Seeing the wood for the trees: what makes a young and old eQTL architecture?

This pitch is based on the outcomes of our projects funded by NIH, ESF, Wellcome Trust and EU on the complex genetic architecture of aging, disease and disorder and stress in *C. elegans*.

The challenge

The identification and characterization of polymorphic genes associated with longevity and senescence has been a hallmark of aging research. Mapping of gene expression regulators (eQTL) has facilitated the detection of genes or quantitative trait nucleotides (QTn) controlling complex aging phenotypes in worms, flies, mice and humans. This has yielded a wide range of potentially causal genes which in most cases are species specific or, but this is seldomly so, are conserved across species.

The quest to search for "causal" genes has been so pervasive that we overlooked the overall genetic architecture which may harbour a more refined insight into the process of aging. In particular the patterns of distant eQTL can help us to understand pathways and networks underlying longevity and senescence. Importantly, it can teach us what the difference is between a young and old eQTL architecture, and *if old architectures are conserved across species?*

By now we have vast amounts of eQTL data covering many species, environments, treatments and ages spread over diverse data bases. *The challenge is to combine these data and perform a meta-analysis and look for eQTL signatures of aging rather than hunting for single genes.*

The opportunity

Over the past years, we have collected many diverse eQTL data for *C. elegans* and made these accessible for computational analysis via different platforms WormQTL, WormQTL-HD and WormQTL-2. This offers the opportunity i) to perform metanalysis using data sets of other species and aim for a cross-species-environment-age approach. We have the biocomputational expertise and we are looking for interested parties in the human and mouse (and others) field to team up in a concerted effort. In my opinion this is a treasure trove yet to be revealed and explored. Since eQTL data are always snapshots in time, we further need to investigate ii) how the dynamics of eQTL architectures change during lifetime and whether there is an *aging fingerprint* of eQTLs.

The offer

We can take the lead in setting up a collaborative consortium that is dedicated to apply for grants and seek funding. It is about time to unlock all hidden and unexplored data across species and take advantage of our complementary expertise's to make the next step in understanding eQTL architectures of aging.