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## **From Single-Cell Multi-Omics Technologies to Functional Phenomics**

Initially, single-cell omics-technologies originated from solving technical key challenges in the field of DNA and RNA amplification, quantification and sequencing. Meanwhile, single-cell omics technologies are available for the analysis of a cell's transcriptome, genome, epigenome, proteome and metabolome which are used to decipher ground-breaking aspects of cellular behaviour. Recent studies include the combination of different omics-technologies at a single-cell level resulting in single-cell multi-omics approaches.

Although these approaches provide already an invaluable tool for biological research and precision medicine, omics-technologies are currently facing an important challenge as they fail to directly link a single-cell's omics data to orchestrated functional phenotypes of the same single-cell. This functional phenotype is for example a time-lapse behaviour of a single-cell represented e.g. by morphological changes, cell-cell interaction events, cell migration, surface marker expression as well as the secretion of molecules such as cytokines or chemokines. Combining this data of a single-cell's functional phenotype with omics data derived from the same cell will enable an approach that we define as functional phenomics. This approach will enable the direct correlation between a cell's biological function and its underlying omics data thereby providing a tool for in-depth analysis of biological systems.

The talk will focus on current developments of the company evorion biotechnologies GmbH in the field of functional phenomics and will present evorion's mission to transform the way how we gain fundamental insights into biological systems.