

BP 9: Evolutionary Game Theory (Joint Session SOE/DY/BP)

Time: Monday 12:15–13:15

Location: H36

BP 9.1 Mon 12:15 H36

Evolutionary ecological-economic modelling: Ecological instability and economic growth — ●SYLVIE GEISENDORF¹, FRANK BECKENBACH², and CHRISTIAN KLIPPERT¹ — ¹ESCP Europe Campus Berlin, Heubnerweg 8-10, 14059 Berlin, Germany — ²University of Kassel

The paper proposes an evolutionary ecological-economic model taking into account the complexity of the ecological as well as the economic system. We argue that Economics should consider ecological complexity and the co-dynamics of the economic and ecological system to better understand drivers and restrictions of economic evolution. At the same time, the development of a regenerative resource is affected by the internal growth dynamics of the economy. Given that no economic activity is conceivable without using natural resources and relying on natural systemic services, there is a surprising simplification of the natural system in economic models. The model we propose has three particularities distinguishing it from traditional resource economic models. (1) it implements a multi-dimensional link between the economic and ecological system, considering side effects of the production process like waste or emissions. (2) it uses a difference equation approach for the biological resource instead of the typical differential one, to allow for the whole range of stability regimes and (3) it links this resource system to an evolving, agent-based economy instead of the standard optimization calculus.

BP 9.2 Mon 12:30 H36

Changing the rules of the game as an emergent feature of the dynamics — ●DARKA LABAVIĆ and HILDEGARD MEYER-ORTMANN — Jacobs University Bremen, Bremen, Germany

We consider (N, r) games of competition with N species and $r < N$ prey and predators. Basic reactions include predation, reproduction, decay, and diffusion, without a hard constraint on the occupation number per site. For special combinations of N and r we observe the option to see games within games for an appropriate choice of parameters. As one of the simplest examples we analyze a $(6, 3)$ game. Once the players segregate from a random initial distribution, domains on a coarse scale emerge, which play a $(2, 1)$ -game at their boundaries, while agents inside the domains play rock-paper-scissors (that is, $(3, 1)$), leading to the formation of spirals with species chasing each other. The $(2, 1)$ -game has a winner in the end, so that the coexistence of domains is transient, while agents inside the remaining domain coexist, until demographic fluctuations lead to the survival of only a single species. This means that we observe a dynamical generation of multiple scales in space and time with an emerging change of rules on the coarse scale starting from a simple set of rules on the unit scale of the grid. In view of predicting these features, we derive the deterministic limit within a van Kampen expansion. A linear stability analysis reproduces the number of forming domains and their composition in terms of species. A comparison of analytical predictions with Gillespie simulations also reveals the impact that the various sources of stochastic fluctuations have on the dynamics, even on its qualitative features.

BP 9.3 Mon 12:45 H36

A synthetic codon replicator with tRNA — ●SIMON ALEXANDER LANZMICH and DIETER BRAUN — Systems Biophysics, Physics Department, Nanosystems Initiative Munich and Center for NanoScience, LMU Munich, Germany

Every evolving system requires the storage and replication of genetic information. Modern biology solves this using an RNA-dominated machinery (ribosome and a pool of tRNAs) to encode proteins. The proteins in turn replicate genetic information. In contrast, early life most probably replicated genes using a pool of short RNA sequences.

To approach above chicken and egg problem, we explore an autonomous, waste-free, and purely thermally driven replication mechanism. Instead of chemical base-by-base replication, it operates on successions of multi-base codons. The molecules used have a hairpin loop at each end and are derived from transfer RNA. They encode and replicate a binary code at the anticodon sites of tRNA.

Replication of a template succession of tRNAs is facilitated by temperature oscillations and proceeds in three logical steps. (1) Strands with matching anticodons bind to the template. (2) Fluctuations in the bound strands' hairpins allow for the hybridization to neighboring strands. (3) Subsequent heating splits the replicate from the template, freeing both for the next cycle. This physical ligation chain reaction proceeds cross-catalytically. Instead of chemical backbone ligation, matching strands are linked by physical base pairing.

BP 9.4 Mon 13:00 H36

Stepwise cooperation of molecular replicators — ●GEORG URTEL and DIETER BRAUN — Systems Biophysics, Ludwig-Maximilians-Universität München, Amalienstr. 54, D- 80799 München, Germany

Life emerged from the ability of informational polymers to pass on sequences to other polymers before they degrade. Before competition between living species, the first selection pressure was to replicate faster than degradation. What were the strategies the molecules could take?

Based on biological evidence, DNA or RNA replicators require a defined binding site to start replication. We study experimentally and theoretically three geometries of the binding site: linear single binding, hairpin binding and two opposing binding locations. The geometries have fundamentally different, increasing replication speeds.

Interestingly, two hairpin replicators cooperate readily and form the fastest replicating geometry. After incomplete replication, they bind by hybridization and cooperate by forming a crossbreed species. This cooperation of two replicators retains most of the sequence information of both hairpins. Under conditions where hairpins are doomed to degrade, their crossbreed is replicating fast enough to survive. As a result, two initially separated hairpins survive by diffusional mixing and the colocalized crossbreeding.

Our experiments show a stepwise evolution of replicator geometries. Already at a molecular level, cooperation was an advantageous strategy under Darwinian evolution.