# Using real data sets to simulate evolution within complex environments

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Target Question: Does the complexity of the environment significantly affect evolutionary processes?

- (here "complexity" means that there are exploitable patterns in the environment but these are difficult to discover)  $\triangleright$
- Adding randomness to the environment (or the fitness function) is not satisfactory and the NK model of fitness  $\geq$ adjusts the difficulty in a uniform manner (second order uniformity)

# Main Ideas:

- Evolutionary data-mining is where ideas from biological evolution are applied to data-mining *finding patterns in data*
- Data sets exist for the purpose of testing different ML algorithms that have patterns in them, albeit difficult to discover
- *Reversing this...* I am suggesting the use of complex data sets as a test bed to investigate how the complexity of the environment might affect evolution

# The Data Set Environment:

- Find a rich data set (preferably one derived from a naturally complex system) with many independent variables Ο
- The gene of an individual is an arbitrary arithmetic expression stored as a tree (or similar technique) Ο
- Resource in the model is modelled by distributing to individuals predicting the outcome variable of local data better than its competitors Ο
- The gene are mutated and crossed as the simulation progresses Ο
- Individuals are selected for/against depending on their total success in predicting Ο

# (1) Evaluation Phase of Model:



# **Data Space**

-For each data point (or a random subset of them) evaluate (a random selection of) near individuals to determine the share of fitness each receive (depending on predictive success)

Sum of fitness determines which breed and die

# (2) Selection Phase of Model:



Gene 7804: (42) (0-(fbs/2))

Gene 10596: (40) (restecg+(fbs+1)

### An example simulation run using the HD data set:

Start of Simulation (HD Data)



Data points from set distributed over space dependent on 2 variables chol (x) & thalach (y)

Individuals each with gene which is an arithmetic expression, e.g.: Gene 516: (1) (trestbps/(9/exang)) Gene 864: (1) ((ca\*trestbps)/0.5) Gene 1538: (1) ((4\*ca)+thalach) Gene 1950: (1) ((cp/3)\*(3-age)) Gene 1950: (1) ((cp/3)\*(3-age)) Gene 1374: (1) ((8-exang)/5) Gene 1222: (1) ((20-slope)\*11) Gene 1978: (1) (restecg+(100-exang Gene 1660: (1) (thal+age) Gene 1986: (1) ((0+cp)\*(100/fbs)



### Illustrative Results:

Using Reduced Cleveland Heart Disease Data Set, 20 runs with each setting, 1000 individuals, 1000 iterations, Locality parameter 0.1 (radius), Comparison of Original vs Ersatz Data Sets (same distribution in each dimension but random), Fixed normal noise (0, 0.1) added to both data sets

#### Fitness

### Gene Complexity/Depth



Questions: That might be explored using this approach

When mighty the complexity of the environment effect evolutionary processes? *How* might the complexity of the environment effect evolutionary processes? Will models with a simple environment tell us about evolution in the wild? •When and about what aspects will models with simple environments be sufficient? •In what *ways* might evolution differ when in complex environments? What *kind* of complexity might we need? *How* might one measure this complexity in the wild (if this is even possible)?