

Reaction Networks

July 19, 2018

Contents

1	Petri Nets	5
1.1	Subclasses	5
1.1.1	State Machine	5
1.1.2	Marked Graph	6
1.1.3	Free Choice Net	6
1.1.4	Asymmetric Confusion Net	6
1.2	Combining Petri Nets	6
1.2.1	Disjoint Union	6
1.2.2	Identifying many places into one	6
2	Chemical Reaction Networks	7
2.1	Detailed Balance	7
2.2	Coupling	8
2.2.1	Collapse	9
2.2.2	Affine Toric Varieties Appendix	9
2.3	Identification from Data	12
2.4	Similar Code	13
3	OpenMarkovTensorFlow	15
4	Glauber Couplings.ipynb	17
5	Evolutionary	19
5.1	Evolutionary Graph.ipynb	19
5.2	Evolutionary Game	19
5.2.1	Equilibria	20
5.2.2	Relative Entropy	20

Chapter 1

Petri Nets

1.0.1 Definition (Petri Net) *A Petri net P is a bipartite directed multigraph colored by two letters P and T . The vertices colored P are marked with some natural number of dots each. The multiedges of multiplicity n that go from $p \in P$ to $t \in T$ indicate that when it absorbs transition t needs to take in n dots from the place P . A multiedge of multiplicity m from $t \in T$ to $p \in P$ indicates that when t releases, it will produce m dots on the place p . A transition firing means that it absorbs then releases. At all stages the number of dots on the vertices must be valid. So a transition may either take a marking M_1 to another possibly equal marking M_2 or it may be invalid. In the code this is represented with `Nothing` from the `Maybe` monad.*

1.0.2 Definition (Reachability) *A marking M_2 is reachable from a marking M_1 if there is some sequence of valid transition firings that take one from M_1 to M_2 . The reachability set $R(P, M_1)$ is the set of such M_2 .*

1.0.3 Definition (Bounded Petri Net) *For each place p provide two extended integers $lb_p \leq ub_p$ ($\pm\infty$ allowed). Replace the natural number of dots on p to be any integer in the set $[lb_p, ub_p]$. In a usual Petri net all the lower bounds are 0 and all the upper bounds are $+\infty$. Usually the lower bound of 0 is implicit. Setting that to $-k$ would be like allowing debt, but only so much before one can't borrow anymore.*

This is the case implemented by `PetriNet.hs`

1.0.4 Lemma *If $lb_p = ub_p$, then that vertex p must have exactly lb_p dots which implies no transition can use it as inputs because then there would be too few after the absorption nor can it have any transition which outputs to it which would create too many dots. This effectively removes all transitions neighboring p as well the vertex p itself. This leaves a smaller bounded Petri net with equivalent behavior.*

1.0.5 Definition (Integer Petri Net) *A bounded Petri net with all lower bounds $-\infty$ and all upper bounds $+\infty$.*

1.1 Subclasses

1.1.1 State Machine

1.1.1 Definition (State Machine) *Every transition has one incoming arc, one outgoing arc and all markings have exactly 1 token over the entire graph. There is a single p that is occupied with 1*

dot and all the rest have 0 dots. This last condition is even stronger than making a bounded Petri net with all bounds $0 \leq 1$.

1.1.2 Lemma *Because there is only one dot, only one transition can fire at the same time, but there may still be many options for which transition to choose. There is no concurrency but there is conflict.*

1.1.2 Marked Graph

1.1.3 Definition (Marked Graph) *Every place has one incoming arc and one outgoing arc.*

1.1.4 Lemma *Because each place has one outgoing arc, one can select all the firable transitions by looking at the targets of the outgoing arcs from all the occupied places and picking the firable subset of those. Those can all happen concurrently.*

1.1.3 Free Choice Net

1.1.5 Definition (Free Choice)

1.1.4 Asymmetric Confusion Net

1.2 Combining Petri Nets

1.2.1 Disjoint Union

First step is disjoint union. This is defined in `PetriNet.hs`, but requires specifying `SNats` for the number of places and transitions in each of the constituent nets. This makes sure the types all line up.

1.2.2 Identifying many places into one

This is done by `collapseManyPlaces` which takes the initial net with `n` places, a list of `n` booleans that say true for the places that are subject to identification. The last argument is the number of places that will be there at the end.

Chapter 2

Chemical Reaction Networks

2.0.1 Definition *Same underlying graphical structure of the Petri net. However instead of marking the places with natural numbers or integers between lb_p and ub_p , they are marked with non-negative real numbers for the concentrations. The transitions indicate reactions and are marked with two real numbers t_{fwd} and t_{bwd} so that the rate of the forward reaction is proportional to t_{fwd} through the law of mass action and the backward is proportional to t_{bwd} .*

2.0.2 Lemma *For a chemical reaction network on N number of places, we get a polynomial vector field on $\mathbb{R}_{\geq 0}^N$. The N components of this vector field in the coordinate vector fields $\frac{\partial}{\partial X_i}$ are $\frac{d}{dT}[X_i]$ as determined by the law of mass action*

$$\begin{aligned} \frac{d}{dT}[X_p] = & - \sum_{t|(pt) \in E} mult(pt)t_{fwd} \prod_{(qt) \in E} [X_q]^{mult(qt)} \\ & + \sum_{t|(tp) \in E} mult(tp)t_{fwd} \prod_{(qt) \in E} [X_q]^{mult(qt)} \\ & + \sum_{t|(pt) \in E} mult(pt)t_{bwd} \prod_{(tq) \in E} [X_q]^{mult(qt)} \\ & - \sum_{t|(tp) \in E} mult(tp)t_{bwd} \prod_{(tq) \in E} [X_q]^{mult(qt)} \end{aligned}$$

Because of the similar data structure used, this is also contained in PetriNet.hs

2.0.3 Definition (Equilibrium) *A point in $\mathbb{R}_{\geq 0}^N$ is called an equilibrium if it is a 0 for this vector field.*

2.0.4 Definition (Conserved Quantities) *Keep only the data of the bipartite directed multi-graph. Define the R by N integer matrix whose ij entry is the difference of how many molecule j reaction i outputs minus the number that it inputs. The kernel of this matrix defines conserved quantities.*

2.1 Detailed Balance

Let there be N total possible molecules in the network and R reactions. We may ask for each reaction in the network to be in detailed equilibrium.

2.1.1 Definition (Detailed Balance) A reaction $X_1 + \cdots X_r \rightarrow Y_1 \cdots Y_p$ (possible repeats for multiplicities) with forward rate k_{fwd} and backwards rate k_{bwd} is said to be in detailed balance if

$$k_{fwd}[X_1] \cdots [X_r] = k_{bwd}[Y_1] \cdots [Y_p]$$

The entire network is in detailed balance if this is true for all reactions.

2.1.2 Remark This is a priori stronger than simply equilibrium where it is possible for multiple transitions to conspire to cancel out. In detailed balance, each t contributes 0. \diamond

2.1.3 Definition (Detailed Balance Variety) The equations for each reaction is a difference of monomials. We can ask for the subset in $\mathbb{R}_{\geq 0}^N$ cut out by all these R equations.

We can forget the nonnegativity and define a variety over any field containing \mathbb{R} . We need at least \mathbb{R} because all the rate constants come as real numbers. If they came as rationals, then we would have been able to define the variety over any field containing \mathbb{Q} . Call this variety over the reals, the detailed balance variety. Call the subset of the closed points that satisfy the nonnegativity constraints as the nonnegative part of the detailed balance variety.

2.1.4 Lemma (Gibbs) For each reaction $X_1 + \cdots X_r \rightarrow Y_1 \cdots Y_p$, with constants k_{fwd} and k_{bwd}

$$\frac{k_{fwd}}{k_{bwd}} = \frac{[Y_1] \cdots [Y_p]}{[X_1] \cdots [X_r]} = e^{-\frac{\Delta G^\circ}{RT}}$$

2.2 Coupling

2.2.1 Definition (Coupling) Let R_1 be a reaction network and R_2 be the same reaction network but with the addition of a few more transitions to represent additionally allowed reactions. In this case, call R_2 a coupling of R_1 .

2.2.2 Example R_1 is the reaction network with places for ATP, ADP, P, XP, X, Y and XY. The transitions in R_1 are $\alpha = X + Y \rightarrow XY$ and $\beta = ATP \rightarrow ADP + P$. The place XP is just an isolated vertex with no transitions.

Then add two more transitions $\gamma = ATP + X \rightarrow XP + ADP$ and $\delta = XP + Y \rightarrow XY + P$

2.2.3 Definition (Quasi-conserved quantities) If R_2 is an addition of transitions from R_1 , then all of the conserved quantities of R_2 remain as conserved quantities for R_1 . In addition, there may be new conserved quantities. Call these additional quantities quasi-conserved quantities. An extreme example, would be if R_2 had all chemistry reactions that involved those N molecules. In that case the only conserved quantities would come from conservation of numbers of different atoms because R_2 would have extreme reactions that break everything into constituent atoms and put them back together. One could go even further if one wants to allow all physical process including radioactivity as well. In that case there would be even fewer conserved quantities.

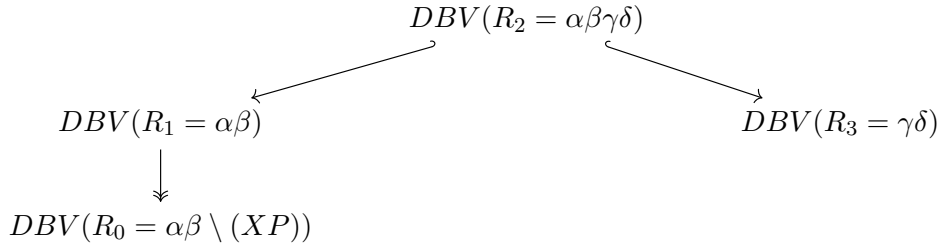
2.2.4 Lemma The detailed balance variety of R_2 is given by adding more equations from the detailed balance variety of R_1 . This gives the map $DBV(R_2) \hookrightarrow DBV(R_1)$.

2.2.5 Definition (Inclusion) Let R_3 be a reaction network and R_4 the result of adding some number of isolated places disjoint without any transitions connected to them.

2.2.6 Lemma *The conserved quantities for R_4 are the direct sum of the conserved quantities for R_3 and the span of the coordinate vectors for the new molecules.*

2.2.7 Lemma *If you add a disjoint place, then there is a projection from the nonnegative part of the detailed balance variety for R_4 to that of R_3 given by forgetting the concentrations of the new molecules. That is $DBV(R_4) \rightarrow DBV(R_3)$*

2.2.8 Example *Continuing the notation of the ATP example. $R_1 \cdots R_3$ have all the molecules and the reactions they are labelled by. R_4 does not have XP .*



2.2.1 Collapse

2.2.9 Definition (Collapse) *Suppose R_6 is given by imposing an equivalence relation on the places of R_5 . If $X_1 \cdots X_n$ get identified and given the new name Y_1 , then either $[Y_1] = \frac{1}{L} \sum L[X_i]$ if one is thinking they should all be in a volume L and the total volume remains L or $[Y_1] = \frac{1}{nL} \sum L[X_i]$ if one is thinking that the volume should grow to nL from mixing. Call whatever that map is ϕ from $\mathbb{R}_{\geq 0}^N$ to $\mathbb{R}_{\geq 0}^M$ where the N different molecules of R_5 have been collapsed into M equivalence classes for R_6 . The vector field pushes forward. Does it match with what expect from R_6 ????*

2.2.10 Lemma *Let $\Delta_{R_5 \rightarrow R_6}$ be the product of diagonals in $\mathbb{R}_{\geq 0}^N$ given by imposing $x_{i_1} = x_{i_2}$ for all pairs that get identified under the equivalence relation. Is this a useful definition?????? How are $DBV(R_5)$ and $DBV(R_6)$ related??????*

2.2.2 Affine Toric Varieties Appendix

Coordinate Expression

2.2.11 Definition (Affine Toric Variety) *For $m \in M = \mathbb{Z}^n$*

$$\begin{aligned}
 \phi_m &\in (\mathbb{C}^*)^n \rightarrow (\mathbb{C}^*) \\
 \phi_m(t_1 \cdots t_n) &= \prod_i t_i^{i_i}
 \end{aligned}$$

For an integer $n \times s$ matrix A define the map

$$\begin{aligned}
 \phi_A &\in (\mathbb{C}^*)^n \rightarrow (\mathbb{C}^*)^s \\
 \phi_A &= (\phi_{m_1}, \cdots \phi_{m_s})
 \end{aligned}$$

where each m_i is a column of A .

Then take the Zariski closure in $(\mathbb{C})^s$. That variety is called Y_A .

2.2.12 Example

$$A = \begin{pmatrix} 1 & 3 \\ 2 & -1 \\ 3 & 0 \end{pmatrix}$$

$$\phi_A(t_1, t_2, t_3) = (t_1^1 t_2^2 t_3^3, t_1^3 t_2^{-1} t_3^0)$$

2.2.13 Theorem *Generated by differences of monomials.*

Proof Let L be the lattice of linear dependencies for the columns m_i .

$$\begin{aligned} \ell &\in \mathbb{Z}^s \\ \sum \ell_i m_i &= 0 \end{aligned}$$

This is the kernel of A as a map $\mathbb{Z}^s \rightarrow \mathbb{Z}^n$.

Write $\ell = \ell_+ - \ell_-$

$$\begin{aligned} \ell_+ &= \sum_{\ell_i > 0} \ell_i e_i \\ \ell_- &= - \sum_{\ell_i < 0} \ell_i e_i \end{aligned}$$

The difference of monomials $\prod_i x_i^{\ell_+, i} - \prod_i x_i^{\ell_-, i}$ vanishes on the image of ϕ_A and it's Zariski closure.

These are in the ideal for Y_A and in fact generate that ideal.

Coordinate Free

For Y_A , let Q be the lattice spanned by the m_i columns of A . This gets included into \mathbb{Z}^n .

$$0 \longrightarrow Q \longrightarrow \mathbb{Z}^n \longrightarrow B \longrightarrow 0$$

where B is the cokernel to finish off the exact triangle. B is $\mathbb{Z}^{n-s} \oplus \text{Torsion}$. Applying $\text{Hom}(-, \mathbb{C}^*)$

$$1 \longrightarrow G = B^\vee \longrightarrow (\mathbb{C}^*)^n \xrightarrow{\phi_A} \text{Hom}(Q, \mathbb{C}^*) \longrightarrow 1$$

of abelian groups written multiplicatively.

2.2.14 Definition (Invariant Ring) $S^G = \mathbb{C}[x_1 \cdots x_n]^G$ with associated affine variety.

$\text{Spec} S^G = \mathbb{C}^n //_{\text{affine}} G = \text{Spec}(\mathbb{C}[\mathbb{N}^n \cap Q])$. $\mathbb{C}^n //_{\text{affine}} G$ indicates affine GIT quotient. Expect dimension $n - (n - s) = s$.

Apply $\text{Hom}(-, \mathbb{Z})$ instead gives

$$0 \longrightarrow \text{Hom}(B, \mathbb{Z}) \longrightarrow \mathbb{Z}^n \longrightarrow \text{Hom}(Q, \mathbb{Z}) \longrightarrow \text{Ext}^1(B, \mathbb{Z}) \longrightarrow 0$$

$$0 \longrightarrow \text{Hom}(B, \mathbb{Z}) \longrightarrow \mathbb{Z}^n \longrightarrow Q^\vee \longrightarrow \text{Ext}^1(B, \mathbb{Z}) \longrightarrow 0$$

2.2.15 Definition (Projective Toric Variety) For $b \in B$, define $S_{(b)} = \bigoplus_i \mathbb{C}[x_1 \cdots x_n]_{i \cdot b}$ because S is graded by B . $S_{(b)}$ is graded by \mathbb{N} . $\text{Proj} S_{(b)}$ is the projective GIT quotient at b . One automatically has a map $\mathbb{C}^n //_{\text{proj}, b} G \rightarrow \mathbb{C}^n //_{\text{aff}} G$

Categorical aspects

One can ask for morphisms between toric varieties in three obvious ways.

- Polynomial maps in local coordinates as for usual varieties.
- Polynomial maps in the global homogenous coordinates.
- Toric morphisms are algebraic morphisms that respect the torus action.

The second and third are more specialized cases of the first.

2.2.16 Definition Let *Toric* be the category with objects (not necessarily affine) toric varieties over k . Denote an object X_1 with $T_1 \subset X_1$ and morphisms are equivariant morphisms $X_1 \rightarrow X_2$ extending a homomorphism of tori $T_1 \rightarrow T_2$.

2.2.17 Definition Let the category *Fan* be the category whose objects are fans Δ_1 in $N_1 \otimes \mathbb{R}$. The morphisms are group homomorphisms $N_1 \rightarrow N_2$ that send each cone $\sigma \in \Delta_1$ into some cone $\tau \in \Delta_2$.

2.2.18 Theorem The correspondence between fans and toric varieties gives an equivalence of categories between *Toric* and *Fan*.

Proof As theorem 2.1 of <https://arxiv.org/pdf/1503.04343.pdf>. See sources cited within. \square

Relation to Detailed Balance Varieties

There are coefficients k_{fwd} and k_{bwd} so not directly of the form differences of monomials as above. Treat them as variables, then later impose $k_{fwd} = k$ for it's values. This gives a specific kind of subscheme of a toric variety.

It is intersecting a toric variety with a bunch of complex codimension 1 hyperplanes by setting all the rate constants to their values.

$$\begin{array}{ccc} \text{DetBalVar} & \longrightarrow & pt \\ \downarrow & & \downarrow \\ \text{AffTorVar} & \longrightarrow & \mathbb{F}^{2R} \end{array}$$

The arrow $pt \rightarrow \mathbb{F}^{2R}$ picks out the reaction rates for all $2R$ forward and backward reactions. The arrow $\text{AffTorVar} \rightarrow \mathbb{F}^{2R}$ tells all of the reaction rates from the affine toric variety where they are treated as variables. The Detailed Balance Variety sits inside the affine toric variety by matching these two.

2.2.19 Lemma *What sort of morphism is the one for adding an extra equation as in coupling for reaction networks by adding extra reactions????*

What sort of morphism is the one for adding an extra molecule that simply drops one of the variables??????

2.2.20 Theorem *Looks like we have a functor from reaction networks and inclusions thereof to specific kind of subschemes of affine toric varieties and scheme maps.*

2.3 Identification from Data

This is in rxnNtwkId.py

Suppose one is given many observations of concentrations $[X_1] \cdots [X_n]$ such that each observation is of a detailed balance equilibrium. The goal is to form a plausible reaction network.

$$\begin{aligned}
 k_{fwd}[X_1]^{in_1} \cdots [X_n]^{in_n} &= k_{bwd}[X_1]^{out_1} \cdots [X_n]^{out_n} \\
 \sum (in_i - out_i) \log[X_i] &= \log \frac{k_{bwd}}{k_{fwd}} \\
 \begin{pmatrix} \log[X_1]_{o1} & \log[X_2]_{o1} & \cdots & \log[X_n]_{o1} \\ \log[X_1]_{o2} & \log[X_2]_{o2} & \cdots & \log[X_n]_{o2} \\ \cdots & \cdots & \cdots & \cdots \\ \log[X_1]_{oM} & \log[X_2]_{oM} & \cdots & \log[X_n]_{oM} \end{pmatrix} \begin{pmatrix} in_1 - out_1 \\ in_2 - out_2 \\ \cdots \\ in_n - out_n \end{pmatrix} &= \begin{pmatrix} 1 \\ 1 \\ \cdots \\ 1 \end{pmatrix} \left(\log \frac{k_{bwd}}{k_{fwd}} \right) \\
 \begin{pmatrix} \log[X_1]_{o2} - \log[X_1]_{o1} & \log[X_2]_{o2} - \log[X_2]_{o1} & \cdots & \log[X_n]_{o2} - \log[X_n]_{o1} \\ \cdots & \cdots & \cdots & \cdots \\ \log[X_1]_{oM} - \log[X_1]_{o1} & \log[X_2]_{oM} - \log[X_2]_{o1} & \cdots & \log[X_n]_{oM} - \log[X_n]_{o1} \end{pmatrix} \begin{pmatrix} in_1 - out_1 \\ in_2 - out_2 \\ \cdots \\ in_n - out_n \end{pmatrix} &= \begin{pmatrix} 0 \\ 0 \\ \cdots \\ 0 \end{pmatrix}
 \end{aligned}$$

Solve that last equation over the integers to get $in_i - out_i$. In particular find the solution with the smallest ℓ^1 norm possible. Then plug that into the second to last equation to recover $\log \frac{k_{bwd}}{k_{fwd}}$

If $A_i \equiv in_i - out_i < 0$ take $in_i = 0$ and $out_i = -A_i$. If $A_i > 0$ then take $in_i = A_i$ and $out_i = 0$. If it is 0 then take both to be 0. Solve for $K \equiv \frac{k_{fwd}}{k_{bwd}}$ and set $k_{fwd} = K * r$ and $k_{bwd} = r$ where $r > 0$ is a free parameter that we will optimize over.

This is the basic reaction. Also add reactions that have the same net behavior but add $\sum n_i [X_i]$ to both sides of the equations for all \vec{n} with $|\vec{n}|_1 \leq N$ for some small $N \approx 2$ (up to you). They have their own r values. This adds $f(N, n)$ reactions for every basic reaction. We expect only 1 of them will be correct. One of the $[X_i]$ might be a catalyst that is on both sides of the reaction, so the basic reaction is not correct.

Repeat for the solution with the next smallest ℓ^1 norm and keep doing this until we have enough candidate reactions. Do not check if this is in the span of those already found. For example, in terms of net vectors $\alpha + \beta = \gamma + \delta$, but all four are in the example reaction network.

Use the number of reactions that one expects the reaction to be made up of (based on intuition from similar systems like a citric acid cycle or urea cycle) to get a gauge of how many times to repeat. Actually each candidate reaction is a 1 parameter family with their own r values. We want some extra because data from nonequilibrium dynamics will eliminate some of the possibilities.

2.4 Similar Code

<https://github.com/enricozb/python-crn>

<https://github.com/barronh/permm>

<https://arxiv.org/pdf/1509.05153.pdf>

<https://arxiv.org/ftp/arxiv/papers/1412/1412.6346.pdf>

Chapter 3

OpenMarkovTensorFlow

There is a Jupyter and a regular py version.

http://math.ucr.edu/home/baez/coarse_graining.pdf

`timeStep` takes care of the operation $p \rightarrow e^{Ht}p + inRate * t - outRate * t$ for H the stochastic matrix and provided vectors of the inflow and outflow rates. Those are initialized with `tf.scatter` to put them in the correct entries of the vector.

Disjoint union is implemented, but unlike `PetriNet.hs` identifying multiple places into one is not implemented. That is the function `coarseGrain` that just returns 0.

`displayGraph` makes a directed graph where the blue vertices have `inFlow`, the red vertices have outflow, the black vertices are the ordinary vertices. There are edges between vertices i and j whenever the stochastic matrix H has $|H_{ij}|$ bigger than some numerical cutoff. That prevents cluttering the graph with edges that are essentially not there.

Chapter 4

Glauber Couplings.ipynb

<https://arxiv.org/pdf/1803.04738.pdf>

4.0.1 Definition (Glauber Dynamics) $\vec{s}(t)$ are the ± 1 variables representing Ising spin state of atom i at time t .

$$\begin{aligned} P(\vec{s}(t+1) \mid \vec{s}(t)) &= \prod_{i=1}^N \frac{e^{s_i(t+1)H_i(t)}}{e^{H_i(t)} + e^{-H_i(t)}} \\ H_i(t) &= h_i(t) + \sum J_{ij}s_j(t) \end{aligned}$$

This does an effective magnetization H_i by an external h_i combined with the effect of the neighbors.

We just see a sample trajectory from this dynamics. From this J is estimated.

$$\begin{aligned} J^{est} &= A^{-1}DC^{-1} \\ A_{ij} &= (1 - m_i^2)\delta_{ij} \\ m_i &= \langle s_i(t) \rangle \\ C_{ij} &= \langle s_i(t)s_j(t) \rangle - m_i m_j \\ D_{ij} &= \langle s_i(t+1)s_j(t) \rangle - m_i m_j \end{aligned}$$

Chapter 5

Evolutionary

5.1 Evolutionary Graph.ipynb

<https://www.quantamagazine.org/mathematics-shows-how-to-ensure-evolution-20180626/>

Make an Erdos-Renyi random graph with numNodes as the number of individuals. pErdosRenyi is a parameter for the probability of edges. If there is an edge that represents that those two individuals can compete where one dies and the other gets to reproduce and have it's child occupy that node. The individuals are all initialized with some random fitnesses. The edges are randomly weighted.

doARound carries out the following procedure

- Randomly choose an individual A to reproduce with probability distribution weighted based on fitness.
- Select a neighbor B of that individual with probability distribution based on edge weights.
- Replace that neighbor B with the child of A who has the same fitness that A did.

Repeat this round for timeLength times and plot the average fitness as a function of time. It tends to increase because the more fit reproduce more and replace the less fit. But it is not completely monotone because there are small chances for less fit individuals to reproduce.

5.2 Evolutionary Game

[?]

Let there be a two player symmetric game where each player has K strategies counted as $1 \cdots K$. The payoffs p_{ij} are the probabilities for survival when you play strategy i and they play strategy j . If the opponent dies, there are simply p_{i0} probabilities when you play strategy i and you're opponent is dead. There are N rounds of this.

Suppose you have to choose one of those pure strategies at the beginning of those N rounds and can't change it. Then the probabilities of survival become a payoff matrix for a symmetric game with K strategies with entries being functions of N . Call these $q_{ij}(N)$. To find $q_{ij}(N)$, make a Markov model and take it to the N 'th power and use that to find you're probability of survival with you in strategy i and opponent in strategy j . For $j \neq i$, this is the sum of probabilities where $ij \rightarrow ij$ and $ij \rightarrow i$. Those account for the probability you both survive and the second for the probability only you survive. If $i = j$, then do 1/2 the probability of $ii \rightarrow i$ plus the probability of $ii \rightarrow ii$.

Imagine a population of these. Let x_i be the proportion of the population choosing strategy i . There fitness is the probability of survival when they play this game with a random other member of the population.

5.2.1 Definition (Replicator Equation)

$$\begin{aligned}\dot{x}_i &= x_i(f_i(\vec{x}) - \sum x_j f_j(\vec{x})) \\ \sum x_i &= 1\end{aligned}$$

where $f_i(\vec{x})$ is the fitness of strategy i in the population with given proportions. The last term in the parenthesis is the average fitness of the population. So better than average is rewarded and worse is punished.

In this example,

$$f_i(\vec{x}) = \sum_m x_m q_{im}(N)$$

As N changes, the equilibria for this differential equation change.

$$\dot{x}_i = \sum_m x_i x_m q_{im}(N) - \sum_{j,m} x_i x_j x_m q_{jm}(N)$$

This is the general structure whenever the fitness is a linear function of the proportions.

5.2.1 Equilibria

For equilibria, set all $\dot{x}_i = 0$, to get K polynomial equations on these K variables as well as the normalization $\sum x_i = 1$.

Homogenize with an additional variable z .

$$\begin{aligned}0 &= \sum_m z x_i x_m q_{im}(N) - \sum_{j,m} x_i x_j x_m q_{jm}(N) \\ 0 &= \sum x_i - z\end{aligned}$$

Intersecting K cubic hypersurfaces and a hyperplane in $\mathbb{P}(F^{K+1})$. This is $K + 1$ equations applied to a K dimensional projective space. Want there to only be isolated points as equilibria so if all $K + 1$ of these equations are needed, won't be a complete intersection.

5.2.2 Relative Entropy

Let $I(p(t) \mid q)$ be the relative entropy

$$\begin{aligned}
I(p(t) \mid q) &= \sum q_i \log \frac{q_i}{p_i(t)} \\
\frac{d}{dt} I(p(t) \mid q) &= - \sum q_i \frac{\dot{p}_i}{p_i} \\
&= - \sum q_i (f_i(\vec{p}) + \sum p_j f_j(\vec{p})) \\
&= - \sum q_i f_i(\vec{p}) + \sum p_j f_j(\vec{p}) \\
&= \sum f_j(\vec{p}) (p_j - q_j)
\end{aligned}$$

5.2.2 Lemma (Shahshahani) *If $q_{im}(N) = q_{mi}(N)$ so can find a V such that $f_i = \frac{dV}{dx_i}$ with mixed partials being equal. If this is done then the replicator equation is a gradient flow equation with respect to the Fisher information metric.*