**Simulation paper outline: The evolution of kin preference**

**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 ....

**Methods (copies from Julian’s document in dropbox)**

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

population all individuals are related.

Let i denote the cooperative tendency of individual i, and gi denote her 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:

Pij =

\_

1 : if j is empty

h(j) \_ k(rij ; \_ gj) : otherwise

where h(j) is one if group j is below the optimal group size (\_=c), 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 k(rij ; \_ gj) considers the kinship

preferences of the group, \_g 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 de\_ned 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 aproximates 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 o\_spring that each individual will contribute to the pool, using the following function:

fi (n; ; i) = ere􀀀cnn (1 + \_ ( 􀀀 i)) (1)

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 and group size are correlated, relatedness and kin preference area correlated, but that kin preference and relatedness are counter-correlated with cooperation and group size

Figure 1: representative graph

*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 | <<0.00001 (2.11e-293) |
| Average group size | 1380.3 | <<0.00001 (reported as 0) |
| Relatedness | 730.1 | <<0.00001 (2.11e-319) |
| Kin preference | 1757.4 | <<0.00001 (reported as 0) |

*Anova tests*

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)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 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:

**Need to test whetheh rt just tth hewd application of anothte repbome ewth itwi iht thh the tht tht tht thtthh the tht tht etth hee thh eth hhe ehe ete ete eth hhet tte ttet tth**

**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.

D:\RFile\RplotFULL.tiff

**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.)