Blog Posts

This is a collection of blog posts from our website that you might find of interest.

How to select the best single cell quality control thresholds

The answer no one wants to hear

Using trajectory analysis to study cellular differentiation in single cell RNA-Seq experiments

Using trajectory analysis to determine their fate

Tissue transcriptomics—what's the big deal and why you should do it

Transcriptome-wide studies of gene expression certainly provide invaluable insight into biology on a molecular level, particularly when performed at the single-cell level

Less is more: detecting differential gene expression in single cell RNA-Seq analysis

Which tools to use for single cell analysis

Batch remover for single cell data

Can nuisance batch effects or undesirable numeric or categorical factors be removed?

How to perform single cell RNA sequencing: exploratory analysis

Step one in performing single cell analysis

Bioinformatics approach to spatially resolved transcriptomic

A review of spatial transcriptomic analysis

Pathway Analysis: ANOVA vs. Enrichment Analysis

Comparing gene expression levels across samples

Studying Immunotherapy with Multimodal Omics: Simultaneous Measurement of Gene and Protein Expression

We discuss the advantages of simultaneous gene and protein expression measurement.

How to Integrate ChIP-Seq and RNA-Seq Data

Let's discuss how to make multi-omics integration analysis and integration seamless by bringing all your analysis tools and data together.

Enjoy Responsibly!

Using tasting results of 86 different Scotch malts, let's explore how you can apply statistical tools to non-genomic data.

To Boldly Go…

With the human genome being extensively described and studies of the proteome well under way, is the glycome is the final frontier?

Get to Know Your Cell

Cells are sometimes mysterious and do not readily reveal their true identity. Here's how to identify their biological nature.

How One Researcher Identified a Novel Cancer Prognostic Marker Using 6,260 Small Non-coding RNA Samples

Custom smRNA-Seq pipeline in Partek Flow to deduce expression of ~32,000 human piRNAs per sample.

Aliens Among Us: How I Analysed Non-Model Organism Data in Partek Flow

How well does Partek Flow software analyze non-model organism data, without having to deal with any command-line tools?