

# Functional Analysis of Transcriptional Response During Cutaneous Wound Healing in db/db Mice

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## ABSTRACT

Wound healing is an extremely intricate and highly dynamic process. High throughput molecular screening technologies such as DNA microarrays hold great potential in enhancing our understanding of complex biological processes, and thus have been extensively exploited in wound healing research. Previous attempts at analyzing transcriptional response during cutaneous wound healing have been limited to conventional statistical methods that are oblivious to the temporal and longitudinal aspects of time-course data. Functional data analysis (FDA) is a branch of statistical methods that treats the entire sequence of time-course data as a single functional entity rather than a set of discrete measurements. By directly utilizing the time structure of data and borrowing information across all time points, FDA can more accurately elucidate transcriptional response during cutaneous wound healing. In this talk, I will present a comprehensive functional approach to analyze time-course microarray data of impaired wound healing in a murine model of diabetes. First, I will demonstrate how functional observations can be constructed from discrete measurements. Second, I will use these functional observations to explore gene expression dynamic from a single-gene perspective. Lastly, I will show how FDA can be utilized to explore the architecture of gene expression and regulatory networks during cutaneous wound healing. Overall, this talk aims to introduce FDA as a novel and extremely powerful statistical analysis framework that may enhance the existing knowledge on transcriptional regulation during pathophysiologic wound healing and lead to identification of novel candidate biomarkers and potential targets with implications in diagnostic and therapeutic applications.