

NOTE TO FILE:  
Garvin H Boyle  
Dated: R1:170224 R5:170309 R7:170322

# TpLab Change Log

## Frontispiece

**PANEL 01: THE MODEL**

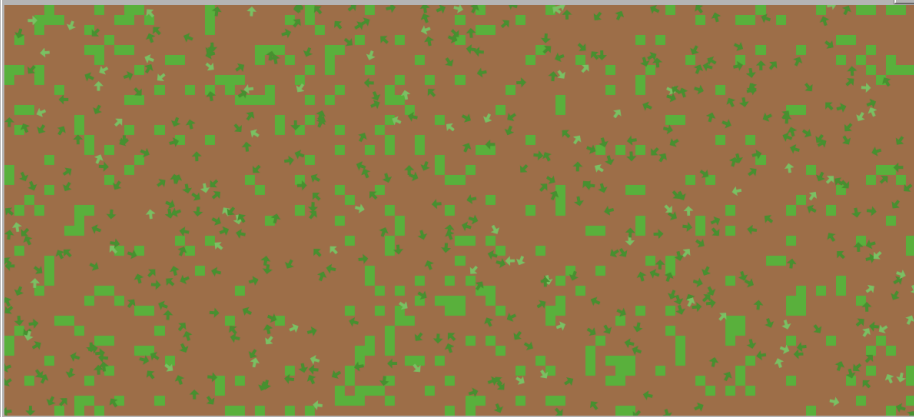
**TpLab**  
(NetLogo Platform)

**THE ECOSYSTEM**

QUICK START INSTRUCTIONS  
 1. Select a scenario.  
 2. Select a PRNG seed.  
 3. Optionally, set the advanced switches.  
 4. Push the "Setup" button.  
 5. Push the "Go" button.

SETUP CONTROLS  
 gs-scenario  
 Seekers  
 g-use-this-seed 7  
 Setup

OPERATIONS SWITCHES  
 On  
 Off  
 gb-plot-data



ticks: 28568

Be sure other 'Go' buttons are off before you turn this on.

One Tick  
Go

g-halt-at-tick  
-1

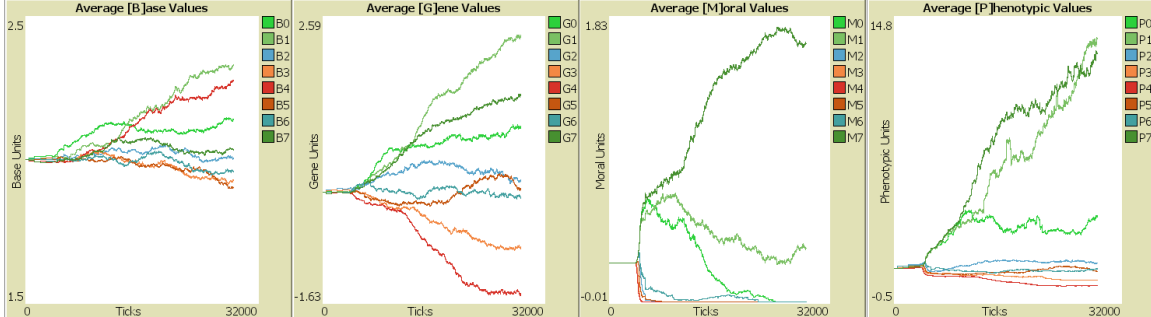
<<--- To halt the run at a pre-specified tick., enter it here.

2-Sliders; 3-Debug; 4-Clock; 5/6/7/8-Graphs --->>>

**PANEL 06: AVERAGE VALUES, COMPOUND GENES, BY TYPE OF COMPONENT.**

All values in this panel are averaged instantaneously across all currently living agents.

$[P]=[B]^{([G]+[M])}$



**Average [B]ase Values**  
Base Units vs Ticks (0 to 32000). Legend: B0, B1, B2, B3, B4, B5, B6, B7.

**Average [G]ene Values**  
Gene Units vs Ticks (0 to 32000). Legend: G0, G1, G2, G3, G4, G5, G6, G7.

**Average [M]oral Values**  
Moral Units vs Ticks (0 to 32000). Legend: M0, M1, M2, M3, M4, M5, M6, M7.

**Average [P]henotypic Values**  
Phenotypic Units vs Ticks (0 to 32000). Legend: P0, P1, P2, P3, P4, P5, P6, P7.

These are the [B]ases of the eight compound genes, averaged across all currently living seekers. All start at a value of 2. Evolutionary pressure is mild.

These are the exponents of the eight compound [G]enes, averaged across all currently living seekers. All start at a value of 0. These play a significant role in any effective search pattern.

These values encode the [M]oral imperatives or beliefs of the agents as to which swiveling behaviour is best, averaged across all currently living seekers. False beliefs impervious to change from experience may be adaptive, or may not be.

These [P]henotypic characters are the external face of the genes, and they control the search pattern of agents. Those agents with the most effective search pattern usually increase their numbers, while those with less effective search patterns are selected against.

Clear All Plots

Setup One Tick Go

Be sure other 'Go' buttons are off before you turn this on.

Ticks  
28568

7-Power/EROI; 8-Nrg Hist/COD --->>>

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## 1 - References

- A. TpLab\_V1.xx.nlogo; The “Teleological Pruning” Laboratory – An NetLogo ABM
- B. PSoup – A C++ model demonstrating evolution
- C. XXX

## 2 - Background

Sholto Maud suggested I try to model TP. So the Ref A application is my first attempt.

I started Wednesday, 22<sup>nd</sup>. It is now the 24<sup>th</sup> and I am on version 1.03, and I have it running. A number of things still need to be addressed, but I have populations of hunters and gatherers who live and reproduce sustainably as long as the energy keeps flowing. The goal now is to tweak it to demonstrate:

- The development of heuristics that are unique to the experience of each agent, that guides their decisions about search patterns.
- The pruning of those heuristics by evolution.

It’s time to put some configuration management on this project.

## 3 - Purpose

To keep track of changes as I make them starting with V1.03.

## 4 - Discussion

### 4.1 - Changes to V1.03

In version 1.xx I have two breeds, hunters and gatherers. My thought was to have the hunters actually hunt and eat animals, requiring another breed not yet introduced. But, on second thought, that would mask the issues that I want to demonstrate around teleological pruning. In addition, I have heuristics that are essentially learned behaviour as the “teleological” ideals to be pruned. My idea was that, as the genes were pruned, the knowledge would also be pruned. But, that gets into issues of how much weight I assign to heuristics, which is a means of loading the results. However much that might in fact demonstrate TP, it would require some careful explanations, and a lot of data runs and statistical arguments. It would be a lot of work, and perhaps only convincing to those who care enough to read through a dense note.

So, I need to abandon that idea and see if I can come up with a better one. And, I think I have.

No	Description	Status
1	The gatherers feed before the hunters, and, when the food becomes scarce, there is none for the hunters and they all starve. I need to feed them in random order to make it less biased. I inserted an agent list called active-agents into the do-feed routine, and it includes both hunters and gatherers, only if appropriate, and I use an “ask” on that list. They are addressed in random order.	Done 170224
2	When all of the hunters died out, there was still energy in the variable g-nrg-in-hunters. There is some leakage. Was in the move step.	Done 170224

3a	Phenotypes of genes should, I imagine, rise for some genes and fall for others, but they all seem to fall. They do not follow the pattern of behaviour seen in PSoup. Perhaps there is too much nrg available, and the heuristics are more potent. I.e. perhaps there is too much nrg building up in the “leaves”, the hidden store of energy. So, I will (a) start with a larger population – bigger than 10 – maybe 40, and (b) discard all energy not deposited as fruit at the end of the energize step.	Done 170224 Did not help a lot, but the graphs are more reasonable.
3b	Trying to address the same problem as in 3a. Will try to debug the geno/pheno/heuristic translation.	
4	Agents do not respect the EPA limit on the total energy obtained. They gather immense amounts of energy prior to reproduction. I need to put a check into the do-feed step.	Done 170225
5	Not all sliders are updated to default values in the startup routine.	
6	There is a problem translating gene values into phenotypic values. I am using the formula (phenotypic value) = (gene value) ^ 2. This is not happening for hunters. I was putting the gene value into the list of pheno values. Oops! This was a bug.	Done. 170224
7	Heuristic values are HUGE and drown out any effect of the genes, as expressed via the phenotypic numbers. They need to be balanced – maybe. Reduce the size of the increment for heuristic success. Raise the power of the initial phenotypic values.	Not done. I need a different approach.
8	Mutation rate at 10% is too low. Try raising the default value to 0.5 – i.e. 50%. Is now [0, 0.001, 1, 0,500]	Done 170225
9	I need a smaller minimum for nrg-per-tick. Was 2000. Now [50, 50, 12000, 500]. Oops! There was a bug. Added a check to ensure I did not deposit more energy than was in the sunshine for the tick. I had an endless flood. Back to [1000, 40, 12000, 2000]. This enables $1000/4 = 250$ agents to move per turn, at carrying capacity, at minimum.	Done 170225
10	The agents’ heading is not being adjusted correctly. This is a bug. Record old heading and calculate heading-delta, then add then.	Done 170225
11	Added graphs for c1-genes, c1-pheno and c1-heuri.	Done 170225

## 4.2 - Changes to V2.00

It’s back to the drawing board.

I have copied V1.03 into V2.00 and will continue from there. My plan is to have nine breeds, all identical except for a built-in bias to depend on an heuristic (a search strategy) that distinguishes them. There will be one vanilla breed for which there is no bias. Each of the other eight breeds will have a bias to use one of the eight directional genes more often than the genes themselves indicate. So, the genes will be under the same evolutionary pressure in all cases, but the heuristic bias (representing an ideal that changes behaviour slightly) that does not line up with evolutionary effects will be selected out of the population. I will need to be able to turn the bias on and off, and do comparative runs for a given seed.

I've copied the above table, removed the items that were done, and carry on.

No	Description	Status
1	Change the version number from V1.03 to V2.00	Done 170225
2	Remove the hunters, change the gatherers to seekers, and add gene preferences and a composite set of values (genetic plus preference) to determine heading deltas. There are now gene preferences coded for each seeker, and they can be distinguished by their gene preferences.	Done 170225
3	Audit check on nrg accounting at end of setup asserts. Bug. Fixed. Replaces native logicals (true/false) with numeric logicals (1/0). Works now.	Done 170225
4	Averages of mores are bad. Bug. Fixed	Done 170226
5	<p>Add calculations of EROEI and associated graphs. EROI could be on a per agent lifetime basis. Or it could be on the basis of some time-averaged rate, for a shorter time. It will only make sense when there is competition for nrg. If all agents are near EPA then they stop feeding and the individual EROEI will be depressed. So, I suppose I need:</p> <ul style="list-style-type: none"> <li>• A slider to set <math>\Delta T</math>;</li> <li>• In each agent: <ul style="list-style-type: none"> <li>○ a counter to determine when the time (<math>\Delta T</math>) is up – say when 100 ticks has passed – and to determine when to remove old entries;</li> <li>○ a variable for ER (calculated on feeding);</li> <li>○ a list for <math>\Delta ER</math>;</li> <li>○ a variable for EI (calculated on moving);</li> <li>○ a list for <math>\Delta EI</math>;</li> <li>○ a variable for EROI</li> </ul> </li> <li>• a routine that records ER and EI, by adding the deltas at time T and removes them again at time T + <math>\Delta T</math>.</li> </ul> <p>The average EROEI (for a single agent) should be rather stable over time, once competition has set it. But, the EROEI should rise as the agents become more proficient at collecting energy. Eventually, the Red Queen Effect will kick in and EROEI will be a factor in survival, but may not increase over time. If all agents are more efficient, they will still just get a fair share. So, the individual EROEI is only useful when comparing with contemporary cohort, in a post-mortem study. Hmmm!?</p> <p>I will also need some a global aggregator variable, for graphing.</p>	Done 170226
6	Add calculations of MPP and associated graphs. This would be at the hierarchic level of $H_{PA}$ , and so would be on a system-wide basis. I.e. this is the expended power. This would be extremely simple, as the power is the rate of expenditure of nrg, which happens only in the “move” step. I can put a sink monitor and record the nrg used per tick for metabolic activities. The interesting question would be, once the system is at carrying capacity,	Done. 170226

	<p>does the power continue to increase after serious competition for survival sets it. So, I suppose I need:</p> <ul style="list-style-type: none"> <li>• An nrg sink, for moves;</li> <li>• A routine that records all expenditures to sink; and</li> <li>• A graph of nrg expended, per tick, over time.</li> </ul> <p>This proved to be less than surprising or interesting. It tracks the total population very closely, because each agent expends precisely EPM units of nrg per tick.</p>	
7	I could also do a system-wide EROI calculation. This would be different, having the aggregates in the system rather than in the agents own variable lists.	Done 170226
8	Set the value of dt-for-eroi to 400. [10,10,800,400]	Done 170226
9	Age should be random RAT instead of DAT.	Done 120226
10	Not all sliders are updated to default values in the startup routine.	Done 120226
11	The sink graph (power, showing maximum power) needs to be added.	Done 170227
12	The old MppLab interface needs to be ripped out and replaced.	Done 170227
13	Startup is very sensitive to initial conditions. If agent is randomized at the beginning, then some runs are NOT as expected. So, I have made the initial age = RAT / 2, and the initial nrg = RET / 2.	Done 170226
14	To access more of genospace, I should mutate bases as well as powers. I'll use a technique similar to what I did in PSoup. I think a list of factors made of prime numbers will be the tool to use. I want to vary the bases by just a little. They are all 2's at initialization. So for example if I randomly decide on one factor out of eight, all close to 1.0, and then randomly multiply by the factor, the bases will all experience a random walk around the value of 2. I am unsure what evolutionary pressure will do to them. The six primes are 7, 11, 13, 17. I'll produce the factors (F) from the primes (P) as $F=1+(1/P)$ or $F=1+(1/P)$ , for a total of eight possible factors.	Done 170226
15	Code colours – green for forwards – red for backwards – blue for middlin'.	Partly Done 170227

### 4.3 - Changes to V2.01

Some things in NetLogo are not working right. E.g. text is not being displayed as indicated. I worry something is wrong either with the interpreter, or with my application. I hope a new name, and a re-boot of everything will clear it up. So, an incrementally new version is established.

It seems a re-boot cleared it up. It seems that the NetLogo ADE gets a bit confused after long usage (I leave it running overnight) and it gets the fonts wrong. So, a mental note, I really should reboot it before I start fussing about the user interface. I spent a LOT of time trying to get it to not look trashy, and much of that is now wasted. It seems to be working well again. I have noticed this before.

No	Description	Status
1	Change the version number, in two places.	Done 170227
2	Rebuild the user interface from end to end to organize it much better.	Done 170227
3	Better code colours – green for 3 forwards – red for 3 backwards – blue for 2 middlin’s.	Done 170227
4	<p>I should add a button or a scenario which lets you inject morals into a population in a state of equilibrium.</p> <p>I have given this quite a bit of thought over the past couple of days. The base scenario, at the moment, has 8 inflexible mores. The evidence of TP in action is strong, but only if you know how to interpret the statistics, and that need for a complex interpretation makes the model less impressive than it could be. So, the question is, how can I make the evidence of TP more obvious, and less a matter of complex explanations. My conclusion is I should have three scenarios, as follows:</p> <ul style="list-style-type: none"> <li>• Scenario 1 – As is, with 8 morals;</li> <li>• Scenario 2 – As is, with 0 morals;</li> <li>• Scenario 3 – New scenario with only 1 moral.</li> </ul> <p>The first two can be handled by simply adjusting a slider in the current scenario. But, to make it obvious, I will list this as a separate scenario in the scenario chooser. I will add a “reset defaults” routine unique to type of scenario, and a monitor beside it to tell me what scenario is active.</p> <p>The third requires a different routine for setup, but that can be done with a switch within the current setup. So, it should be easy to do this.</p> <p>The effect will be this, a user can run a 0-mores scenario to equilibrium, then inject a moral preference into half the population and see what that does to the population, and who is selected by natural selection.</p>	Done 170228
5	Insert “C2” into all genes for chromosome #2.	Done 170228
6	Check and resolve each piece of code marked as xxx.	Done 170228
7	The CSV stuff needs to be ripped out or adjusted for TpLab data.	
8	I need to write the info tab.	
9	I need to write user documentation.	
10	I note a variety of phrases of similar meaning. The code uses “mores” and “beliefs” but there are others that come to mind: moral suasion, morals, mores, social norms, beliefs, belief systems, moral preferences, moral alignments, moral imperatives, moral compass, moral convictions, plans, intentions, desires. I also note that my “seekers of fruit” are also “seekers	

	of truth”, and they interact with (noumenal? and) phenomenal reality. These should all be discussed in the user documentation.	
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## 4.4 - Changes to V2.02

Back to the Drawing Board! I had a moment of synthesis, yesterday, as I had to take a day away from this stuff. I need at least one scenario in which the belief systems are both passed on from parents but also spread through the population. I need a scenario for which the spread of belief systems is an inter-familial social process, and not just an intra-familial process.

### 4.4.1 - Two Questions

The problem is with this ‘spread through the population’ bit. On what basis? How fast? It seems that if I design anything that responds to those specific questions, I am going to get the answer that my design builds into it. So it won’t really support an argument that TP **MUST** happen in all circumstances, but would demonstrate that TP could happen under certain select circumstances. That would make the model less compelling. But, perhaps any demonstration I could present would suffer that same weakness.

### 4.4.2 - On What Basis?

**Perceived Success of Daily Contacts** – The seekers might be swayed by the apparent success of the other seekers that happen to arrive in the same cell as them:

- They could check which other seekers share a cell with them, and form an agent-list of coincident seekers.
- They would then choose from that list the seeker with the most apparent success so far – the highest nrg.
- If that seeker has more nrg (more success) than them they would want to emulate the successful seeker.
- They could then compare the belief systems ([M] values) of the more successful seeker with their own and make adjustments. The adjustments could be done in many ways, and that gets into the issue of “How Fast?”

**Perceived Wisdom of Daily Contacts** – The seekers might be designed to recognize differences in experience, and respect the wisdom of elders or of the most experienced:

- They could check which other seekers share a cell with them, and form an agent-list of coincident seekers.
- They would then choose from that list the seeker with the greatest age, or with the greatest number of previous contacts, presumably having collected wisdom from the most contacts so far in their long lives.
- If that most wise seeker has more opportunities to obtain wisdom (more ticks, or more contacts) than them they would want to emulate the wiser seeker.
- They could then compare the belief systems ([M] values) of the wiser seeker with their own and make adjustments. The adjustments could be done in many ways, and that gets into the issue of “How Fast?”

**Social Networks** – I could, perhaps, figure out how these NetLogo links work, and set up a potential for social networks of competing widely-shared systems of beliefs. This is essentially



what I have in the 8-mores scenario, but the shared systems cannot currently make converts, or modify their beliefs. They must live with received wisdom of their type.

I could do it this way. I could set up N competing groups of seekers, all having identical systems of beliefs at the beginning. Each of the N groups would contain exactly 8 seekers owning one strong belief each. All 8 possible discrete beliefs would then exist in every group, so all groups are equally (dis)advantaged, though members within groups would be variously advantaged due to the pathological nature of some discrete beliefs. The N competing groups would then seek to enhance their proprietary wisdom, sharing it within their group, but not sharing it outside of their group:

- They could check which other seekers of the same group share a cell with them, and form an agent-list of coincident seekers of their own group.
- They would then choose from that list the seeker with the greatest success (nrg), age (ticks), or with the greatest number of previous contacts (experience), presumably having collected wisdom from the most contacts so far in their long lives.
- If that most august seeker of the social group has more opportunities to obtain wisdom (more ticks, or more contacts) than them they would want to emulate the wiser seeker.
- They could then compare the belief systems ([M] values) of the wiser seeker with their own and make adjustments. The adjustments could be done in many ways, and that gets into the issue of “How Fast?”

### 4.4.3 - How Fast?

There is a problem with time scales that needs to be managed, and it is a BIG problem when it comes to credibility, or even comprehension, of the results. In real life genetic variation happens every generation (assuming sexual reproduction), and less often when fission is the mode of reproduction. In most of my models I use fission as the mode of reproduction, but with an extremely high rate of genetic “mutation” to demonstrate evolution on the desk. In real life, again, belief systems of people can vary on a daily basis, or on a minute-to-minute basis if experiences are intense. So cycle times vary by approximately six orders of magnitude.

So, I think I need to:

- (a) Speed up genetic rates of variation, which I do by having high genetic mutation rates. But that does not affect the mores.
- (b) Throttle back the rate of change of belief systems, which I do currently by holding them static within an individual’s lifetime. If I move towards a sharing of wisdom, in some fashion, I need to figure out whether and how to throttle it.

### 4.4.4 - When is wisdom transferred?

**Instantaneous transfer at a distance** – At the moment of any contact in which wisdom is to be transferred, it happens as widely as needed (which may be the contactee only, or to a whole group if groups are implemented)

**Transfer at end of tick** – At the end of each tick, collected wisdom is integrated into the seekers belief system. This might be the belief system of a single contactee, or of a group, if groups are implemented.

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**Transfer only on contact** – Within a group, the spreading of group-think would happen only when members of the same group happen to be in the same cell at the same time.

#### 4.4.5 - How is wisdom transferred?

Wisdom will always be transferred from the wiser to the seeker of wisdom. I assume that each seeker has a preferred moral conviction, whatever else I do. There are several options:

##### 4.4.5.1 - Which More?

**Only the preferred more is affected** – the transfer of wisdom alters only the preferred more of the seeker. This would limit all transfers to seekers of the same preferred more. Hey, that would be cool, setting up two social networks – one based on preferred mores, and one based on social adhesion (group belonging). So wisdom is acquired by the group from other groups through their experts in each more.

**A random more is affected** – wisdom would spread slowly in this fashion.

**All mores are affected** – wisdom would spread much more quickly if all mores are adjusted in every transfer.

##### 4.4.5.2 - How Much?

**Direct full transfer** – The seekers more(s) is(are) replaced in their entirety with that(those) of the wiser seeker.

**Partial transfer** – There is a small (how small) adjustment of the seekers more in the direction of the more of the wiser seeker.

#### 4.4.6 - Decision

So, what to do?

##### 4.4.6.1 - My Goal

My goal is to show that, in any society, the belief systems of the society are pruned to coincide with and enhance the effects of the MPP. Do I need the complicated groups, as conceived of above, or is the simple approach demonstrative enough? I think that I **MUST** have the ability of individual seekers of wisdom to change their belief systems independently of their genetic heritage. The orientation of the belief system would then, effectively, replace or overwhelm their genetic heritage, and we will see the genetic heritage becoming irrelevant.

So, I'll have transfer of wisdom, but only on contact. Each seeker may be part of two groups:

- Those with the same preference for a more; and
- Those with the same social group allegiance.

But, I do not want an explicit bias due to nrg consumption to be built in. So success (nrg) cannot be a criterion for selecting a guru. Age must be the only such criterion.

##### 4.4.6.2 - Preferred More and Success

Transfer of wisdom due to similar belief - I will have transfer of wisdom from guru to seeker of a non-group when age of guru is greater than the age of the seeker. Appropriate more of seeker takes a fractional step towards more of guru – say  $1/10^{\text{th}}$  of the difference.

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#### 4.4.6.3 - Familial Connection and Age

Transfer of wisdom due to familial connection – a random more takes a step in the direction of the appropriate more of the familial guru – say  $1/10^{\text{th}}$  of the difference in mores.

#### 4.4.6.4 - Rising beliefs

With the two mechanisms stated above, in no case does the more of the guru rise. When success (nrg) is the criterion for selecting the guru, the seekers more might rise or fall, but will only rise if the guru has a higher more. When age is the criterion for selecting the guru, any more may rise, but only if the guru has a higher more. So, in both cases, the seeker who is at the top in all mores can never go higher. That is the case at the start. I must therefore have a mechanism to also allow the highest mores in the population to gain strength. At the end of each tick, the seeker with the highest age will gain a small amount – say  $1/RAT^{\text{th}}$  – added to the preferred more.

That would be interesting and is not TOO difficult. KISS. But I think it is also necessary to answer the charge that I may be simply loading the dice to fall in my favour. A full sharing of wisdom, as it were, puts the moral conviction in the same arena as the genes, and they will be shaped by the same forces in the same way.

Change the scenarios to:

0 – No mores – genes only

1 – 8 belief systems – no sharing of wisdom

2 – 8 belief systems – social sharing of wisdom between similar faiths

3 – Tribal groups encompassing 8 belief systems each – faith and tribal sharing of wisdom

In all of these, allow for injection of a specified more in a random half of the population at any time, as exists now in V2.01.

The first two scenarios are easily done by reshaping existing scenarios. The third will require addition of sharing logic. This fourth will also require the addition of a family number in each seeker, and some logic around family sharing.

The transfer of wisdom from seeker to seeker will require additional logic.

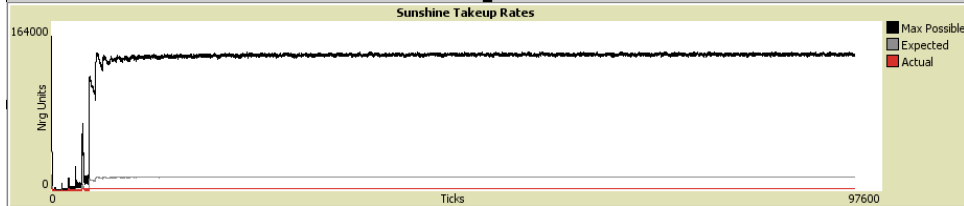
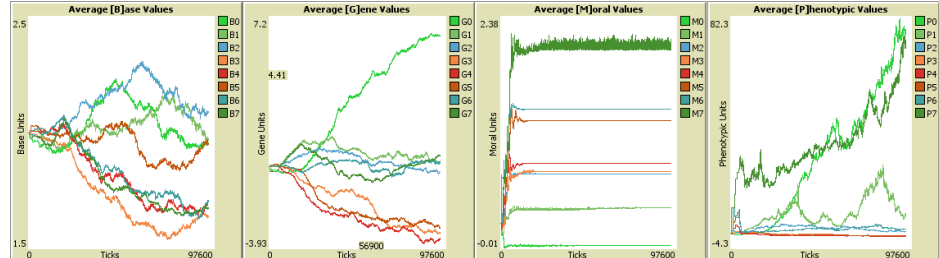
No	Description	Status
1	Change the version number to V2.02, in two places.	Done 170302
2	Change the scenario numbers and names to the new versions.	Done 170302
3	Redo scenario 0. All seekers have preferred-gene 0, but $[M0] = 0$ , so this has no effect on the phenotype. Change all graphs to only shown the data for preferred-gene = 0. Test it.  Results: I ran it to 125,000 ticks. Seed was 7. Phenotypes were $p0=257.5$ ; $p1=0.117$ ; $p2=0.472$ ; $p3=0.738$ ; $p4=0.232$ ; $p5=0.284$ ; $p6=3.183$ ; $p7=157.3$ . This is a kind of bent arrow. The gene bases varied from $b3=1.7$ to $b0=2.7$ .	Done 170303

	So there was very little movement there, with mostly random change, but b0 was the most significant change. The Mxs all remained zeros, as expected and intended. At steady state the population varied from 440 to 500, and the nrg in the seekers varied from 260,000 to 318,000 approximately.	
4	Show graph for Sunshine uptake max, estimated and actual. It reveals another bug, it seems, in that the actual is 1/10 <sup>th</sup> of the expected value. Did I apply the prob-of-deposit twice?	BF
5	Fix bug in nrg histogram that does not show highest value. A Bug.	Done 170303
6	Test, can I reset the variables min-pxcor, max-pxcor, min-pycor and max-pycor using code? No. It says I cannot set that using code.	Done 170303
7	Redo scenario 1 – 8 mores; no sharing of wisdom; belief systems fixed at birth. This was the standard scenario 0 of the previous version. It should require no work.	Done 170304
8	<p>Build logic for scenario 2 – 8 mores; belief systems morph over lifespan; sharing of wisdom between seekers of same moral persuasion; age-based determination of gurus.</p> <p><b>ABOUT THROTTLING THE RATE OF TRANSFER OF WISDOM.</b></p> <ul style="list-style-type: none"> <li>- Max-pxcor=45; Max-pycor=20.</li> <li>- There are <math>(1+(2*X))*(1+(2*Y))=3731</math>.</li> <li>- At steady state: <ul style="list-style-type: none"> <li>o There are approximately <math>500/8=63</math> seekers having the same moral conviction.</li> <li>o The probability that two seekers of the same moral conviction are in the same cell during on tick is <math>(63*63)/(3731/3731) = 0.00281</math>.</li> <li>o A transfer will happen with probability <math>(800*0.000281)=0.2245</math> during a seeker's lifetime.</li> <li>o One of them will be a guru. One will not. Prob of enlightenment is 0.5, so the probability of enlightenment, per seeker, is <math>0.2245/2 = 0.1122</math>.</li> <li>o I.e. approximately 1 in ten seekers will be enlightened by a guru, per lifetime. Compare this with approximately 1 in 10 receiving advantage via genetic mutation.</li> </ul> </li> <li>- Seems about right.</li> </ul> <p>Roughly the same logic applies to both scenario 2 and 3, the two sharing scenarios.</p> <p>When there is no alteration of moral convictions, the guru is too often at a value of 2 (the default value) and no change happens. There needs to be a mechanism for the moral codes to vary, so natural selection can act upon them.</p>	Done 170304
9	Build logic for scenario 3 – tribes in which all 8 moral convictions are shared.	Done 170304

	<p>It would seem logical that the tribes would need to number 8 per tribe, due to the number of directional genes, and the parallel structure, and the desire to have every moral perspective accessible to every tribe. However, there can be any number of tribes. It seems, at carrying capacity for the current set of parameters (nrg-from-sun, deposit size, prob-of-deposit, arena size) that up to 63 tribes can be afforded at once.</p> <p>I already have a slider that determines how many seekers of each moral conviction are launched on setup. This would be the number of tribes. I just need to re-purpose it and alter the logic around it slightly.</p>	
10	Simplify the debug interface to one control vice two.	Done 170304

### 4.5 - Changes to V2.03

I needed to preserve the progress so far, so started a new build number – V2.03.

No	Description	Status
1	Change the version number to V2.03, in two places.	Done 170305
2	<p>Show graph for Sunshine uptake max, estimated and actual. It reveals another bug, it seems, in that the actual is 1/10<sup>th</sup> of the expected value. Did I apply the prob-of-deposit twice?</p>  <p>The limit is g-sun-nrg-per-tick = 2000 in this run, and the actual is 1960. There are two sources of limitations: allowed nrg-per-tick limit, and calculated based on # of empty spaces. With a low nrg-per-tick, the graphs looks like this, which is OK. I have added one more line called 'Limit' which plots g-sun-nrg-per-tick.</p>	BF from 2.02 OK 170305
3	Devise a few graphs to display/provide insight into scenario 3 – in which tribal wisdom is shared.	Done 170306
4	<p>In scenario 3, the averaged [M]oral values are astoundingly stable. Is this an artifact of bad design, or is this a reasonable outcome? The [B]ase and [G]ene values continue to vary. What is the explanation?</p> 	Done 170305

	A couple of bugs. Fixed.	
5	Not getting more than one tribe on setup of scenario 3. Bug. Fixed.	Done 170305
6	I oopsied at the beginning. My 'pheno' is okay, but I should also have a 'strength' set of values in which the actual strength is displayed, and then percentages only in the phenotype values.. I need to add a new list, perhaps c1-weights, and alter the display. This will require a few hours of re-write. Well, better now than after I write the user docs!	Done 170306

## 4.6 - Changes to V2.04

I needed to preserve the progress so far, so started a new build number – V2.04. While working on the text in the 'info' tab I save a lot, but when working on the various runs, I also tend to save small changes to the UI. I am worried that one will destroy the progress on the other. So, I will do the info tab changes in this version and the UI changes in V2.03, and merge them later.

A kind of “code checkout” mechanism.

No	Description	Status
1	Change the version number to V2.04, in two places.	Done 170307
2	Review and address all issues marked with xxx.	Done 170307
3	Review and re-write the partial info tab material, and finish it.	Done 170307
4	Remove the -dpx- and -dpt- code. It is now obsolete.	Done 170307
5	Review and re-write the partial users documentation, and finish it.	In progress
6	Perform a variety of runs, up to 15,000 ticks for different scenarios and different seeds. Write some analysis.	In progress

## 4.7 - Changes to V2.05

While writing the user documentation I realized that there were a number of instances of jargon that I wanted to change. Version 2.04 is very close to completion, and I did not want to screw it up while making substantial changes throughout the code. So, I have started a new version.

No	Description	Status
1	Change the version number to V2.05, in two places.	Done 170307
2	Review and re-write the partial users documentation, and finish it.	In progress
3	Perform a variety of runs, up to 30,000 ticks for different scenarios and different seeds. Write some analysis.	In progress
4	Move all CSV related controls to a single panel. Re-write the user documentation around those controls and panels.	Done 170311

5	Simplify the jargon around the c1-mores gene components and c1-genes gene components. <ul style="list-style-type: none"> <li>• Change c1-mores to c1-learn</li> <li>• Say learned belief affiliations (or just belief affiliations) and tribal affiliations</li> <li>• Say [B]ase, [G]enetic, [L]earned, [S]trength and [P]henotypic</li> <li>• Separate the population graphs from the nrg graphs, making a new panel</li> <li>• This requires a LOT of very minor changes to code, info UI tabs.</li> </ul>	Done 170310
6	Minor additional changes to UI panels necessitating a new version.	Done 170311

#### 4.8 - Changes to V2.06

Started over doing a variety of runs.

No	Description	Status
1	Change the version number to V2.06, in two places.	Done 170311
2	Review and re-write the partial users documentation, and finish it.	In progress
3	Perform a variety of runs, up to 30,000 ticks for different scenarios and different seeds.	Done 170314

#### 4.9 - Changes to V2.07

No	Description	Status
1	Change the version number to V2.07, in two places.	Done 170322
2	Review and re-write the partial users documentation, and finish it.	In progress
3	Use Behaviour Space (BS) tools to collect a lot of data.	