Using machine learning to determine the association of maternal characteristics & serum biomarkers with newborn outcomes

Presenter: Javairia Khalid
2024 IDM Annual Symposium

Dr. Fyezah Jehan, Dr. Imran Nisar,
Dr. Waqasuddin Khan, Samiah Kanwar,
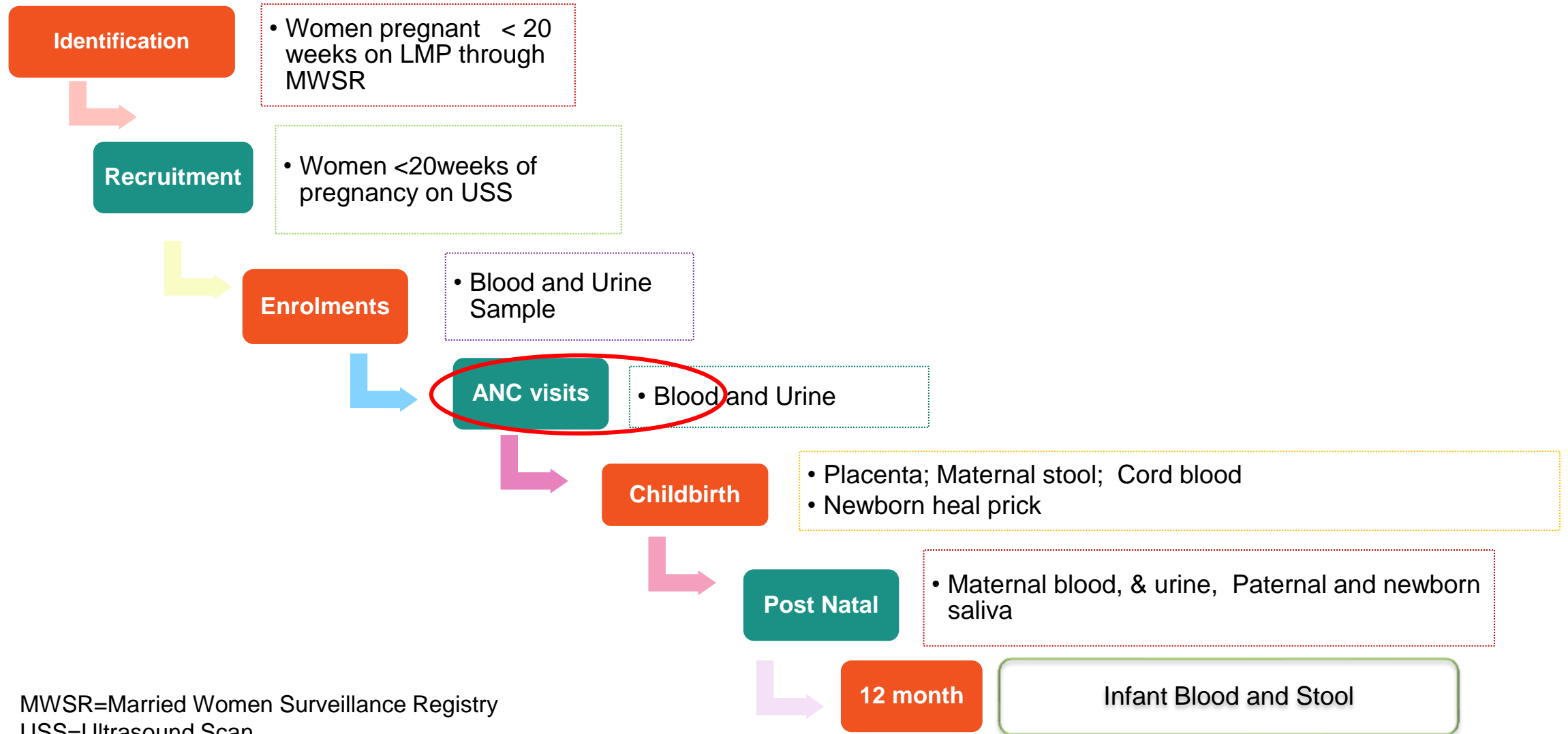& Farrukh Qazi.

Background

- Pro-inflammatory biomarkers have a role in the molecular pathways that lead to the onset of labour

- Differential expression linked to adverse outcomes such as hypertension, preeclampsia and preterm birth which may result in SGA babies with stunting and/or wasting

- Growth restriction begins in utero and has been correlated with cognitive decline and vaccine immunogenicity in later years

AMANHI Bio-repository study

Identification
- Women pregnant < 20 weeks on LMP through MWSR

Recruitment
- Women <20weeks of pregnancy on USS

Enrolments
- Blood and Urine Sample

ANC visits
- Blood and Urine

Childbirth
- Placenta; Maternal stool; Cord blood
- Newborn heal prick

Post Natal
- Maternal blood, & urine, Paternal and newborn saliva

12 month
Infant Blood and Stool

MWSR=Married Women Surveillance Registry
USS=Ultrasound Scan

Objectives

i. Using retrospective data to generate predictive models for newborn outcomes at birth through various machine learning methods

ii. To identify maternal serum biomarkers that are strong predictors of growth outcomes for newborns
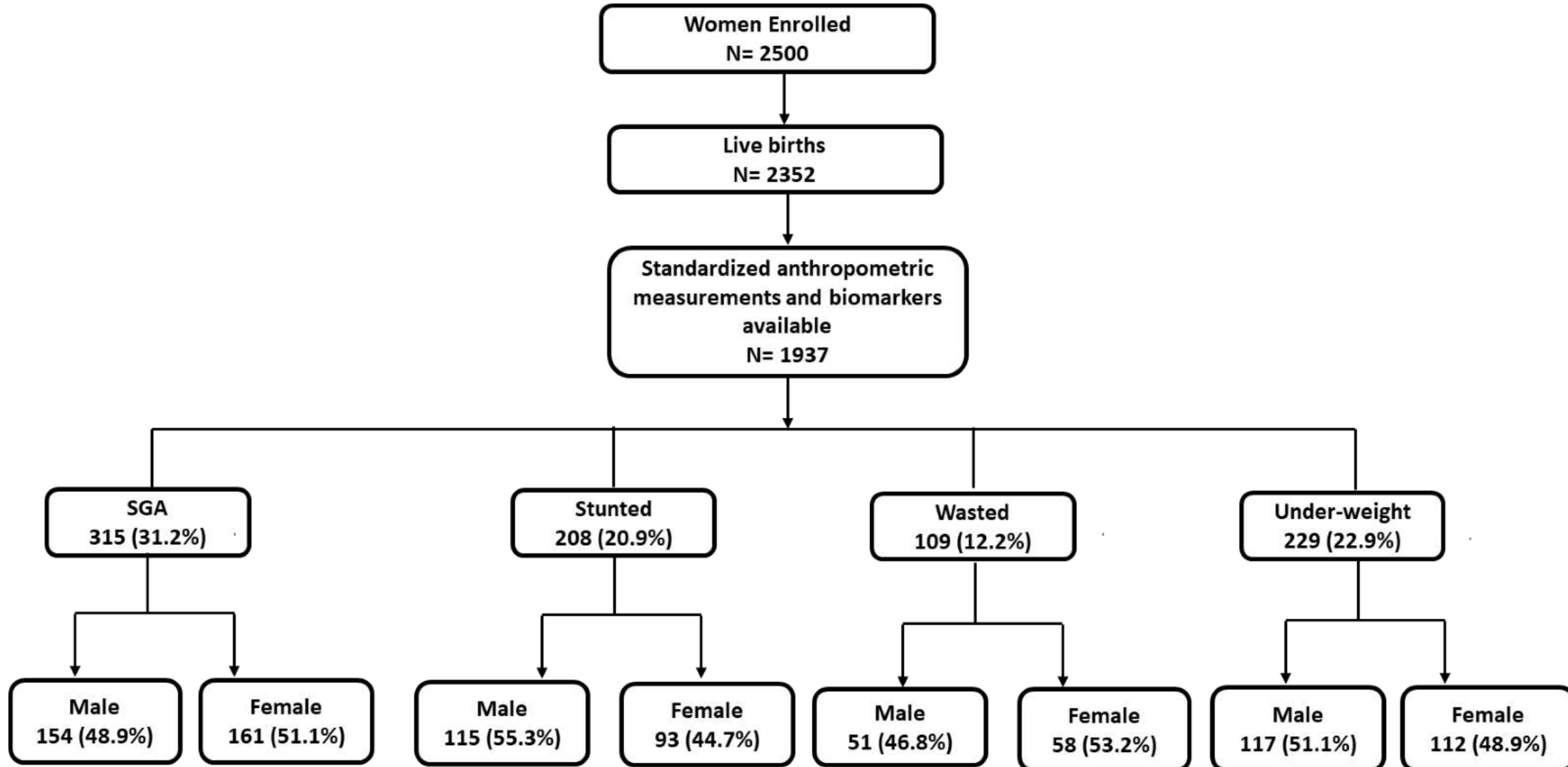
Outcomes

I. Anthropometric measurements at birth

    I. Stunting (HAZ <-2)

    II. Underweight (WAZ < -2)

    III. Wasting (WHZ < -2)

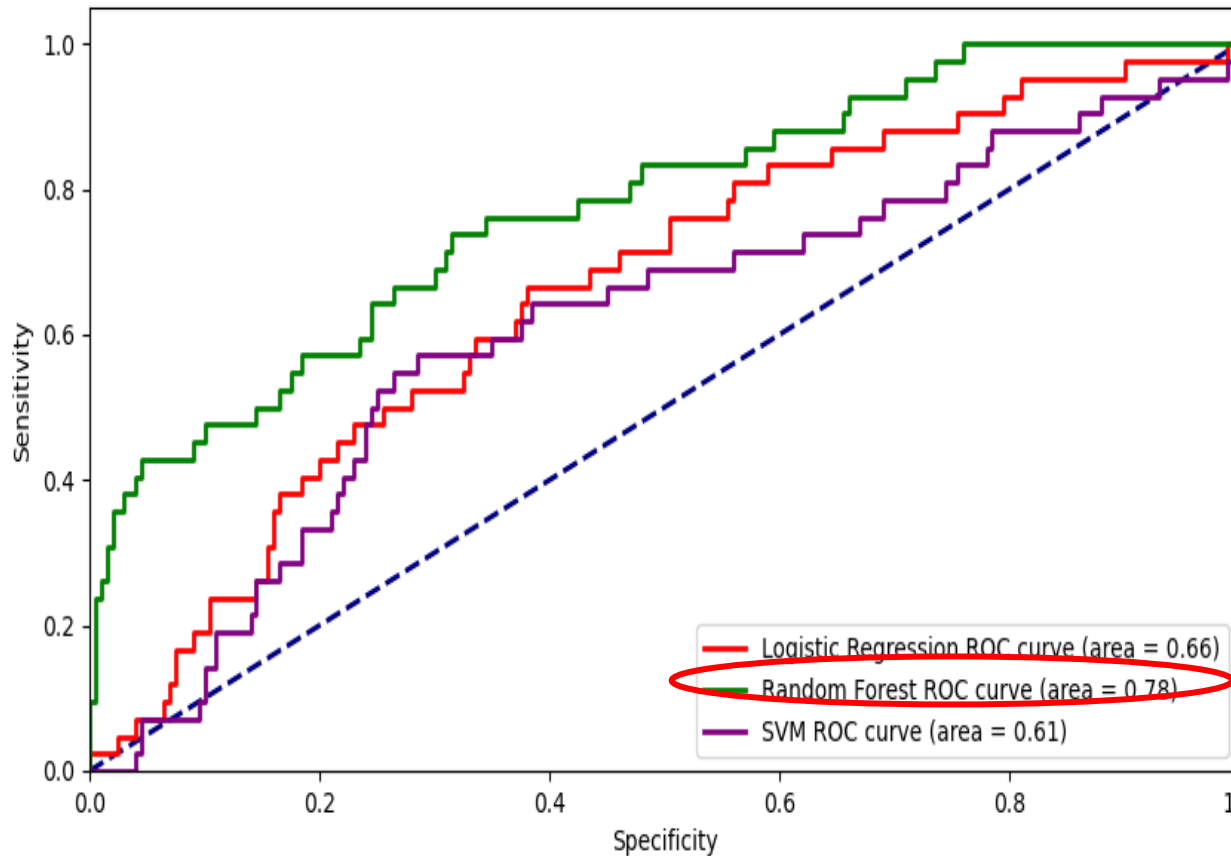II. SGA (Birth weight < 10th centile for gestational age)

Methods

i. 3 models were applied:

    i. Logistics Regression

    ii. Random Forest

    iii. Support-vector Machine

ii. Each model integrated maternal:

    i. Serum biomarkers measured at 24-28 weeks i.e. PLGF, SFLP,VEGF,SGOT, Calcium, Ferritin, TSH, Albumin, CRP, Blood Urea, Creatinine, PAPP-A & Hb and;

    ii. Phenotypic variables (e.g., socioeconomic status, parity, BMI, gravidity, MUAC, height, age etc.)

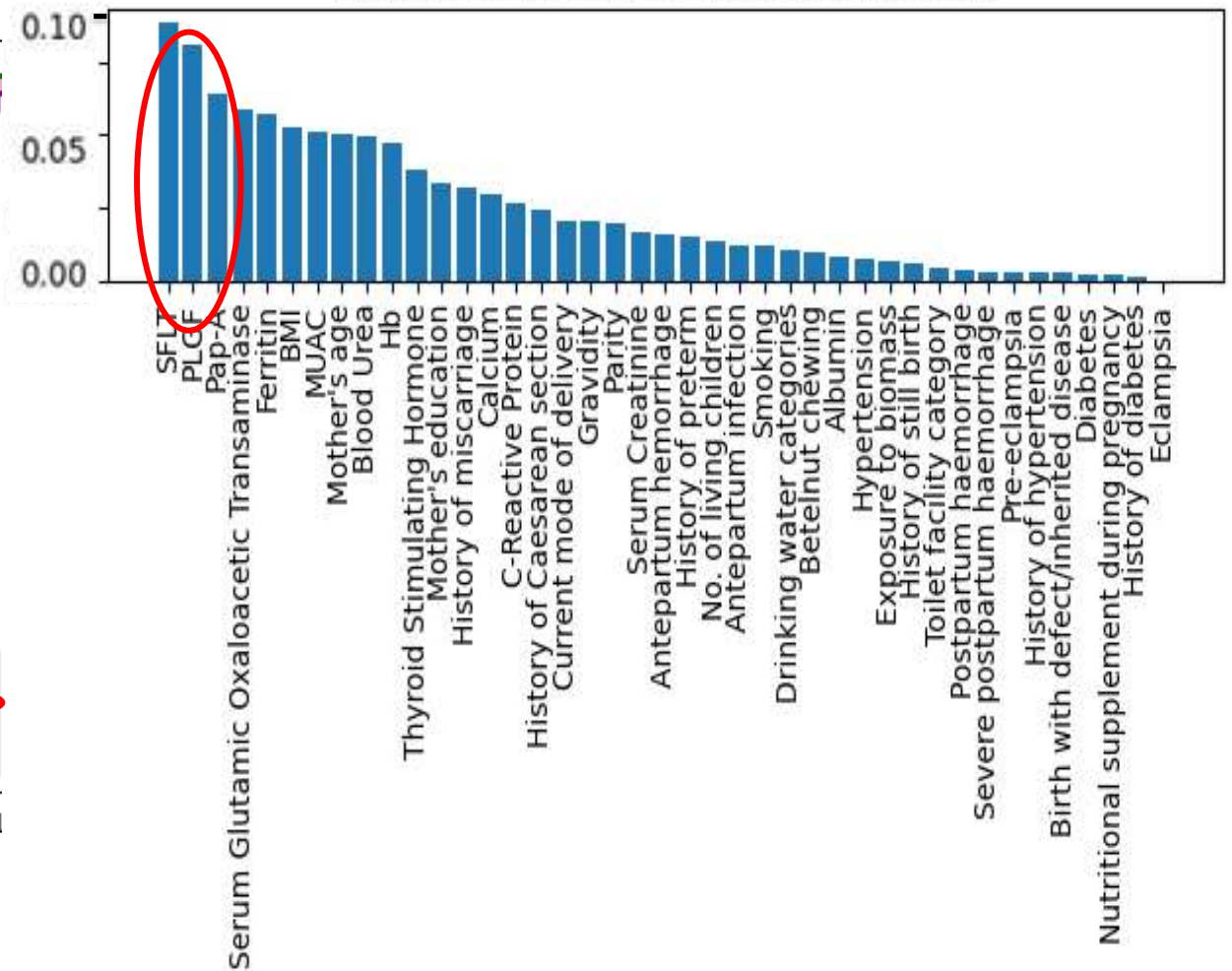iii. For all models, a 70–30 test-train split was used

Result – Study population

Women Enrolled
N= 2500

Live births
N= 2352

Standardized anthropometric measurements and biomarkers available
N= 1937

| SGA 315 (31.2%) | Stunted 208 (20.9%) | Wasted 109 (12.2%) | Under-weight 229 (22.9%) |

Male 154 (48.9%) | Female 161 (51.1%)

Male 115 (55.3%) | Female 93 (44.7%)

Male 51 (46.8%) | Female 58 (53.2%)

Male 117 (51.1%) | Female 112 (48.9%)

Models for Stunting

Models for Wasting

Models for Underweight

Underweight ROC after hyperparameter tuning

- Logistic Regression ROC curve (area = 0.60)
- Random Forest ROC curve (area = 0.75)
- SVM ROC curve (area = 0.64)
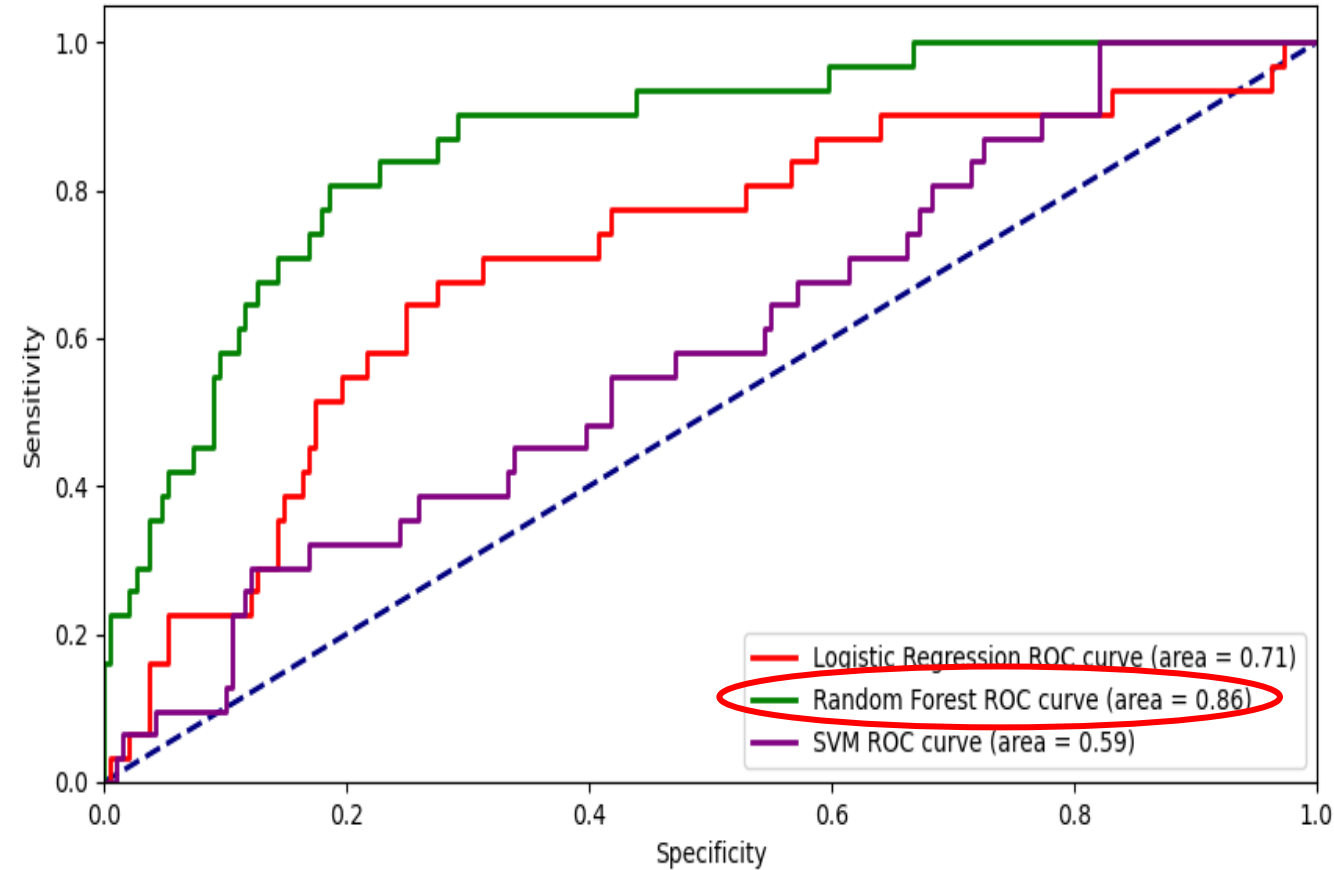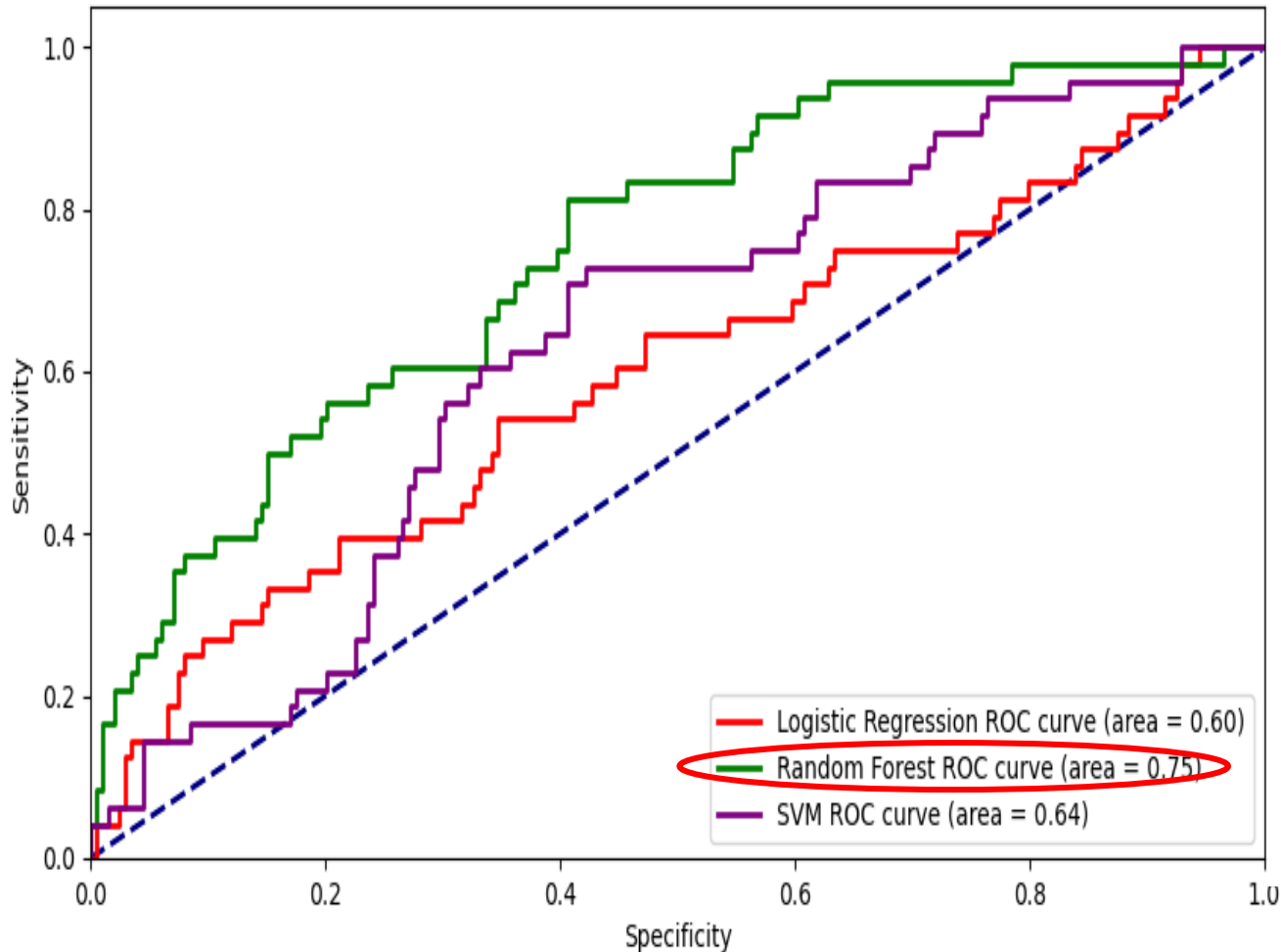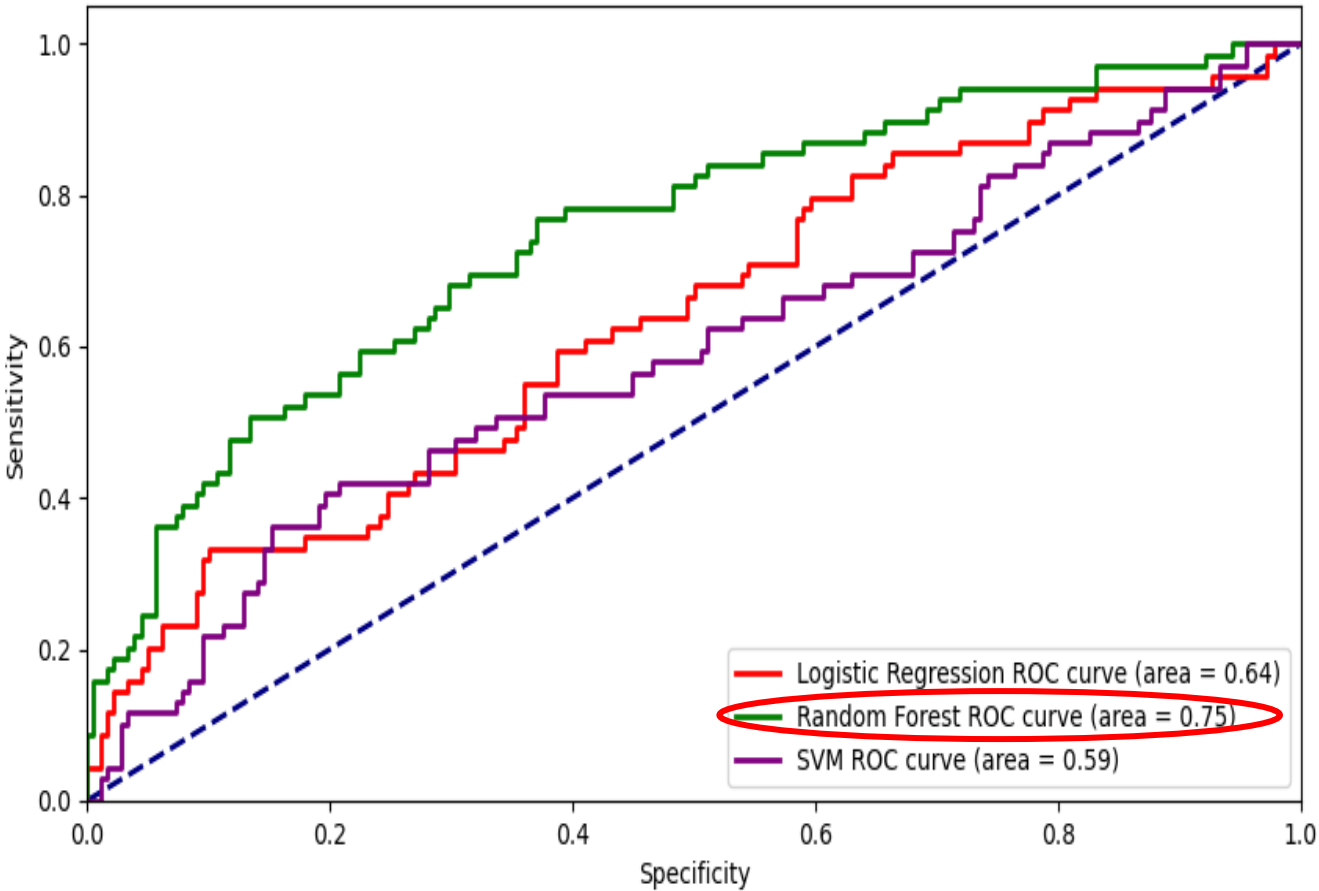
Features Importance in Underweight at Birth

Models for SGA
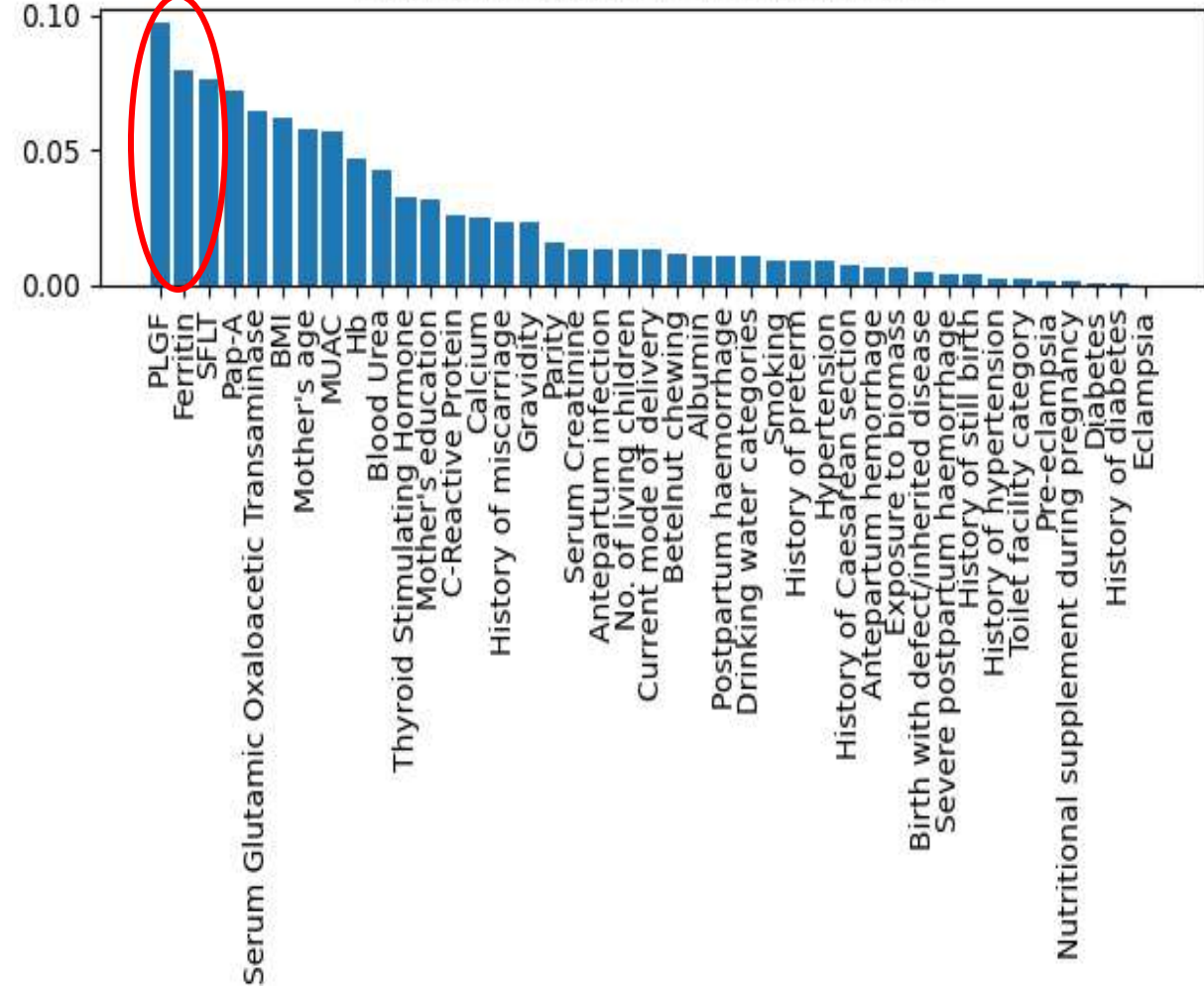
Conclusion

- Biomarkers such as PLGF, sFLT and PAPP-A are strong predictors of malnourishment in children at birth.

- Specific biomarkers that need to be factored in during planning of future trials targeted towards improvement of growth.

- Random Forest models can accurately predict malnourishment which can be further calibrated before being used as a screening tool in pregnant women.

- Encourage the use of pre-existing data, innovative tools and technologies to accelerate progress in maternal and newborn health towards the prevention and diagnosis of adverse outcomes.

Thank you!