

# **DEGASeq: Graph-based identification and visualization of differentially expressed alternative splicing events from RNA-Seq**

Charny Park<sup>1,2</sup>, Byungwook Lee<sup>1</sup>, Wankyu Kim<sup>2</sup>, Sanghyuk Lee<sup>1,2\*</sup>

<sup>1</sup>Korean Bioinformation Center (KOBIC), Korea Research Institute of Bioscience and Biotechnology (KRIBB), 111 Gwahangno, Yuseong-gu, Daejeon 305-806

<sup>2</sup>Ewha Research Center for Systems Biology (ERCSB), Ewha Womans University, 11-1 Daehyun-dong, Seodaemun-gu, Seoul 120-750

There is an immediate need for tools to both analyze and visualize the alternative splicing (AS) events from RNA-Seq data. We present DEGASeq (Differential Expression Graph for Alternative Splicing) software that identifies AS events, performs a statistical test for differential expression, and visualizes differentially expressed AS events in an intuitive and interactive manner. All possible AS events are obtained by analyzing the graph structure of exon connectivity in the user-supplied general transfer format (GTF) file. Each AS event is tested for differential expression using only the junction reads associated to the AS event of interest. A novel visualization scheme was devised to illustrate condition-specific AS events on the exon graph that can be customized interactively by user.