Step 1: Set up the parameters of MGA for the optimization of process

Planning.

*Step 2*: Generate an initial population (i.e. *regular population, P*) .

The *regular population* *P*, is formed by randomly creating

individuals at the beginning of the algorithm until its maximum

size Nis reached. It may contain both nondominated and

dominated individuals.

Step 3: create the *archive population A.*

The *archive* *A*, consists of only nondominated individuals.

It is created from the copies of the nondominated individuals

of *P*. Although its size is not explicitly restricted by a fixed

number, it depends on *τ* that defines the size of the territory

of an individual. Only the individuals that are accepted to the

regular population are eligible to be evaluated to enter the

archive.

Step 4: Evaluate the initial population: calculate the objective

Function.

*Step 5*: Parent Selection: The selection scheme is different for the two populations. In the regular population, the binary tournament selection is used.

Pick two individual *s1* and *s2* from the regular population and parent p1 is determined according to the following procedure:

1. Test for dominance between *s1* and *s2*. If one dominates the other, denote the dominating individual as the first parent *p1.*
2. If there is no dominance relation, then select randomly among *s1* and *s2*.
3. The second parent *p2* is randomly archive population.

Since all individuals in the archive are nondominated relative

to each other, we randomly choose one individual as p2.

In this selection tournament size is not strict. If a larger selection pressure is desired, a larger tournament size can be set. Also, parents that compete in the tournament selection can be chosen from any

population freely.

Step:6 Two point crossover is used for process planning as well as scheduling chromosome.Since crossover and mutation operators are not specific to our algorithm,we have not used them.

This step includes:

(i)Two random point are selected for process planning.

(ii)for scheduling level the genes corresponding to process planning level,are randomly generated again & replaced by their previous values.

In this way crossover is done on the individuals selected from the step 5 and then forwarded for mutation.

Step:7 Mutation is performed on the offspring.

Now the individuals created by (mutation+crossover) and only(crossover) are checked for their fitnesses.Hence fittest offspring is allowed to propagate further to enter into the regular and archive population.

*Step 8*: *Population Updates*

An offspring, *c*, is first evaluated for acceptance into the

regular population. The evaluation procedure is as follows.

1) Test *c* against each individual *si* ∈ *P*(*t*) for dominance.

Mark the individuals dominated by *c*. If *c* is dominated

by at least one *si*, reject *c*. Otherwise, go to the next

step.

2) Remove one of the marked individuals randomly from

*P*(*t*). If no individuals are marked, choose and remove

an individual randomly from *P*(*t*).

3) Insert *c* into *P*(*t*) and test for acceptance in *A*(*t*).

If *c* is rejected in the above procedure, then it is not

evaluated for archive acceptance at all. The archive evaluation

process consists of two stages.

First, the offspring *c* is checked

for dominance against the members of the archive. If it is not

dominated by any individual in the archive, then we proceed

to the second stage. The second stage begins with the removal

of individuals dominated by *c* from the archive. After that,

we determine the closest individual, *si*\*, to *c* in terms of the

scaled rectilinear distance. Then, we check whether *c* is in the

territory of *si*\*. If it is, we reject *c*. Otherwise, *c* is accepted.

1. Test *c* against each individual ∈*A*(*t*) for dominance. Mark the individuals dominated by *c*. If *c* is dominated by at least one, reject *c*. Otherwise, go to the next step.
2. Remove all marked individuals from *A(t).*
3. If *A*(*t*) is empty, accept and insert *c* into *A*(*t*) and stop. Otherwise, continue to next step.
4. Defining as the scaled value of individual *i* in objective *j*. Calculate the rectilinear distance  of c to each individual ∈*A(t).*
5. Find, that is, the individual closest to *c*.
6. Find the maximum scaled absolute objective difference between *c* and  . That is, find 
7. In TDEA, *τ* defines the territory size, if, accept and insert c into A(t). Otherwise, reject c.

For scaling i have used exponential scaling function

F(x)=e-xa

Where a is any constant & x is objective value.