**Study design, size, duration:** Retrospective cohort analysis from 2013 to 2020 of 193 cycles with 386 embryos used in double ETs on day 5 at POMA fertility clinic with positive live birth outcome. ML model, xgboost, was trained to predict multiple live birth (N=54) versus single live birth (N=139). Detailed embryology data from day 1 to day 5 were used as input.

**Participants/materials, setting, methods:** Input of the machine learning model included patient age and 18 morphological parameters collected on days I, 2, 3 and 5 (symmetry, number of cells, blastocyst status, fragmentation, ICM and troph grades) from the two transferred embryos. An xgboost algorithm was trained on 80% of the data (n= 154) and tested on 20% of blind data (n=39). **Main results and the role of chance:** Xgboost machine learning algorithm predicted multiple live birth on the blind dataset with an accuracy of 72%, with an AUC of 0.60, showing better results than random. PPV (true prediction of multiple births) was 64% and NPV (true prediction of single birth) was 75%.

The following parameters ranked high in the predictive power of the machine learning (in order of predictive power): blastocyst status on day 5 of both embryos, symmetry on day 3, number of cells on day 2, scores on day 2 and 3. Limitations, reasons for caution: The dataset was derived from a single clinic with manual annotations and may not be transferable to other clinics. The risk of bias is important as the model was trained only àon embryos that were transferred and led to at least one birth

Wider implications of the findings: A tool to help identify which patients are at increased risk of MP with MET would be clinically useful to help patients and clinical team make the best personalised decision for a specific embryo, finding the balance between maximising success rate whilst minimising multiple pregnancy rate and its associated risks.

Trial registration number: not applicable

P-378 Using a machine learning tool (72% accuracy with 64% PPV) to predict multiple live birth when transferring multiple embryos, based on embryo specific data

<u>C.A. Pena<sup>1</sup></u>, J. Chambost<sup>1</sup>, C. Hickman<sup>2</sup>, C. Jacques<sup>1</sup>, K. Wiemer<sup>3</sup>, K. Kelley<sup>4</sup>

<sup>1</sup>Apricity, AI team, Paris, France ; <sup>2</sup>Apricity, AI team, London, United Kingdom ; <sup>3</sup>POMA Fertility, Laboratory, Kirkland, U.S.A. ; <sup>4</sup>POMA Fertility, Data Analytics, Kirkland, U.S.A.

**Study question:** Can Machine Learning predict multiple pregnancy based on data specific to the embryos and the patient?

**Summary answer:** Embryo data are useful in determining which embryos are likely to lead to multiple pregnancy. Patient age has low predictive value compared to embryo data.

What is known already: Our previous assessment of the HFEA data demonstrated that single embryo transfer (SET) in the UK occurred in a minority (45%) of fresh cycles, with a marginal increase in live birth rate (LBR) in some patient cohorts in favor of multiple embryo transfer (MET). Current policies on determining number of embryos for transfer tend to be generic and do not account for detailed embryology data. Generic policies may compromise LBR for some patients that would benefit from MET. Artificial Intelligence has the potential to assist in this decision process.