Ecological modelling of elasmobranch population dynamics in the Mediterranean Sea.
Contacts: Dr Alberto Barausse and Prof. Carlotta Mazzoldi, e-mail: alberto.barausse@unipd.it - carlotta.mazzoldi@unipd.it

The recently realized decline of elasmobranch abundance worldwide due to human overexploitation has been particularly strong in the Mediterranean Sea. Yet few studies integrate the ample empirical evidence on the decline of Mediterranean elasmobranchs (fishery time series, bycatch and sexual maturity estimates, etc.) in a coherent modelling framework to support conservation. This project aims to develop novel modelling tools to better understand elasmobranch population dynamics and their largely unexplored impact on marine ecosystems, and apply them to selected Mediterranean sub-basins. Such tools include: adaptations of classical population dynamics models to simulate the effect of ecological processes; Individual Based Models, explicitly simulating single individuals, their interactions and life history; food web models simulating trophic interactions. This project will advance the state of the art in marine ecological modelling and will generate knowledge-based advice for marine conservation and management.

Family life: an intricate system of signals.
Contact: Prof. Matteo Griggio, e-mail: matteo.griggio@unipd.it

Although the family is the commonest social structure, a considerable amount of work is still required to understand this fascinating system. Family life is only possible through cooperative behaviour such as joint offspring investment by parents but conflicts of interests, with at least three different origins, are an inherent part of the family system: sexual conflict between the parents over parental investment, parent-offspring conflict and sibling competition. The rock sparrow (Petronia petronia) is an excellent species to investigate these conflicts and the behavioural interactions between parents and offspring in response to modification of different intraspecific signals. Field work will be performed in Spain and the results will significantly contribute to our understanding of how conflicts arise and are dealt within a family.

Exploring photosynthetic biodiversity of the Ross Sea (Antarctica): how environmental changes affect it?
Contact: Prof. Isabella Moro, e-mail: isabella.moro@unipd.it

In recent years, Antarctic continent is going towards complex environmental changes, mostly related to global warming. Consequently, the native biota, undergoing to this challenge, is adapting itself to these modifications. In this context it is important to investigate the biodiversity of this area, to detect possible changes in the future. The focus of this project will be study the marine and terrestrial photosynthetic biodiversity (cyanobacteria, microalgae and seaweeds) of selected sites of the Ross Sea in Antarctica through classical and modern approaches (DNA barcoding and metabarcoding). Particularly, the research will focus on dynamics of phytoplankton community in the water column during the Austral summer through metabarcoding analyses based on samples from filters of the desalination plant of the Italian Antarctic Station (Mario Zucchelli Station) in Terra Nova Bay.

Homo sapiens in Eurasia between 60.000 and 40.000 years ago: where did everyone go?
Contact: Prof. Luca Pagani, e-mail: luca.pagani@unipd.it

Several layers of genetic, palaeoanthropology and palaeoclimatology evidence point to ~60.000 years ago as the most likely time window for the major colonization of Eurasia by Homo sapiens. The same evidence, however, also show that until 45.000-40.000 human populations did not expand much, both from a demographic and a geographic perspective. This PhD project aims at exploiting patterns of homozygosity and the signature of Neanderthal introgression within contemporary and ancient human populations, to reconstruct ~20.000 years of human demography between the out of Africa expansion and the broader colonization of Eurasia. The reconstructed scenario will be complemented through comparison with palaeoclimatic and palaeoanthropological evidence to refine our understanding of human occupation in Eurasia until 40.000 years ago. Requirements: bioinformatics skills (familiarity with Unix environment, commandline skills and basic coding abilities) and the ability to manage genomic data are mandatory.

Sexual selection and the evolutionary trade-offs in male life-history strategy.
Contact: Prof. Andrea Pilastro, e-mail: andrea.pilastro@unipd.it

Sexual selection, the main evolutionary explanation for sexual dimorphism, also contribute explaining sex differences in longevity and senescence rate. Life-history (L-H) theory predicts that reproductive senescence is shaped by evolutionary trade-offs with growth rate, survival and intrinsic longevity. While empirical evidence of L-H trade-offs is abundant for females, studies on male reproductive senescence are limited by the logistic difficulty of measuring genetic covariation among multiple sexual traits' senescence rates and longevity. We will overcome these problems by using a Pareto optimization approach, which allows to detect evolutionary trade-offs based on the phenotypic (co)variance of life-history traits from a random sample of unrelated individuals. We will focus on male pre- and postcopulatory traits in male guppies, which are characterized by an unusual pattern of senescence (Gasparini, Devigili & Pilastro. 2019. Sexual selection and ageing: interplay between pre- and post-copulatory traits senescence in the guppy. Proc. R. Soc. B 286:20182873).

Population genomics of Venice lagoon fish and mollusks for conservation and traceability.
Contact: Prof. Lorenzo Zane, e-mail: lorenzo.zane@unipd.it

The project will focus on the population genomics of a fish Atherina boyeri) and a mollusk species (Mytilus galloprovincialis), using ddRAD markers. The two species have strongly different features, but their lagoon populations critically depend on the exchange with the nearby sea. The microgeographic area considered will be the Venice lagoon and the neighboring estuaries in the North Adriatic Sea. Genomic markers (SNPs) will be used to detect genetic temporal variation using a multiyear sampling design and to estimate the effective population size of the two species. In addition, SNPs will provide a useful source of markers for the traceability of commercial products of the two species.