

Master project opportunities with TRÊS 2025-2026

Master project opportunities with the [TRÊS group](#) 2025-2026,
Groningen Institute for Evolutionary Life Sciences [GELIFES](#), University of Groningen

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For general orientation on master projects, make an appointment with your mentor or with one of the scientific staff members of the TRÊS group:

[Martijn Egas](#), [Yagmur Erten](#), [Rampal Etienne](#), [Ido Pen](#), [Koen van Benthem](#), [Sander van Doorn](#)

If you are interested in one of these projects, contact the daily supervisor for more information.

Note that you can only start with a project after meeting with / approval of the responsible scientific staff member.

The starting dates and ECTS size of projects below are approximate, in many cases this is flexible.

Editing note: insert a link or email address by marking a block of text and selecting ctrl-k

Keep projects (rows) together for each staff member

Please add if needed

Title: Maintenance of alternative reproductive tactics in two-spotted spider mites Type of work (experimental/theoretical/field work): experimental and/or theoretical Abstract: The study of ARTs has always drawn much attention, if only because males in those study systems typically differ in morphology: fighters develop a weapon and are not afraid to use it to monopolize females, whereas cheaters lack the weapon and try to sneak matings. The interesting aspect of ARTs in the two-spotted spider mite is that both fighters and sneakers are morphologically indistinguishable (and both have a weapon: their sword-like mouth parts with which they can fence) but display their strategy purely in terms of behaviour. How the polymorphism is maintained requires further explanation. This project is aimed to figure out if an eco-evolutionary feedback loop would allow for maintenance of the ART-polymorphism. Using the two-spotted spider mites we rear in our climate room, you will either 1. quantify behavioural traits displayed by fighter and sneaker males, and/or 2. create selection lines for fighting and sneaking, and/or 3. model the population dynamics of fighting and sneaking in a population and analyze evolutionary changes in fighting and sneaking.	Responsible staff member: Martijn Egas (martijn.egas@rug.nl) Daily supervisor: Koen Freerks / Martijn Egas ECTS: 30 or more Start: Jan/Feb 2025	Illustration 
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Methods: behavioural experiments and AI analysis of video material from the experiments, and/or theoretical modelling and simulation

Title: Origin and evolution of the genetic code – a theoretical framework

Type of work (experimental/theoretical/field work): theoretical

Abstract: A main feature in the origin of complex life is the translation system by means of the near-universal genetic code: stored information contained in large molecules (DNA) is copied onto smaller molecules (RNA) that are “read” by ribosomes, which make proteins based on the information. How this translation system originated and how it evolves, still poses many important questions. Evidence suggests that the translation system is highly adaptive and appears optimized by natural selection. What is missing, however, is an overall theoretical framework for the evolution of the translation system, which could predict the outcomes of experimental and bio-informatic efforts and thereby really test our insight into the evolution of translation. This project aims to build such a theoretical framework, based on existing models for protein synthesis and ideas on the evolution of the genetic code.

At the core of the translation system are codons, triplets of nucleotides of the RNA molecule that are recognized by tRNA molecules (because they have the mirror image of the codons: anticodons) in the ribosome. These codons cause the ribosome to add the amino acid that the tRNA molecule was charged with (through the enzyme AARS) to the emerging protein. The genetic code links each individual codon to one specific amino acid. There is quite some redundancy in the translation system, with multiple codons coding for the same amino acid. Open question are what level of redundancy is selected for, and what factors (e.g. growth rate, G-C content of the genome) drive the optimization of codon usage. Furthermore, experimental approaches in microbes, e.g. inserting or deleting specific tRNA genes to measure the effects on cellular function, showed that deletion of a non-mandatory tRNA gene does not strongly affect the functioning of the cell, but it does typically result in the evolution of a new tRNA gene with the same anticodon (by duplication of a tRNA gene followed by point mutation). Also, experiments have “resurrected” putative ancestral genes (“primordial genes”) for tRNA and AARS to test their function in

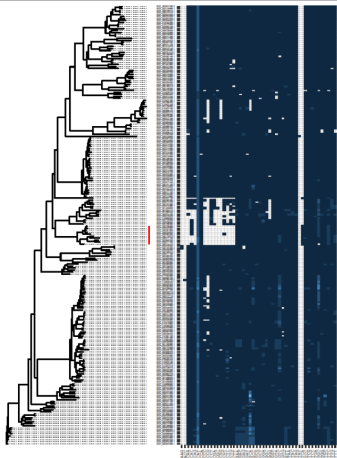
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Daily supervisor: Martijn Egas

ECTS: 30 or more

Start: Jan/Feb 2025

		Second letter codon							
		U		C		A		G	
First letter codon	U	UUU Phe	UUC Phe	UUA Leu	UUG Leu	UUC Ser	UUA Tyr	UGU Cys	UGA Cys
	C	UUC Phe	UCC Ser	UUA Leu	UUG Leu	UUA Ser	UUA stop	UGA stop	UGA stop
	A	UUA Leu	UUA Ser	UUA Ser	UUA stop	UUA stop	UUA stop	UGG Trp	UGG Trp
	G	UUG Leu	UUG Ser	UUG Ser	UUG stop	UUG stop	UUG stop	UGG Trp	UGG Trp
C	U	CUU Leu	CUU Pro	CUU Pro	CUU Pro	CAU His	CAU His	CGU Arg	CGU Arg
	C	CUC Leu	CCC Pro	CCC Pro	CCC Pro	CAC His	CAC His	CGC Arg	CGC Arg
	A	CUA Leu	CCA Pro	CCA Pro	CCA Pro	CAA Gln	CAA Gln	CGA Arg	CGA Arg
	G	CUG Leu	CCG Pro	CCG Pro	CCG Pro	CAG Gln	CAG Gln	CGG Arg	CGG Arg
A	U	AUU Ile	ACU Thr	AAU Asn	AAU Asn	AGU Ser	AGU Ser	AGU Ser	AGU Ser
	C	AUC Ile	ACC Thr	AAC Asn	AAC Asn	AGC Ser	AGC Ser	AGC Ser	AGC Ser
	A	AUA Ile	ACA Thr	AAA Lys	AAA Lys	AGA Arg	AGA Arg	AGA Arg	AGA Arg
	G	AUG Met	ACG Thr	AAG Lys	AAG Lys	AGG Arg	AGG Arg	AGG Arg	AGG Arg
G	U	GUU Val	GUU Val	GCU Ala	GCU Ala	GAU Asp	GAU Asp	GGU Gly	GGU Gly
	C	GUC Val	GUC Val	GCC Ala	GCC Ala	GAC Asp	GAC Asp	GGC Gly	GGC Gly
	A	GUA Val	GUA Val	GCA Ala	GCA Ala	GAA Glu	GAA Glu	GGA Gly	GGA Gly
	G	GUG Val	GUG Val	GCG Ala	GCG Ala	GAG Glu	GAG Glu	GGG Gly	GGG Gly



translation. This project aims to develop theoretical predictions for these experimental approaches. Using publicly available high-quality genome sequences of Archaea, you will either 1. analyze why most Archaea have a set of 46 tRNA genes in single copy?, and/or 2. study phylogenetic changes in Archaeal tRNA gene use, and/or 3. model evolutionary dynamics of tRNA gene sets in relation to codon usage. Methods: bio-informatic analysis, phylogenetic comparative statistics, and/or theoretical modelling and simulation		
Title: Reputation-based cooperation: how to explain the polymorphism in reciprocation strategies? Type of work (experimental/theoretical/field work): theoretical Abstract: Human cooperation in large groups can emerge when help is channeled towards individuals with a good reputation of helping others. Evolutionary models suggest that, for reputation-based cooperation to be stable, the recipient's reputation should be based not only on his past behaviour (1st-order information) but also on the past behaviour of the recipient's recipient (2nd-order information). Second-order information reflects the context of others' actions, and allows people to distinguish whether or not giving (or denying) help was justified. Little is known yet about how people actually condition their cooperation on 2nd-order information. With a behavioural experiment, we show that people actively seek 2nd-order information and take this into account in their own helping decisions. In an anonymous iterated helping game, donors learned if their recipients helped others in the past and could obtain 2nd-order information about these actions. Donors often requested this 2nd-order information and were especially interested to know why help was denied (i.e., defection). Justified defection was rewarded: help was generally directed towards those who defected against the selfish, and away from those who defected against helpful individuals. A detailed analysis of individual strategies reveals that many subjects based their decisions solely on 1st-order information about their recipients' past behaviour. However, a substantial fraction of subjects consistently considered also the 2nd-order information about their recipients'	Responsible staff member: Martijn Egas (martijn.egas@rug.nl) Daily supervisor: Martijn Egas ECTS: 30 or more Start: Jan/Feb 2025	

behaviour. Our results provide strong empirical support for the mechanisms that theoretically underpin reputation-based cooperation, and highlight pronounced individual variation in human cooperative strategies. This last finding, in return, asks for new modelling effort to search for explanations of such behavioural polymorphisms.

Using the available experimental data on effects of information use on human helping behaviour, you will

1. model evolutionary dynamics of behavioural strategies that reciprocate acts of (non-)helping in simple game-like interactions.

Methods: game-theoretical modelling and simulation

Title: Changes in son preference in the Dutch nobility

Type of work (experimental/theoretical/field work): Data analysis and simulations

Abstract:.

A preference for sons is still present in many communities across the globe (Le & Nguyen, 2022). Such a preference could emerge when men are perceived to have an advantage throughout their life. In the Netherlands, a specific group for which this may hold is the Dutch Nobility. Their title, which has been shown to convey benefits (Dronkers, 2000), is inherited through the male line only. As such it would not be surprising if the nobility has had a preference for sons. Studying such a preference is possible by analysing how the current family composition of a couple affects their choice in having another child. In this project, together with Maurice de van der Schueren from the faculty of economics and business, we will analyse the presence of son preference based on an extensive dataset that he has digitised. This dataset contains the male lines of the Dutch nobility. A preliminary analysis (see figure) has shown that families of two whose second child was a daughter (F) are more likely to have a third child compared to other families of two. In this project we will analyse whether this preference for sons is heritable and perform simulations to test whether factors such as selective reporting could already lead to the found son preference. For the former question we will fit an animal model (see e.g. Wilson et al. 2010). As this project evolves undoubtedly new questions will show - and we are excited and open to exploring these too!

Methods: Data analysis, simulations

Responsible staff member:

Koen van Benthem

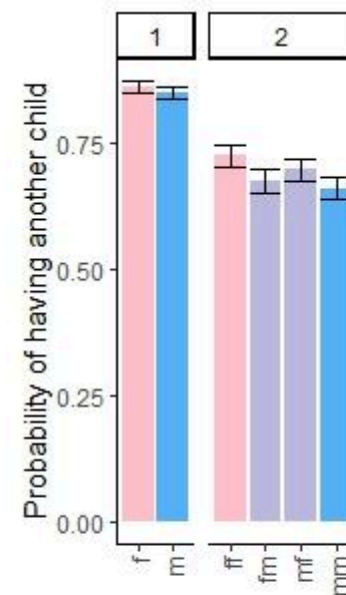
(k.j.van.benthem@rug.nl)

Daily supervisor: Koen van Benthem

ECTS: flexible

Start: flexible

Illustration



Title: Effect of a herbicide on the 14-spotted ladybird Type of work (experimental/theoretical/field work): experimental, analysis Abstract: The 14-spotted ladybird (<i>Propylea quatuordecimpunctata</i>) is used as a biocontrol agent. Preliminary results suggest that larvae of the species avoid drinking from droplets that contain glyphosate. In this experiment we aim to explore whether repeated exposure to a droplet with glyphosate leads to learning, in the sense that larvae start avoiding droplets altogether. In the future we would also like to explore other research questions, such as drivers for cannibalism, strength of inbreeding, and dietary preference. Methods: video tracking, experiments	Responsible staff member: Koen van Benthem Daily supervisor: Koen van Benthem ECTS: flexible Start: flexible	Illustration 
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Title: Type of work (experimental/theoretical/field work): Abstract:. Methods:	Responsible staff member: Daily supervisor: ECTS: Start:	Illustration