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A gene regulatory network for ear precursor specification

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During development, the coordinated and sequential action of signals and regulatory factors controls how cells become different from each other and acquire specific fates. This information can be integrated in gene regulatory networks (GRNs) that model these processes over time and consider temporal and spatial changes of gene expression and how these are regulated.

The inner ear is responsible for hearing and balance and its progenitors are specified during early development. This project uses a bioinformatics approach to establish a GRN to model how multipotent progenitors transition through sequential regulatory states until they are committed to the ear lineage. Using RNAseq we have identified new ear-specific genes and established their epistatic relationships by iterating systematic perturbation experiments with network building. This has enriched a preliminary literature-based GRN and predicts new interactions. Using alignment and motif discovery algorithms combined with histone ChIP-seq we have characterized the dynamic enhancer changes as cell acquire ear identity. Focusing on the earliest steps that initiate this process, we have identified two novel enhancers of a known otic specifier, *Foxi3*. These enhancers show spatially and temporally distinct activity *in vivo*, and integrate different transcriptional inputs. Together, we establish the first GRN for otic specification and reveal novel regulatory interactions.

Biography

Maryam Anwar holds an MSc in Bioinformatics and is currently enrolled as a PhD student at King's College London, UK. Her project lies at the interface of developmental biology and bioinformatics with the major aim to uncover gene regulatory networks (GRNs) that control and define the hierarchy of events that commit progenitor cells to an ear lineage.

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