S6.11 Assessing physical habitat characteristics as limiting factors on brown trout (*Salmo trutta*) density

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The relations among brown trout densities and environmental variables have been deeply studied in freshwater ecosystems. These density–environment relations can be used in habitat-based association models to understand ecological dynamics and to predict changes in biological communities, especially when human-induced alterations are involved. However, the models proposed in literature are based on the study of the mean response, deliver information only about the preferences for certain habitat variables and are sometimes based on qualitative sampling. Habitat selection predictive models often do not account for ecological dynamics, especially density dependent processes. In stage-structured population, the strength of density dependent interactions between individuals of different age classes can exert a profound influence. The models produced in this work are based on the study of the limiting response and deliver information about the density that can be reasonably expected for each value of the considered habitat variable. In order to produce quantitative habitat suitability curves, a new sampling procedure has been performed and the acquired data were analyzed using quantile regression. The aim of this work is to demonstrate how the use of quantitative data and quantile regression analysis can be useful to describe the action of hydraulic variables and competition process on brown trout density in Alpine streams, where the flow can be considered as the main driving force.

S6.12 Coupling oceanography and genetics to assess the connectivity of European green crab populations in the Adriatic Sea

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Identifying the spatio/temporal scale of connectivity among populations is crucial to understand the factors driving population dynamics, dispersal patterns and gene flow in marine species. Coupled physical biological models are increasingly used to investigate larval dispersal and contrast alternative hypotheses by simulation. We coupled individual-based Lagrangian simulations incorporating early-life-history traits with a genetic marker analysis to investigate larval dispersal patterns of the European green crab (*Carcinus aestuarii*) in the Adriatic Sea and study the connectivity among seven locations during three years (2006-2008). The coupled physical biological model explicitly allowed for pelagic larval duration, diel vertical migration and synchronization between reproduction and moon phases and provided an assessment of oceanographic connectivity. Genetic analyses, based on eleven polymorphic microsatellite loci, tested for genetic divergence among populations using pairwise F_{ST} and AMOVA. We eventually compared connectivity matrices resulting from the two approaches to point out the role of Adriatic Sea currents in determining retention and spillover patterns and their consequences on the genetic structure of the local European green crab populations. Results revealed the existence of weak but significant differentiation patterns, with three significantly differentiated groups of samples reflecting a oceanographic subdivision of the Adriatic Sea into three sub-basins.