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Artificial Life Research

After running my FrobWorld program in batch mode using both a runThese and a runCount file I collected the following data.

This is the data from running a runThese file with 25 values inside. Just 7 of the populations with the provided seeds lived the full amount of MAX_SIMULATION_LENGTH. As expected there is no correlation between size of the seed and probability to survive (that would be one hell of a bug).

seed	day extinct	mean metabolism	standard deviation
981237	3205		
9182	20101		
92834091		17	5
73465	7635		
81276	18337		
182736	9316		
18273	8338		
123876		21	8
82735	6128		
81276	18337		
812712		16	2
818273	23125		
63571		23	8
3758	9979		
83745	7976		
1234647	17468		
734658		31	0
87576		25	6
6235476	4691		
75676		12	5
2376	6562		
81726	8856		
812736	11007		
1265	10880		
7265	7106		

The frobs created from the runCount file somehow had a slightly better time of it. 9 of the 25 runs had a population that survived to the end however a much larger

portion of the simulations got past 10000 days in their simulation. I have no explanation other than blind chance that the random seeds made better frobs. The seed numbers for these simulations came from System.nanoTime() calls made before the runs.

seed	day extinct	mean metabolism	standard deviation
1973363232		17	10
-259505064	8948		
-29503064	15859		
163746936	10488		
318616936	12334		
557578936	8524		
642313936	7495		
712593936		20	8
782027936	15845		
978218936	10984		
1087298936		32	4
1180743936	14015		
1378358936		23	4
1398769936	10167		
1491435936		16	8
1688714936	9058		
1778417936	12081		
1881829936		21	7
1979981936		25	7
-2090429360	19788		
-1846366360		19	8
-1844905360	10343		
-1721444360	8955		
-1632036360	14043		
-1472496360		23	9

It seems to not be a very high proportion of simulations that have frob populations that survive to MAX_SIMULATION_LENGTH. However there does seem to be a clear level of metabolism that is best for this time frame.

Of the populations that do survive it seems as though a median metabolism is slightly better for the long-term survival of the frobs. Of the frob populations that survived the whole simulation the average metabolism was roughly 21, which is around the middle of the possible range (5 to 37). The average standard deviation was rather big (given the range) at 6. So the average range of metabolisms in the populations that survived was 15 to 27. This makes some sense since we could identify major problems with having really fast metabolisms (like being taxed to death if there is no grass in the area) and really slow metabolisms (like never having

children). It makes sense for the middle of the road metabolisms to become dominant since the bad sides will be slightly mitigated in all cases.

The metabolic rates do seem to play an important role in whether or not a population survives. There are simulation runs in which the standard deviation of the survivors is 0. This could only mean that the surviving frobs were all of the same family and none of them had a mutation that changed their metabolism. It also means that their metabolism was the best for that environment.

Also there is the interesting fact that the standard deviation has such a large possible range (0 to 10). This shows that we are not definitely proving what metabolism is best in all situations in our world. It is likely that we would have to run the simulation far longer to allow the frobs to mutate into an optimal form. Even better would be to put the survivors of a simulation into the next one as initial frobs. This would allow the best more time to mutate into even more optimal frobs (it also seems to be common practice in genetic algorithms).