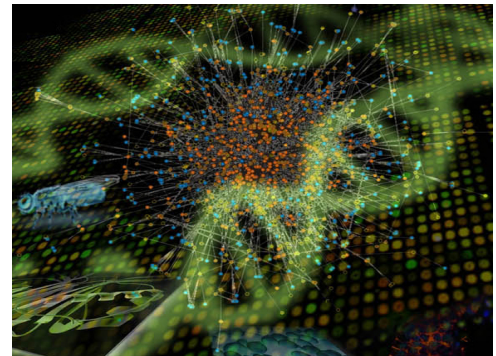


Post-Doctoral position – Bioinformatics

Understanding genome structure and function: Transcription and epigenetics

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Transcriptional networks are a key driving force in development, evolution and disease, yet how they generate robust yet dynamic outcomes remains elusive. The research in the Furlong group focuses on dissecting general mechanisms by which transcription and regulatory networks function during development. For this purpose, we examine chromatin state (using diverse ChIP-Seq experiments), nucleosome positioning (MNase-seq, DNase1), gene expression (RNA-Seq, 5'-CAGE) and 3-dimensional nuclear structure (using 4C and Hi-C).

The Furlong lab is composed of both computational biologists and wet lab biologists, generating a creative environment to promote collaborations and test computational predictions. EMBL is a highly international, multidisciplinary institute where the working language is English.

Recent publications:

1. Ghavi-Helm Y, et al (2014). **Nature**. Jul 2 doi: 10.1038/nature13417. [Epub ahead of print]
2. Rembold M, et al (2014). **Genes & Dev**. Jan 15;28(2):167. Top 5 downloaded G&D article in January
3. Erceg J, et al (2014). **PLoS Genet**. Jan;10(1):e1004060.
4. Spitz F and Furlong EE (2012). **Nature Reviews Genetics**, Sep;13(9):613-26.
5. Junion G*, Spivakov M*, et al (2012). **Cell**, Feb 3;148(3):473-86.
6. Bonn S*, Zinzen RP*, Girardot C*, et al (2012). **Nature Genetics**, Jan 8;44(2):148-56
7. Zinzen RP*, Girardot C*, Gagneur J*, et al. (2009). **Nature**. 2009 Nov 5;462(7269):65-70.

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