**Simulation Paper Outline: The Evolution Of Kin Preference**

**Sept 2012**

**Abstract**

Using an individual-based and genetically explicit model we explore the evolution of kin selection.....

What causes the evolution of kinship in social groups........?

**Introduction**

*Paragraph 1:*  Background on the evolution of kin selection and the evolution of cooperation

*Paragraph 2:*  In our model we did......

*Paragraph 3:* Explanation of function used in simulation....

*Paragraph 4:* Perhaps sub paragraphs explaining in more detail the function and real world parallels.

**Methods (need more information from Julian)**

*The model (methods copied from Julian’s documents)*

The first step at every generation step of the model is group formation. Groups are formed by accretion which is based on kinship in the following manner. Individuals start trying to get into the last non-empty group and continue backwards from there. If they do not find a group they form a new one. The process stops when the last group has been occupied (by one individual). We assume that in the initial population all individuals are related.

*The function*

Let i denote the cooperative tendency of individual *i*, and *gi* denote the kin-interaction preference. These two traits very from 0 to 1. The larger i is the more individual *i* cooperates, and the larger *gi* is the higher the preference of individual *i* to interact with highly related individuals. Let *j* denote the group that *i* is trying to join. The probability that *i* joins group *j* is:

where *h(j)* is one if group *j* is below the optimal group size , zero if the size of j is above the expected stable group size, and linearly decreasing in between. Function *h* ensures that the group size does not explode, and is slightly above the optimal group size (as often observed in the biological world). Function *k* weights the kinship preferences of the group, we assume that the joiner always wants to join the group. The term considers the kinship preferences of the group, is the average kinship preference inside group *j*, and *rij* is the average relatedness of individual *i* to the members of group *j*.

Function *k* is defined as follows:



Figure 1: Kinship weighting function.

For *t* equal to zero relatedness does not play a role, that is, individuals have no preference for kin interactions. For *t* equal to 1 we get the equivalent of sibs- only. For *t* = 0:5 we get a linear function that approximates the kin-preference case, always letting in brothers and letting in cousins with a probability close to 1/4, second cousins with probability 1/16 and so on.

Once the group formation process has taken place, we proceed to determine the number of offspring that each individual will contribute to the pool, using the following function:

Here, *n* is the size of the group the individual is in, therefore it will be assumed to be a positive real value, *n*0. Parameter i is the cooperative tendency of the individual itself. The resulting value of *n*, depends on each individual preference for kin interaction.

**Results**

*Correlations and counter correlations within runs*

Cooperation is correlated with group size and relatedness is correlated with kin preference. However kin preference and relatedness are counter-correlated with cooperation and group size.

**Figure 1: representative graph of correlations within one run**

*Test for white noise*

Significant values of the Fisher's κ statistic allow us to reject the null hypothesis that fluctuations in the series are due to white noise. We tested whether the oscillations apparent in figure 1 were simply due to whitenoise or whether there was intrinsic periodicity.

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Fisher’s κ** | **P value** |
| Average cooperation | 672.3 | <<0.001 |
| Average group size | 1380.3 | <<0.001 |
| Relatedness | 730.1 | <<0.001 |
| Kin preference | 1757.4 | <<0.001 |

*Anova tests*

*(Statistical description of method closely copied from AmNat 2001 paper)*

We used the ANOVA to test for the effect of the various parameters, their second- and third-order polynomial terms and their interactions. We customized the test for each response variable by dropping all nonsignificant terms (P>0.05) terms and their interactions. The of the reduced models was excellent, with r2 values of 92% (see table x). Kin preference and average cooperation were arcsin transformed while relatedness and group size were log transformed.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Parameter | Kin Preference | Relatedness | Group size | Ave Coop |
| r | 88.4 | 90.6 | 15.8 | 11.1 |
| c | 0 | 0.5 | 63.3 | 6.4 |
| β | 2.3 | 0 | 4.7 | 29.9 |
| Interactions | 1.5 | 0 | 10.6 | 36.9 |
| Total (r2) | 92.2 | 91.1 | 94.4 | 84.3 |

Table x:

**Discussion**

**Figures**

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**Fig 1:** Time series showing oscillations for R=0.1, c=0.06, β=0.2. Lines shown are cubic spline fits with flexibility parameter λ= 0.001 on the original data. The first 10000 records of the re run were removed to ensure that the cycle had reached equilibrium.

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**Fig 2:** Graphs of the average of cooperation, group size, relatedness and kin preference for each run with the first 10000 generations removed. Curves are cubic spline fits with λ=0.001 (**Leticia**: I changed λ to be 0.001 because it appears that when β=0.8 and C=0.02 average cooperation is a step function (orange triangles), which is a lost on the graphs if λ=0.01.)