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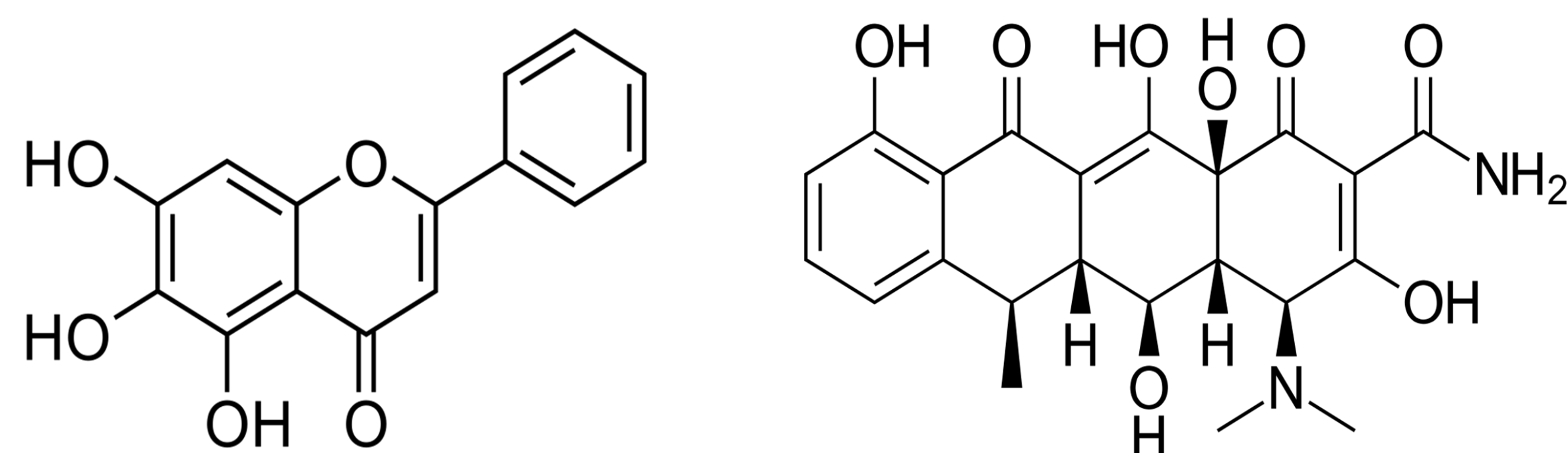
## BACKGROUND

*Caenorhabditis elegans* are microscopic roundworms commonly used to study mechanisms of ageing and extending lifespan interventions. However, the lifespan of *C. elegans* (below) are subject to age related disease and life shortening pharyngeal infection, affecting roughly 40% of the population when under standard culture conditions with *E. coli*.



As a result, there is a possibility a large percentage of similar drug outputs of computational approaches like this are flawed due to effects on bacterial pathogenicity.

Previous studies that have predicted lifespan extension in *C. elegans* do not consider the effect of bacterial pathogenicity on the lifespan of the roundworm. The DrugAge database below lists both Baicalein (left) and Doxycycline (right) as active lifespan extending compounds but ignore Doxycycline's antibacterial activity against *E. coli* which would fight against the pharyngeal infection causing premature death.

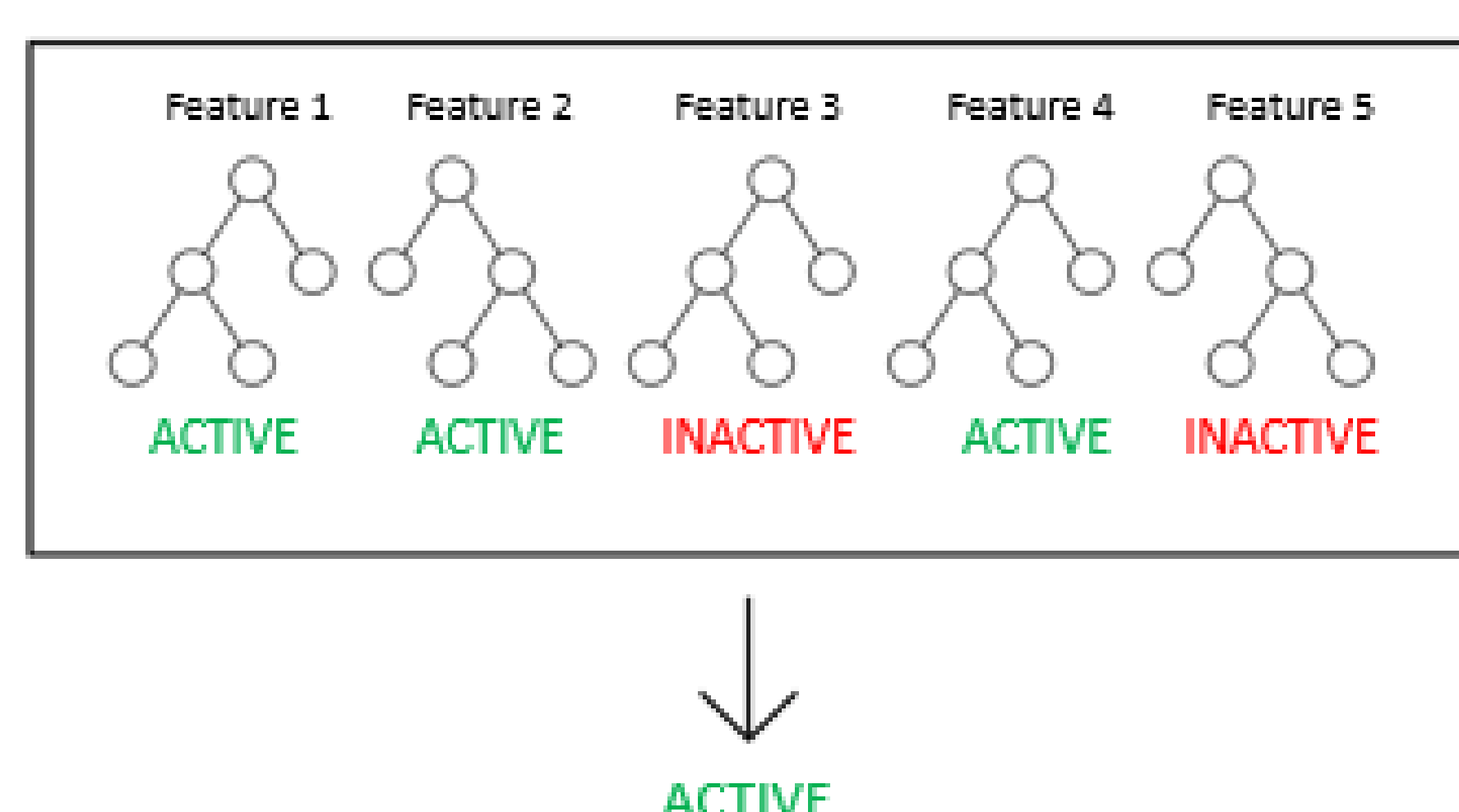


### PURPOSE OF THE STUDY:

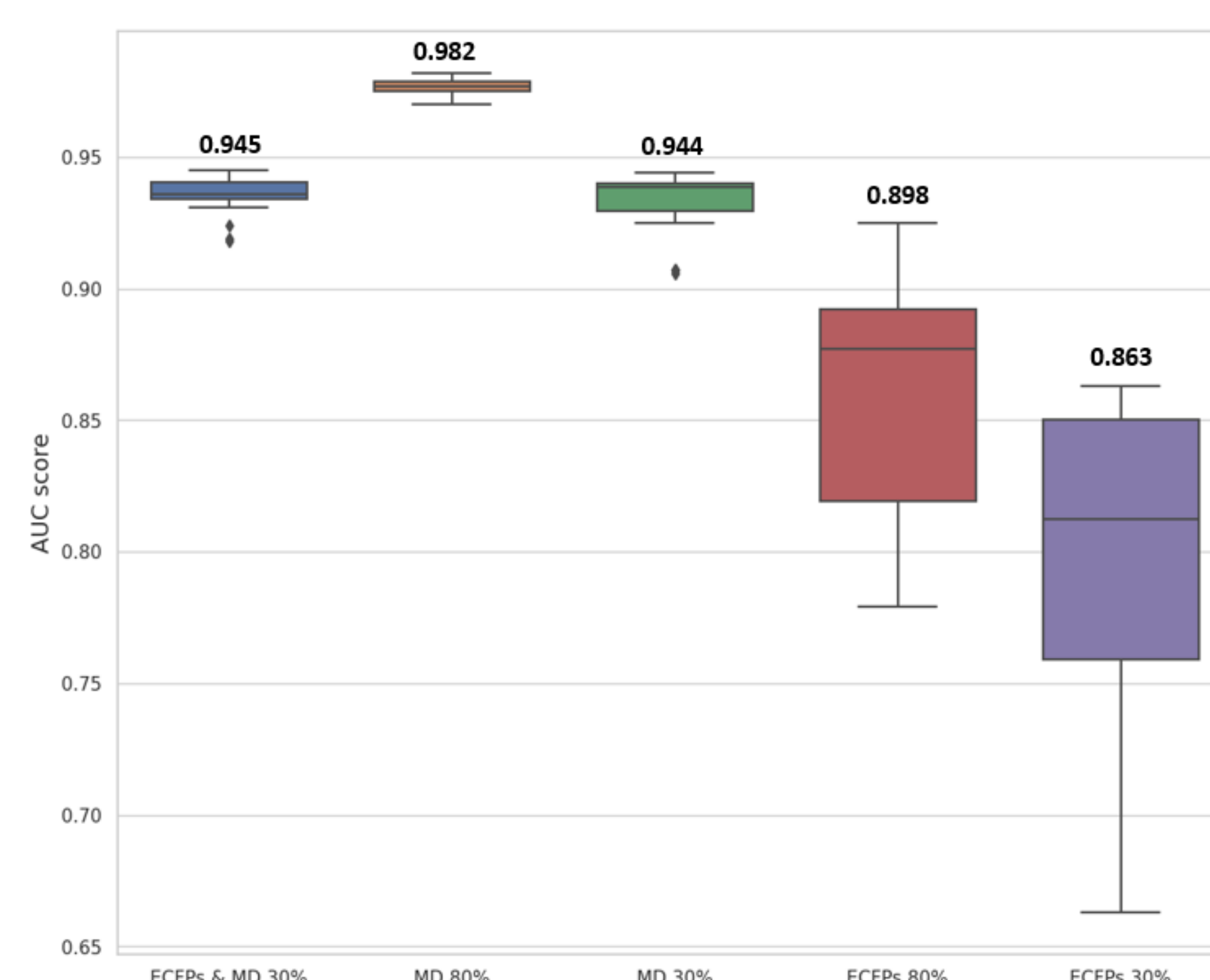
The possibility that drug properties associated with suppression of infection interferes with the detection of potential 'anti-ageing' interventions due to lifespan extension via infection suppression.

## METHOD

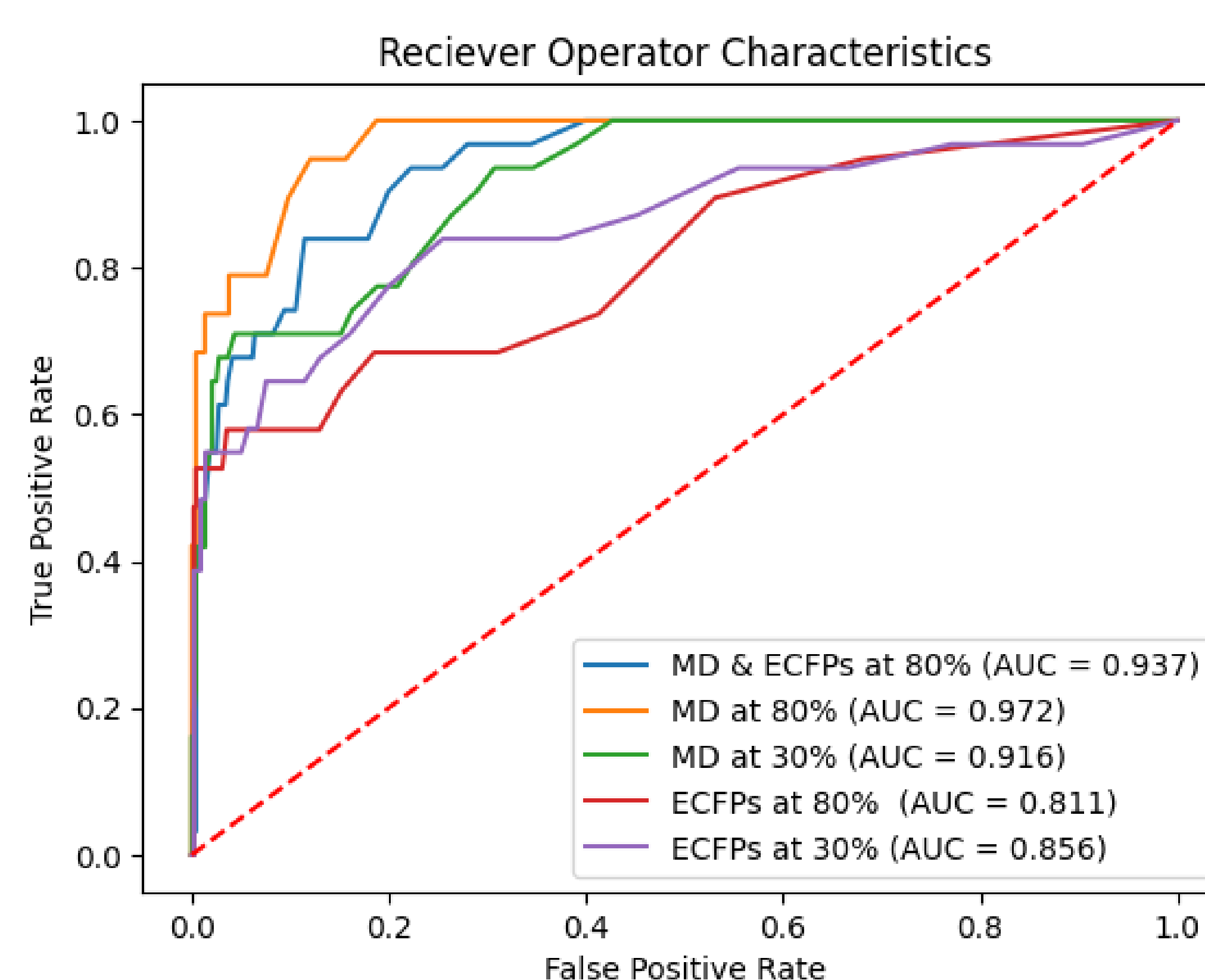
Five random forest classifier models were built in python using the features: molecular descriptors, 1024-bit extended connectivity fingerprints (ECFPs) and a mixture of both at two different activity thresholds. The model was trained on a dataset of 2335 molecules.



## RESULTS



AUC scores for the 10-fold cross validation in the training set.



The ROC curves comparing the performances of the 5 models in the test set.

## CONCLUSION & FUTURE RESEARCH

Of the 5 developed, the best performing model was built with molecular descriptors as the features at an activity threshold of 80%. After consideration, it was decided that the model would be more versatile for deployment using a threshold of 30%, so some accuracy was sacrificed for versatility. The final model selected was built using a mixture of 1024-bit ECFPs and molecular descriptors and had a ROC AUC score of **0.937**. **27 molecules of the 304** active lifespan extending molecules were highlighted as antibiologically active, and subsequently removed from consideration.

With antibiotic resistance a continuing worry, there is scope for this model to be developed to predict antibiotics against more than just *E. coli*. This could lead to a novel technique for scanning large existing drug databases, potentially leading to drug repurposing of existing molecules with antibiotic properties.