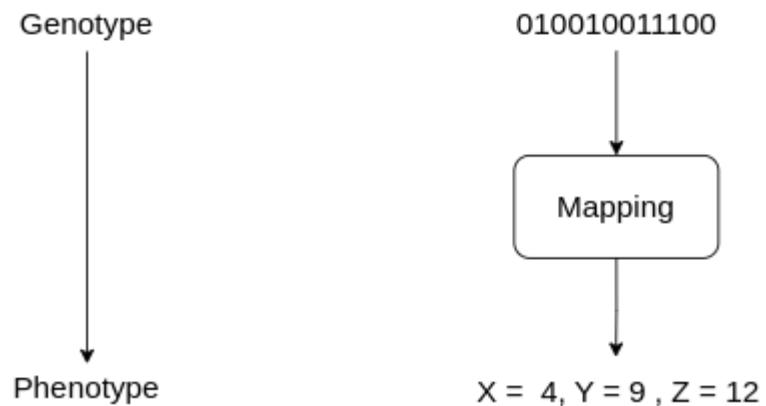
        # print(f'error: {error} fitness {fitness}')
        return fitness
```

Define Phase

```
class Simple_evolutionary_phase(Evolutionary_phase):
    def completed(self, population_fitness: list, epochs: int) -> bool:
        """
        Called to check if the phase has reached its end.
        """
        max_fitness = max(population_fitness)
        if max_fitness > 0.9:
            return True

        if epochs > 5000:
            return True

        return False
```



Define Genetic Operators

```
class Mutation_operator(Genetic_operator):
    """
    This class represents a mutation operator.
    """

    def __init__(self, mutation_rate, rng_seed=9):
        self.mutation_rate = mutation_rate
        self.rng = np.random.default_rng(rng_seed)

    def operate(self, old_population, new_population):
        """
        Apply mutation to all genes of the current op stack.
        """

        for gene in new_population:
            # mutation indexes
            # having at least one mutation
            mutations = int(self.mutation_rate*gene.size)
            if mutations == 0:
                mutations = 1
            indexes = self.rng.integers(low=0, high=gene.size, size=mutations)
            # flip the bits at indexes
            # note, ~ is like np.invert()
            gene[indexes] = ~gene[indexes]
        return new_population
```

Make Configuration

- Instantiation of
 - Genetic Operators
 - Experiment
 - Evolutionary Phases
- Genetic Operator stack/Num Populations
- Individuals per population
 - Genome length
- Initialisation of Genes (predef, random)
- Use MPI ?

```
# -----
# Genetic operator definition
# -----
# Genetic operators can be used for:
# Populations
# Genetic Phases

OP_MUTATION = Mutation_operator(0.06)
OP_REMOVAL = Removal_operator(6)
OP_CROSSOVER = Single_point_crossover_operator(6)

# -----
# Populations
# -----
# how many island populations to use
# is defined by the genetic operators stack length
# used to recombine/produce, mutate, extend...
'genetic_operator_stack': [
    # pop 0
    [OP_REMOVAL, OP_CROSSOVER],
    # pop 1
    [OP_REMOVAL, OP_CROSSOVER, OP_MUTATION],
    # pop 2
    [OP_REMOVAL, OP_REMOVAL, OP_REMOVAL, OP_MUTATION, OP_CROSSOVER, OP_CR]
```

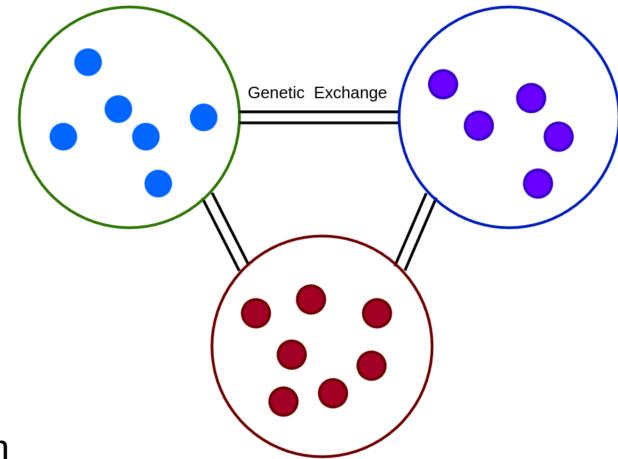
Run Pygma

- mpiexec -n 3 python PyGMA.py
- Evolutionary phase Phase_0
- epoch 0, Pop max fitness [9.925775054145103e-07, 2.12027020723521e-06, 1.6586828731041255e-06]
- epoch 1, Pop max fitness [1.3549254249046132e-06, 1.545657167057718e-06, 1.9955061202172707e-06]
- epoch 2, Pop max fitness [1.3549254249046132e-06, 1.585273443816324e-06, 0.0005668934240362812]
- epoch 3, Pop max fitness [2.2883504654504845e-06, 3.542180282807674e-06, 3.122268015486449e-05]
- ...
- epoch 209, Pop max fitness [3.054386404315237e-06, 0.0002605523710265763, 0.0004068348250610252]
- epoch 210, Pop max fitness [3.054386404315237e-06, 0.00011841326228537596, 4.1221814584278e-05]
- epoch 211, Pop max fitness [3.054386404315237e-06, 0.00013356484573260317, 0.0004730368968779565]
- epoch 212, Pop max fitness [3.054386404315237e-06, 9.994003597841295e-05, 1e+17]
- Finished phase Phase_0
- -----
- stopping mpi workers
- Evolve finished

Parallelization

Parallelization

- Idea
 - If there are multiple populations (Islands), compute each on its own node
 - Genetic operators are applied in parallel
 - But
 - Normally one does not want to use too many Islands
 - Need to evaluate individual genes anyway and as such distribute them
- Idea
 - Applying Genetic operators is fast
 - Fitness evaluation takes time
 - => Distribute individual genes to workers that will evaluate the fitness



Parallelization schemata

- None
- Local Processes
 - Python's ProcessPoolExecutor
- Message Passing Interface
 - MPI calls (utilizing mpi4py)
 - mpi4py MPIPoolExecutor

MPI implementation

```
# will use the cached module and as such the global intercomm
from mpi4py import MPI
from core.mpi_tags import mpi_tags
comm = MPI.COMM_WORLD
world_size = comm.Get_size()

# while we have data distribute it to free workers
# collect finished data as well
# a gene is computed once the result is written back
genes_to_compute = len(worker_tuples)
while genes_to_compute > 0:
    # check all workers
    for worker_index in range(1, world_size):

        # check if worker can compute new data (Is idle) and we have data to compute
        if worker_tuples and comm.iprobe(source=worker_index, tag=mpi_tags.IDLE):
            # eat up that message to clean the pipeline
            comm.recv(source=worker_index, tag=mpi_tags.IDLE)
            # pop the next data to distribute
            data = worker_tuples.pop()
            # signalling the worker that it should continue to work
            comm.send(True, dest=worker_index,
                      tag=mpi_tags.CONTINUE_PROCESSING)
            # send data to worker
            comm.send(data, dest=worker_index,
                      tag=mpi_tags.DATA)

        # check if we can retrieve a result from the worker
        if comm.iprobe(source=worker_index, tag=mpi_tags.DATA_RETURN):
            # retrieve the result
            w_result = comm.recv(
                source=worker_index, tag=mpi_tags.DATA_RETURN)
            # write the fitness result into the appropriate individual
            self.populations[w_result[0]].individuals[w_result[1]].fitness = w_result[2]
            # note that we have computed a gene
            genes_to_compute -= 1

# worker
# work until stop is signalled
while True:
    # print(f'worker {rank} loop')
    # signaling that we are waiting for new work
    self.comm.isend(None, dest=0, tag=mpi_tags.IDLE)

    # we receive a bool if we shall to continue to process
    # to not eat all CPU ressources we sleep a little if no transmission
    # but this will slow down tremendously,
    # don't sleep when you are supposed to be present
    if self.sleep_time > 0:
        while not self.comm.iprobe(source=0, tag=mpi_tags.CONTINUE_PROCESSING):
            # sleep
            time.sleep(self.sleep_time)
        continue_processing = self.comm.recv(
            source=0, tag=mpi_tags.CONTINUE_PROCESSING)

    # if we shall not continue stop the worker
    if not continue_processing:
        break

    # get the working data
    # format will be (pop_index, indiv_index, phase_index, gene)
    data = self.comm.recv(source=0, tag=mpi_tags.DATA)

    # extract data
    pop_index = data[0]
    indiv_index = data[1]
    phase_index = data[2]
    gene = data[3]

    # instantiate the experiment and evaluate the individual
    experiment = self.config['evolutionary_phases'][phase_index].experiment

    # conduct the experiment
    fitness = experiment.conduct(gene)

    # return the result tuple
    self.comm.send((pop_index, indiv_index, fitness),
                  dest=0, tag=mpi_tags.DATA_RETURN)
```

Future Work

- Stagnation check
- Hardware evolving experiment
 - Experiment
 - Operators
 - Phases
- Runtime analysis (Single process, multi process, MPI)

Conclusion

- GA Algorithm works (MPI)
- Defining Fitness function for hardware evolving is not simple
- Diagram's help a lot during implementation