1. **What is the medically relevant insight from the article?**

The medically relevant insight from the article "Reconstruction of Insulin Signal Flow from Phosphoproteome and Metabolome Data" is the identification of the signal flow of insulin and its role in regulating cellular homeostasis. By analyzing time-course phosphoproteome and metabolome data, the study reveals the global control of metabolic homeostasis by insulin. This insight provides a better understanding of how insulin influences various metabolic processes and could potentially lead to the development of more effective treatments for metabolic disorders such as diabetes.

1. **Which genomics technology/ technologies were used?**

The genomics technologies used in the study include phosphoproteomics and metabolomics. Phosphoproteomics involves the detection and quantification of phosphorylated proteins, which play a crucial role in cellular signaling. By analyzing changes in protein phosphorylation in response to insulin, the researchers were able to track the signal flow of insulin. Metabolomics, on the other hand, focuses on the quantitative measurement of small metabolites within a biological system. In this study, metabolomics was used to capture changes in metabolite levels associated with insulin signaling.

1. **List and explain at least three questions/ hypotheses you can think of that extend the analysis presented in the paper**

Three questions/hypotheses that can extend the analysis presented in the paper are: a) What are the downstream signaling pathways activated by insulin that contribute to the regulation of metabolic homeostasis? b) How does the signal flow of insulin differ between healthy individuals and those with insulin resistance or diabetes? c) Can the reconstruction method used in this study be applied to other hormone signaling pathways to gain insights into their regulatory mechanisms?

1. **Devise a computational analysis strategy for (some of) the listed in previous question**

For the computational analysis strategy, several steps can be devised: a) Pre-processing of phosphoproteome and metabolome data: This includes filtering, normalization, and quality control of the raw data to ensure accuracy and reliability. b) Integration of phosphoproteome and metabolome data: The datasets can be merged to establish correlations between changes in protein phosphorylation and metabolite levels, enabling the reconstruction of the signal flow of insulin. c) Network analysis: Constructing a network model to visualize the signal flow and identify key nodes or pathways involved in insulin signaling and metabolic homeostasis. d) Statistical analysis: Performing statistical tests to determine the significance of changes in protein phosphorylation and metabolite levels in response to insulin stimulation. e) Validation and model refinement: Comparing the computational predictions with experimental results and iteratively refining the model to improve accuracy and predictive power.