

MEDC0076 Miscellaneous

October 20: HIV Drug Design

HIV genetics (RNA)

↓reverse transcription

DNA

↓integration

Host reproduction, transcription, expression

↓protein modification

HIV capsids

HIV Drug Targets: Reverse Transcriptase

RT has both polymerase and nuclease activities. Drugs targeting RT can either be *nucleoside analogue reverse-transcriptase inhibitors* (NRTIs) or *non-nucleoside reverse-transcriptase inhibitors* (NNRTIs).

HIV Drug Targets: Integrase

HIV integrase elicits a strand transfer reaction to incorporate the reverse transcribed DNA into the host DNA.

HIV Drug Targets: Protease

The expressed protein is a long polyprotein initially, which must be cleaved by protease to generate proteins with biological activities.

HIV Drug Targets: Capsid

October 21: Omics

October 22: Biological Statistics

Descriptive Statistics

Distribution

The frequency of different values of a variable.

Central tendency: Mode, Mean, and Median

An estimation of the value at the centre of the distribution.

Different methods are used to describe catagorial and continuous data:

Mode→catagorial data

Mode, Mean, Median→continuous data, depending on the shape of the distribution.

Dispersion: Range, Interquartile range, and Standard deviation

A measure of the spread of all the values around the central tendency

Interquartile range→skewed distributions (continuous)

Standard deviation→normal distributions (continuous)

Standard deviation (σ):

σ measures the spead of values about their mean.

$\sigma \downarrow \rightarrow$ higher consistency

Skewness

$$Skewness \begin{cases} < 0 : & Mode > Median > Mean \\ = 0 : & Normal \\ > 0 : & Mode < Median < Mean \end{cases}$$

Inferential Statistics

Estimate the population features using sample features.

Null hypothesis (H_0 , no differences between negative and sample groups)

Alternative hypothesis (H_1)

α : significance value, set before experiment. A larger α value means a lower threshold to reject H_0

$p \geq \alpha \rightarrow \text{accept } H_0$

$p < \alpha \rightarrow \text{reject } H_0 \text{ in favour of } H_1$

$\begin{cases} \text{Type1}/\alpha & \text{error : } & \text{Wrongly reject } H_0, \text{low} & \text{specificity} \\ \text{Type2}/\beta & \text{error : } & \text{Wrongly accept } H_0, \text{low} & \text{sensitivity} \end{cases}$

Supposing that there is a large p-value