Presenter's Name: **Yaseen Arab.**

Presentation Field/Area(s): **Bioinformatics.**

University/College Name: **Baylor University.**

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Presentation Title: **GeneRegulate Tool.**

**Background:**

Gene regulatory elements, such as enhancers and silencers, play a significant role in regulating the degree of gene expression. Identifying these regulatory elements can provide a great understanding of how genes are expressed differently across different tissues and offer possible therapeutic targets for precision medicine.

Understanding the regulatory landscape that controls gene expression is important in advancing precision medicine. GeneRegulate solves this need by connecting enhancer and silencer data with gene expression, to gain a better understanding of the key regulatory components that are associated with tissue-specific expression. Our tool allows researchers to analyze complex genomic data across 6 human tissues.

**Methods:**

GeneRegulate offers two options: users can upload their own gene lists, enhancers, and silencers or use our preloaded datasets. We process the data in Python, connecting regulatory elements with their associated genes using an existing set of chromatin loop annotations.

**Results:**

GeneRegulate users can easily analyze regulatory landscapes for individual genes across multiple tissues, displaying the result with a variety of data visualization options, enabling researchers to easily identify tissue-specific expression patterns and regulatory trends.

**Conclusions:**

GeneRegulate proves to be a powerful tool for studying gene regulation and tissue-specific expression. Analyzing these data can increase our understanding of regulatory mechanisms, with potential implications for precision medicine and drug development.As GeneRegulate evolves, our goal is to add more genome data and analyze more regulatory elements. By doing this, we aim to uncover new findings in gene regulation and contribute to the advancement of precision medicine.