Bio:
Luis Pedro Coelho is a postdoctoral researcher in Peer Bork’s group at the European Molecular Biology Laboratory (EMBL). He has a PhD from Carnegie Mellon University where he worked under the supervision of Prof. Bob Murphy and a MSc from Instituto Superior Técnico in Lisbon. He currently works on the analysis of microbial communities in different environments, such as the marine environment or the human gut using computational methods, namely metagenomic analysis and fluorescence microscopy analysis. Luis is a Fulbright Scholar, a Siebel Scholar, and has won multiple awards for academic or research excellence.

Life in words and pictures: Understanding microbial ecology through sequencing and imaging of communities

Marine microbes are central to several bio-geochemical processes, but only recently has the scientific community developed the high-throughput technologies to ask basic questions such as: who are they? where are they? How are they impacted by their environment? The Tara Oceans project attempts to answer these questions at a global scale. In this context, I have used both sequence-based approaches (metagenomics and metatranscriptomics) and microscopy to understand marine microbial ecology on a global scale.

I present an analysis of 243 metagenomes collected by the Tara Oceans expedition. Given in situ measurements of environmental parameters, we determined that, within the photic layer, temperature is the main determinant of marine prokariotic community structure. When analyzing the data at the level of orthologous groups (OGs), we observed that the majority of the gene abundance stems from a small number of core OGs (OGs present in every sample), which surprisingly largely overlaps with the core of the human gut microbiome.

I then describe a new approach for quantitative fluorescence imaging of whole microbial communities: environmental high content fluorescence microscopy (e-HCFM). This approach uses dyes for major structures in most marine eukaryotic cells and high-resolution three-dimensional confocal microscopy to obtain images of all organisms present in a size-filtered sample. I present an analysis of data from 42 Tara stations (5-20 micron size fraction), which resulted in 57,347 imaged organisms. I present an automated image analysis pipeline which classifies each one of these objects into one of 155 different taxo/morphological classes. Additionally, I extract several measures of biological significance, including total biovolume of each cell or its chloroplasts.

Thursday, March 3
1:00 p.m. GHC 6115

Host: Jian Ma