Evolvability: What Is It and How Do We Get It? 4pm, Wed March 22, Th 391

Biological organisms exhibit spectacular adaptation to their environments. However, another marvel of biology lurks behind the adaptive traits that organisms exhibit over the course of their lifespans: it is hypothesized that biological organisms also exhibit adaptation to the evolutionary process itself. That is, biological organisms are thought to possess traits that facilitate evolution. The term evolvability was coined to describe this type of adaptation. The question of evolvability has special practical relevance to computer science researchers engaged in long-standing efforts to harness evolution as an algorithm for automated design. It is hoped that a more nuanced understanding of biological evolution will translate to more powerful digital evolution techniques. This talk will present a theoretical overview of evolvability, illustrated with examples from biology and evolutionary computing, and discuss computational experiments probing the relationship between environmental influence on the phenotype and evolvability.

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```
individuals.append(ind_init(self.parents[i]
      numpy.dot(self.A[i], arz[i
       individuals[-1]._ps =
  ndom = tools.sortLogNondominated(self.parents), Wen(self).parents),
                                                                                                Wiley, pp. 527-565;
   first_front_only=True)
  for i in range(self.lambda_):
      j = numpy.random.randint(0, len(ndom))
                                                                                              logbook = tools.Logbook()
      _, p_idx = ndom[j]._ps
                                                                                              logbook.header = ['gen', 'nevals'
      individuals.append(ind_init(self.parents[p_idx]
      self.sigmas[p_idx] * numpy.dot(self.A[p_idx], arz[i])))
                                                                                              for gen in xrange(ngen):
      individuals[-1]._ps = "o", p_idx
                                                                                                 population = toolbox.generate
eturn individuals
                                                                                               fitnesses = toolbox.map(toolb
select(self, candidates):
                                                                                                 for ind, fit in zip(populatio
 len(candidates) <= self.mu:</pre>
                                                                                                      ind.fitness.values = fit
  return candidates, []
                                                                                                  if halloffame is not None:
areto_fronts = tools.sortLogNondominated(candidates, len(candidates))
                                                                                                     halloffame.update(populat
hosen = list()
id_front = None
                                                                                                  toolbox.update(population)
ot_chosen = list()
                                                                                                  record = stats.compile(popula
                                                                                                  logbook.record(gen=gen, neval
                                                                                                  if verbose:
                                                                                                     print logbook.stream
                                                                                              return population, logbook
```