

## Epigenetic classifier for twin zygosity

<b>Title</b>	Epigenetic classifier for twin zygosity
<b>Description</b>	Epigenetic modifications alter DNA expression without changing the DNA sequence. While monozygotic twins have the same DNA sequence, they could have different epigenetic modifications. Twins have been suggested to have unique epigenetic features. This project hypothesizes that the zygosity of twins (monozygotic, dizygotic) can be accurately predicted by epigenetic markers, and aims to develop an epigenetic classifier for twin zygosity using high-dimensional DNA methylation data measured by the microarray chip and machine-learning techniques.
<b>Expected outcomes for the project upon completion</b>	A research report easily modified to an article for a scientific journal
<b>Preparation required by students prior to initial meeting (if any)</b>	Become familiar with the structure of DNA methylation data measured by HumanMethylation450 or HumanMethylationEPIC array. Read the paper <a href="https://www.nature.com/articles/s41467-021-25583-7">https://www.nature.com/articles/s41467-021-25583-7</a>
<b>Additional Notes by Host Organisation</b>	Dr Shuai Li is not available for the next couple of weeks. Dr Sue Malta will act as the contact person in the first instance.  Please address correspondence to both Sue and Shuai.  Dr Shuai Li Email: <a href="mailto:shuai.li@unimelb.edu.au">shuai.li@unimelb.edu.au</a>
<b>Course Name</b>	Master of Data Science
<b>What datasets are available and in what format will they be provided?</b>	Several twin datasets of DNA methylation will be available. They will be provided as .txt or .rds file
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<b>Host Organisation Contact Position</b>	Senior Manager and Researcher
<b>Host Organisation Name</b>	Twins Research Centre of Epidemiology and Biostatistics UoM
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<b>Supervisors</b>	Michael Kirley, Jiadong Mao