2019 Research Week Abstract Instructions and Template Posters and Presentations

Research Abstract Instructions

Write a concise summary of the key points of your research. This abstract needs to represent your research well as it could be used as part of the judging criteria during the event. Your abstract should contain a strong literature review or introduction to your research topic, hypothesis or research questions, methods, results, and conclusions. You should also include possible implications of your research and future work you see connected with your findings. Your abstract should be a single paragraph double-spaced. Your abstract should be *between 200 and 300 words*. The second paragraph should address how your research is informed by a Christian worldview. In 250-500 words, describe how your Christian worldview has informed your research design and communication of your results.

Abstract Sample

Title - Motif Analysis Using HOMER of Microarray Data of Mice Under a Folic Acid Diet **Program of Study** – Biomedical Sciences

Presentation Type – Choose one of the following: Physical Poster

Subtype – Choose one of the following for poster or oral presentation types: Basic

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Student name(s) and email(s) -

Abstract example: With the rise of incidence of Alzheimer's disease, various studies have been conducted to determine the genetic factors related to this disease progression. Changes in DNA methylation associated with low levels of folic acid, an oxidized form of Vitamin B9, have been shown to result in cognitive decline. A previous study was conducted to show how DNA methylation and gene expression are changed with the addition of dietary folate in the form of folic acid. During this study, hippocampus tissue from mice was tested for gene expression after given a folic acid diet over the duration of 4 months. Microarray analysis of the RNA from the brain tissue was conducted, providing an outlet into the variation of gene expression. It was hypothesized that changes in dietary folate will modify gene expression via DNA methylation. A command-line program called HOMER, which stands for Hypergeometric Optimization of Motif EnRichment, was used to analyze the RNA sequences of the folate treated mouse

hippocampus after four months of treatment through the use of a motif discovery algorithm. Several differentially expressed genes were identified using this motif analysis. This analysis will be used to identify epigenetically regulated genes of interest related to changes in folate acid metabolism in mice.