



Machine Learning Based Approach for gene expression analysis to predict Intrauterine Growth Restriction (IUGR) and Pre-eclampsia(PE)

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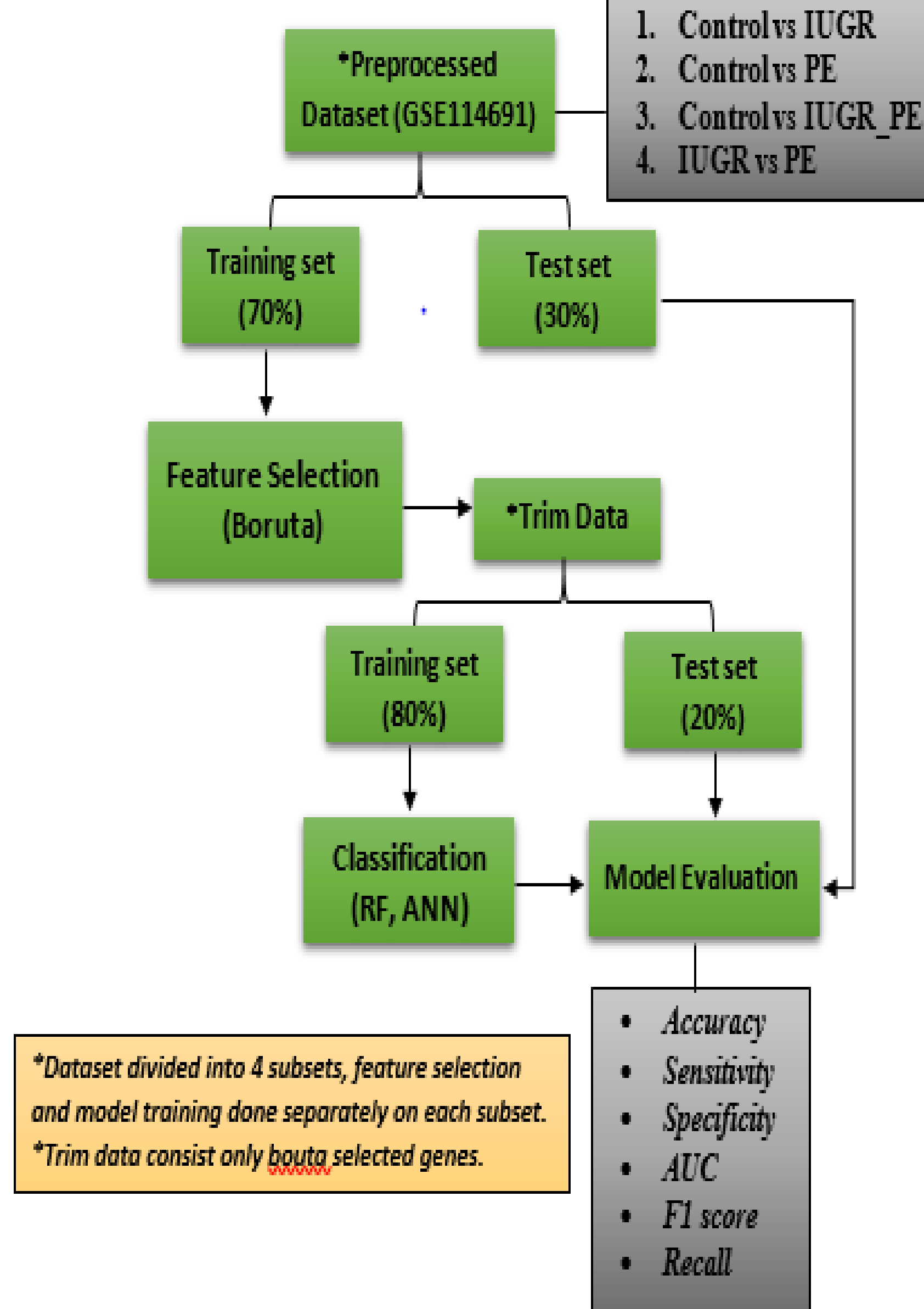
BACKGROUND

Intrauterine Growth Restriction (IUGR) is the leading distresses of global health and chief for maternal and child health. Hypertensive disorders such as pre-eclampsia (PE) of pregnancy are associated with placental blood flow and may lead to IUGR. Up to 24% pregnancies affected with IUGR globally in each year. Fetal growth restriction (FGR) likely to be associated with the onset of several metabolic disorders and non-communicable diseases in adulthood. Poor Maternal nutrition and low socio-economic status are the primary cause of IUGR/FGR in developing nations. Thus the early diagnosis of FGR is crucial for preventing adverse pregnancy outcomes. Since, the machine learning algorithms offers effective ways to excerpt useful information from complex databases and being used to identify risk factors and provide early prediction of PE and IUGR.

OBJECTIVE

We aim to determine utmost genes that involved in pathogenesis of IUGR and PE during gestation by using state of art machine learning(ML) methods.

Workflow

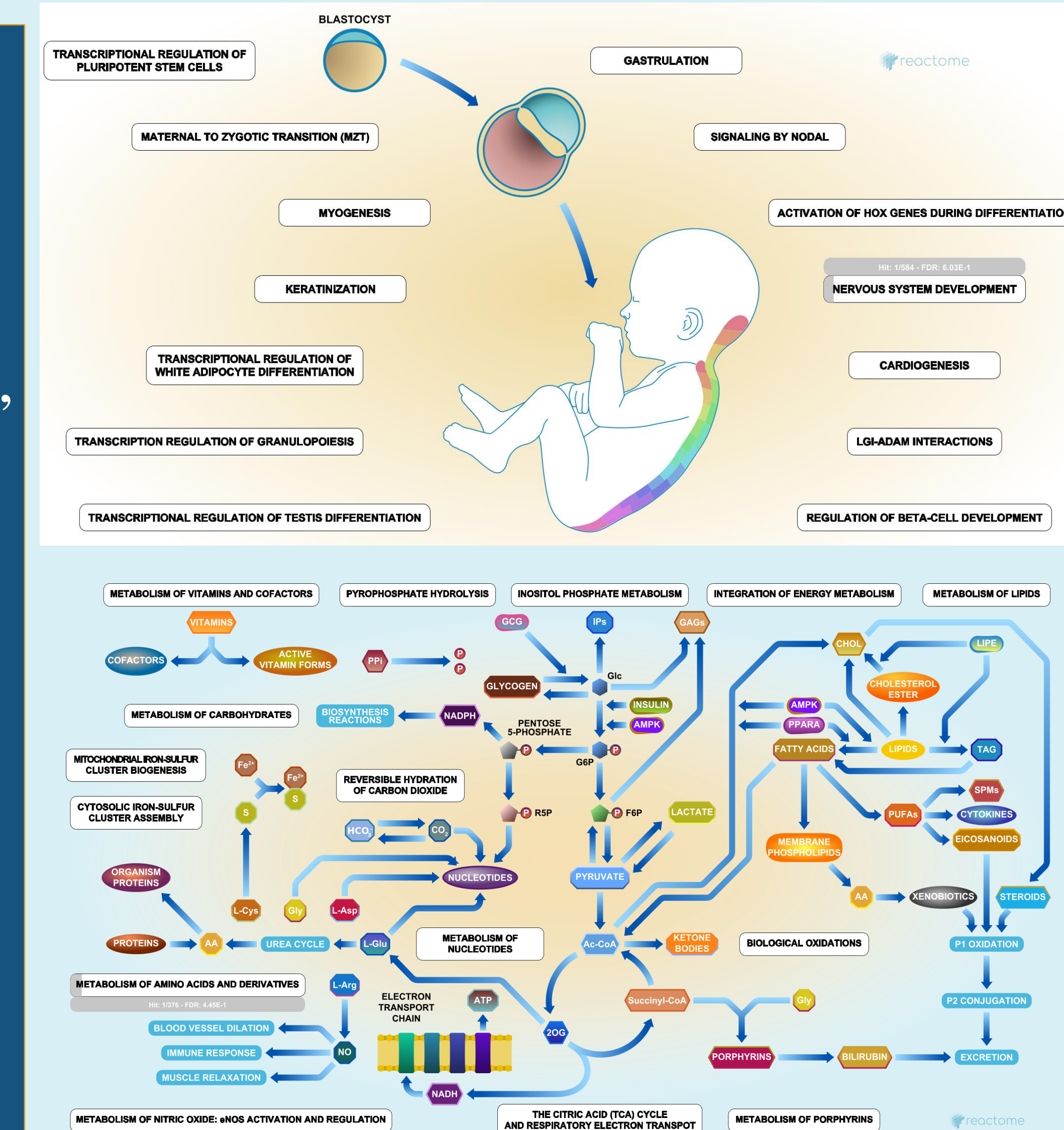


METHODS

- RNA-seq datasets of normal, IUGR and PE pregnancies were obtained from NCBI repository
- Feature selection done with **boruta**
- Random Forest(RF)** and **Artificial Neural Networks(ANN)** algorithms was applied for model training and classification
- Reactome** pathways were also analyzed
- Analysis done by using R programming language

RESULTS

- Boruta selected **TGFB1, CLUH, BCL6, MND4, BIN1, CNM2, XPO6** as key biomarkers
- RF obtained highest AUC = 1.00 with dataset 1, dataset 2 & dataset 3, whereas ANN attained highest AUC = 1.00 with dataset 2 and dataset 3 and for dataset 1 AUC could reach 0.96 with external test set
- We identified 130 up-regulated 306 down regulated. The most significantly upregulated pathways were Tryptophan catabolism, FOXO-mediated transcription of cell death genes, and the most significant downregulated pathways involved metabolism, Developmental Biology, Neuronal System and Immune System pathways



CONCLUSION

The current study demonstrates ML approach possess great potential to classify groups based on their gene expressions. The landmark of genes alongside the biomarker flags of genome which is essential for early diagnosis & treatment of fetal growth restriction and hypertensive pregnancies.

References:

- Murki, Srinivas, and Deepak Sharma. "Intrauterine growth retardation-a review article." *J Neonatal Biol* 3.3 (2014): 1-11.
- Awamleh, Zain, Gregory B. Gloor, and Victor KM Han. "Placental microRNAs in pregnancies with early onset intrauterine growth restriction and preeclampsia: impact on gene expression and pathophysiology." *BMC Medical Genomics* 12 (2019): 1-10

