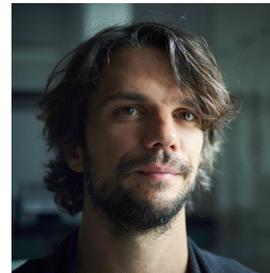


Online - Seminar

“Extensive multiplexing of protein-RNA interactions to comprehensively study post-transcriptional gene expression regulation”

Speaker

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Date and time

Friday, 13th May 2022
10:00 AM

Location

via Zoom
<https://s.gwdg.de/1qUjYq>

Abstract

Characterizing RNA-protein interactions is central to understanding post-transcriptional gene expression regulation. One of the primary methods for studying direct RNA-protein interactions is UV crosslinking and immunoprecipitation (CLIP) coupled with high-throughput sequencing. While powerful, this approach is limited to studying a single RNA-binding protein (RBP) at a time and requires a large number of cells, therefore limiting the study of large classes of RBPs in rare cell populations and disease-relevant patient samples. Here we present SPIDER (Split and Pool Immunoprecipitation for Detection En masse of Rnps), a massively multiplexed method to simultaneously profile the global RNA-binding sites of dozens to hundreds of RBPs in a single experiment, thereby increasing the throughput of current methods by up to two orders of magnitude. SPIDER is based on a split-pool barcoding strategy that maps multiway protein-nucleic acid interactions using high throughput sequencing. Using this approach, we can reliably identify the RNA-binding sites of multiple RBPs simultaneously. Importantly, the use of a single sample to map up to a hundred of RBPs within a single experiment has the potential to eliminate batch effects and dramatically reduces time and resources needed. Moreover, SPIDER allows for mapping of multiple protein-RNA interactions in several samples simultaneously, which provides the means for direct comparison of RNA-protein interactions between different samples with minimal interference of systematic errors. SPIDER thus has the potential to enable rapid, de novo discovery of RNA-protein interactions and to comprehensively define RNA-binding sites across multiple cell types - for known and novel RBPs - at an unprecedented scale.