

Post transcriptional and post translational modifications as drivers for cellular reorganisation upon stress

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Research area: Machine learning, cell biology, RNA and protein relocalisation

Project outline:

Projects on offer focus upon understanding the relationship between post transcriptional modification of RNA (both mRNA and noncoding RNA) and the relocalisation of RNA upon cellular stress, and how this is orchestrated by the proteome. In particular we are keen to dissect core mechanisms from those that are stress-type specific. This study is multidisciplinary and involves cell biology, cutting edge RNA sequencing and quantitative proteomics/mass spectrometry, combined with computational biology and machine learning modelling approaches.

In particular, the project involves development of methods to sample the post transcriptionally modified transcriptome and the post translationally modified proteome localisation on a cell-wide scale and its dynamic response upon stress. It will also entail the application of computational tools and machine learning approaches to determine patterns within the data that can be used to make predictive models of cell behaviour upon stress.

BBSRC DTP main strategic theme: Understanding the rules of life

BBSRC DTP secondary strategic theme: Transformative technologies