Scientific publications without ODD model descriptions

Supplemental material for Exercise 2, Chapter 3 of *Agent-Based and Individual-Based Modeling*

Axelrod, R. 1997. The dissemination of culture, a model with local convergence and global polarization. *Journal of Conflict Resolution* 41:203-226.

Despite tendencies toward convergence, differences between individuals and groups continue to exist in beliefs, attitudes, and behavior. An agent-based adaptive model reveals the effects of a mechanism of convergent social influence. The actors are placed at fixed sites. The basic premise is that the more similar an actor is to a neighbor, the more likely that that actor will adopt one of the neighbor's traits. Unlike previous models of social influence or cultural change that treat features one at a time, the proposed model takes into account the interaction between different features. The model illustrates how local convergence can generate global polarization. Simulations show that the number of stable homogeneous regions decreases with the number of features, increases with the number of alternative traits per feature, decreases with the range of interaction, and (most surprisingly) decreases when the geographic territory grows beyond a certain size.

Bryson, J. J., Y. Ando, and H. Lehmann. 2007. Agent-based modelling as scientific method: a case study analysing primate social behaviour. *Philosophical Transactions of the Royal Society London B* 362:1685-1698. http://rstb.royalsocietypublishing.org/content/362/1485/1685.full

A scientific methodology in general should provide two things: first, a means of explanation and, second, a mechanism for improving that explanation. Agent-based modelling (ABM) is a method that facilitates exploring the collective effects of individual action selection. The explanatory force of the model is the extent to which an observed meta-level phenomenon can be accounted for by the behaviour of its micro-level actors. This article demonstrates that this methodology can be applied to the biological sciences; agent-based models, like any other scientific hypotheses, can be tested, critiqued, generalized or specified. We review the state of the art for ABM as a methodology for biology and then present a case study based on the most widely published agent-based model in the biological sciences: Hemelrijk's DomWorld, a model of primate social behaviour. Our analysis shows some significant discrepancies between this model and the behaviour of the macaques, the genus used for our analysis. We also demonstrate that the model is not fragile: its other results are still valid and can be extended to compensate for these problems. This robustness is a standard advantage of experiment-based artificial intelligence modelling techniques over analytic modelling.

Deffuant, G., F. Amblard, G. Weisbuch, and T. Faure. 2002. How can extremism prevail? A study based on the relative agreement interaction model. *Journal of Artificial Societies and Social Simulation* 5. http://jasss.soc.surrey.ac.uk/5/4/1.html

We model opinion dynamics in populations of agents with continuous opinion and uncertainty. The opinions and uncertainties are modified by random pair interactions. We propose a new model of interactions, called relative agreement model, which is a variant of the previously discussed bounded confidence. In this model, uncertainty as well as opinion can be modified by interactions. We introduce extremist agents by attributing a much lower uncertainty (and thus higher persuasion) to a small proportion of agents at the extremes of the opinion distribution. We study the evolution of the opinion distribution submitted to the relative agreement model. Depending upon the choice of parameters, the extremists can have a very local influence or attract the whole population. We propose a qualitative analysis of the convergence process based on a local field notion. The genericity of the observed results is tested on several variants of the bounded confidence model.

Epstein, J. M. 2002. Modeling civil violence: An agent-based computational approach. *Proceedings of the National Academy of Sciences of the United States of America* 99:7243-7250. http://www.pnas.org/content/99/suppl_3/7243.full

This article presents an agent-based computational model of civil violence. Two variants of the civil violence model are presented. In the first a central authority seeks to suppress decentralized rebellion. In the second a central authority seeks to suppress communal violence between two warring ethnic groups.

Jackson, A. L., G. D. Ruxton, and D. C. Houston. 2008. The effect of social facilitation on foraging success in vultures: a modelling study. *Biology Letters* 4:311-313. http://dx.doi.org/10.1098/rsbl.2008.0038

The status of many Gyps vulture populations are of acute conservation concern as several show marked and rapid decline. Vultures rely heavily on cues from conspecifics to locate carcasses via local enhancement. A simulation model is developed to explore the roles vulture and carcass densities play in this system, where information transfer plays a key role in locating food. We find a sigmoid relationship describing the probability of vultures finding food as a function of vulture density in the habitat. This relationship suggests a threshold density below which the foraging efficiency of the vulture population will drop rapidly towards zero. Management strategies should closely study this foraging system in order to maintain effective foraging densities

Janssen, M. A., N. P. Radtke, and A. Lee. 2009. Pattern-oriented modeling of commons dilemma experiments. *Adaptive Behavior* 17:508-523.

A major challenge in the development of computational models of collective behavior is the empirical validation. Experimental data from a spatially explicit dynamic commons dilemma experiment is used to empirically ground an agent-based model. Three distinct patterns are identified in the data. Two naive models, random walk and greedy agents, do not produce data that match the patterns. A more comprehensive model is presented that explains how participants make movement and harvest decisions. Using pattern-oriented modeling the parameter space is explored to identify the parameter combinations that meet the three identified patterns. Less than 0.1% of the parameter combinations meet all the patterns. These parameter settings were used to successfully predict the patterns of a new set of experiments

Kerr, B., M. A. Riley, M. W. Feldman, and B. J. M. Bohannan. 2002. Local dispersal promotes biodiversity in a real-life game of rock-paper-scissors. *Nature* 418:171-174.

One of the central aims of ecology is to identify mechanisms that maintain biodiversity. Numerous theoretical models have shown that competing species can coexist if ecological processes such as dispersal, movement, and interaction occur over small spatial scales. In particular, this may be the case for nontransitive communities, that is, those without strict competitive hierarchies. The classic non-transitive system involves a community of three competing species satisfying a relationship similar to the children's game rock-paper-scissors, where rock crushes scissors, scissors cuts paper, and paper covers rock. Such relationships have been demonstrated in several natural systems. Some models predict that local interaction and dispersal are sufficient to ensure coexistence of all three species in such a community, whereas diversity is lost when ecological processes occur over larger scales. Here, we test these predictions empirically using a non-transitive model community containing three populations of *Escherichia coli*. We find that diversity is rapidly lost in our experimental community when dispersal and interaction occur over relatively large spatial scales, whereas all populations coexist when ecological processes are localized.

Kreft, J.-U., G. Booth, and J. W. T. Wimpenny. 1998. BacSim, a simulator for individual-based modelling of bacterial colony growth. *Microbiology* 144:3275–3287. http://www.socgenmicrobiol.org.uk/MIC/144/3275/1443275H.HTM

The generic, quantitative, spatially explicit, individual-based model BacSim was developed to simulate growth and behaviour of bacteria. The potential of this approach is in relating the properties of microscopic entities – cells – to the properties of macroscopic, complex systems such as biofilms. Here, the growth of a single *Escherichia coli* cell into a colony was studied. The object-oriented program BacSim is an extension of Gecko, an ecosystem dynamics model which uses the Swarm toolkit for multi-agent simulations. The model describes bacterial properties including substrate uptake, metabolism, maintenance, cell division and death at the individual cell level. With the aim of making the model easily applicable to various bacteria under different conditions, the model uses as few as eight readily obtainable parameters which can be randomly varied. For substrate diffusion, a two-dimensional diffusion lattice is used. For growth-rate-dependent cell size variation, a conceptual model of cell division proposed by Donachie was examined. A mechanistic version of the Donachie model led to unbalanced growth at higher growth rates, whereas including a minimum period between subsequent replication initiations ensured balanced growth only if this period was unphysiologically long. Only a descriptive version of the Donachie model predicted cell sizes correctly. For maintenance, the Herbert model (constant specific rate of biomass consumption) and for substrate uptake, the Michaelis–Menten or the Best equations were implemented. The simulator output faithfully reproduced all input parameters. Growth characteristics when maintenance and uptake rates were proportional to either cell mass or surface area are compared. The authors propose a new generic measure of growth synchrony to quantify the loss of synchrony due to random variation of cell parameters or spatial heterogeneity. Variation of the maximal uptake rate completely desynchronizes the simulated culture but variation of the volume-at-division does not. A new measure for spatial heterogeneity is introduced: the standard deviation of substrate concentrations as experienced by the cells. Spatial heterogeneity desynchronizes population growth by subdividing the population into parts synchronously growing at different rates. At a high enough spatial heterogeneity, the population appears to grow completely asynchronously.

LeBaron, B. 2000. Agent-based computational finance: Suggested readings and early research. *Journal of Economic Dynamics and Control* 24:679-702. http://www.sciencedirect.com/science/article/pii/S0165188999000226

The use of computer simulated markets with individual adaptive agents in finance is a new, but growing field. This paper explores some of the early works in the area concentrating on a set of some of the earliest papers. Six papers are summarized in detail, along with references to many other pieces of this wide ranging research area. It also covers many of the questions that new researchers will face when getting into the field, and hopefully can serve as a kind of minitutorial for those interested in getting started.

LeBaron, B. 2012. Heterogeneous gain learning and the dynamics of asset prices. *Journal of Economic Behavior & Organization* 83:424-445. http://www.sciencedirect.com/science/article/pii/S0167268112000546

This paper presents a new agent-based financial market. It is designed to be both simple enough to gain insights into the nature and structure of what is going on at both the agent and macro levels, but remain rich enough to allow for many interesting evolutionary experiments. The model is driven by heterogeneous agents who put varying weights on past information as they design portfolio strategies. It faithfully generates many of the common stylized features of asset markets. It also yields some insights into the dynamics of agent strategies and how they lead to market instabilities.

Rands, S. A., R. A. Pettifor, J. M. Rowcliffe, and G. Cowlishaw. 2004. State-dependent foraging rules for social animals in selfish herds. *Proceedings of the Royal Society of London Series B* 271:2613-2620. http://dx.doi.org/10.1098/rspb.2004.2906

Many animals gain benefits from living in groups, such as a dilution in predation risk when they are closely aggregated (referred to as the 'selfish herd'). Game theory has been used to predict many properties of groups (such as the expected group size), but little is known about the proximate mechanisms by which animals achieve these predicted properties. We explore a possible proximate mechanism using a spatially explicit, individual-based model, where individuals can choose to rest or forage on the basis of a rule-of-thumb that is dependent upon both their energetic reserves and the presence and actions of neighbours. The resulting behaviour and energetic reserves of individuals, and the resulting group sizes, are shown to be affected both by the ability of the forager to detect conspecifics and areas of the environment suitable for foraging, and by the distribution of energy in the environment. The model also demonstrates that if animals are able to choose (based upon their energetic reserves) between selecting the best foraging sites available and moving towards their neighbours for safety, then this also has significant effects upon individuals and group sizes. The implications of the proposed rule-of-thumb are discussed.

Rose, K. A., W. J. Kimmerer, K. P. Edwards, and W. A. Bennett. 2013. Individual-Based Modeling of Delta Smelt Population Dynamics in the Upper San Francisco Estuary: I. Model Description and Baseline Results. *Transactions of the American Fisheries Society* 142:1238-1259. http://dx.doi.org/10.1080/00028487.2013.799518

Many factors have been implicated in the decline of Delta Smelt *Hypomesus transpacificus* in the upper San Francisco Estuary, and the importance of each factor is difficult to determine using field data alone. We describe a spatially explicit, individual-based population model of Delta Smelt configured for the upper estuary. The model followed the reproduction, growth, mortality, and movement of individuals over their entire life cycle on the same spatial grid of cells as the Delta Simulation Model (DSM2) hydrodynamics model. Daily values of water temperature, salinity, and densities of six zooplankton prey types were represented on the spatial grid. Reproduction was evaluated daily, and new individuals were introduced into the model as yolk sac larvae. Growth of feeding individuals was based on bioenergetics and zooplankton densities. Mortality sources included natural mortality, starvation, and entrainment in water diversion facilities. Movement of larvae was determined using a particle tracking model, while movement of juveniles and adults was based on salinity. Simulations were performed for 1995?2005. The baseline simulation was generally consistent with the available data. Predicted daily fractions of larvae entrained and annual fractions of adults entrained were similar in magnitude to data-based estimates but showed less interannual variation. Interannual differences in mean length at age 1 had large effects on maturity and subsequent egg production. Predicted and observed spatial distributions in the fall showed moderately good agreement for extremely low- and high-outflow years. As indicated by the population growth rate, 1998 was the best year and 2001 was the worst year. Water year 1998 (i.e., October 1997?September 1998) was characterized by fast growth in fall 1997, low entrainment, and high stage-specific survival rates, whereas water year 2001 had opposite conditions. Our analysis further shows how multiple factors can operate simultaneously to result in the decline in abundance of Delta Smelt. Received November 9, 2012; accepted April 18, 2013

Stockholm, D., R. Benchaouir, J. Picot, P. Rameau, T. M. A. Neildez, G. Landini, C. Laplace-Builhé, and A. Paldi. 2007. The origin of phenotypic heterogeneity in a clonal cell population in vitro. *PLoS ONE* 2. http://dx.doi.org/10.1371/journal.pone.0000394

Background. The spontaneous emergence of phenotypic heterogeneity in clonal populations of mammalian cells in vitro is a rule rather than an exception. We consider two simple, mutually non-exclusive models that explain the generation of diverse cell types in a homogeneous population. In the first model, the phenotypic switch is the consequence of extrinsic factors. Initially identical cells may become different because they encounter different local environments that induce adaptive responses. According to the second model, the phenotypic switch is intrinsic to the cells that may occur even in homogeneous environments. Principal Findings. We have investigated the "extrinsic" and the "intrinsic" mechanisms using computer simulations and experimentation. First, we simulated in silico the emergence of two cell types in a clonal cell population using a multiagent model. Both mechanisms produced stable phenotypic heterogeneity, but the distribution of the cell types was different. The "intrinsic" model predicted an even distribution of the rare phenotype cells, while in the "extrinsic" model these cells formed small clusters. The key predictions of the two models were confronted with the results obtained experimentally using a myogenic cell line. Conclusions. The observations emphasize the importance of the "ecological" context and suggest that, consistently with the "extrinsic" model, local stochastic interactions between phenotypically identical cells play a key role in the initiation of phenotypic switch. Nevertheless, the "intrinsic" model also shows some other aspects of reality: The phenotypic switch is not triggered exclusively by the local environmental variations, but also depends to some extent on the phenotypic intrinsic robustness of the cells

Troisi, A., V. Wong, and M. A. Ratner. 2005. An agent-based approach for modeling molecular self-organization. *Proceedings of the National Academy of Sciences of the United States of America* 102:255-260. http://www.pnas.org/content/102/2/255.full

Agent-based modeling is a technique currently used to simulate complex systems in computer science and social science. Here, we propose its application to the problem of molecular self-assembly. A system is allowed to evolve from a separated to an aggregated state following a combination of stochastic, deterministic, and adaptive rules. We consider the problem of packing rigid shapes on a lattice to verify that this algorithm produces more nearly optimal aggregates with less computational effort than comparable Monte Carlo simulations

Tyre, A. J., H. P. Possingham, and D. B. Lindenmayer. 2001. Inferring process from pattern: can territory occupancy provide information about life history parameters? *Ecological Applications* 11:1722-1737.

A significant problem in wildlife management is identifying “good” habitat for species within the short time frames demanded by policy makers. Statistical models of the response of species presence/absence to predictor variables are one solution, widely known as habitat modeling. We use a “virtual ecologist” to test logistic regression as a means of developing habitat models within a spatially explicit, individual-based simulation that allows habitat quality to influence either fecundity or survival with a continuous scale. The basic question is how good are logistic regression models of habitat quality at identifying habitat where birth rates are high and death rates low (i.e., “source” habitat)? We find that, even when all the important variables are perfectly measured, and there is no error in surveying the species of interest, demographic stochasticity and the limiting effect of localized dispersal generally prevent an explanation of much more than half of the variation in territory occupancy as a function of habitat quality. This is true regardless of whether fecundity or survival is influenced by habitat quality. In addition, habitat models only detect a significant effect of habitat on territory occupancy when habitat quality is spatially autocorrelated. We find that habitat models based on logistic regression really measure the ability of the species to reach and colonize areas, not birth or death rates.

People interested in economics and finance are encouraged to look for additional publications at Dr. Leigh Tesfatsion’s Agent-based Computational Economics web site: http://www2.econ.iastate.edu/tesfatsi/aapplic.htm