

# Translating Animal Transcriptomic Data to Inform Human Infection and Immunity Studies

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## Abstract

Studies looking to understand human health and disease are often individually limited in scope due to ethical and practical considerations in designing experiments. Ethically, the number of animals or patients studied are minimalised. However, studies using high content biological data such as microarray data potentially contain a wealth of untapped information beyond their original aims. This includes a plethora of historical data of infectious states that could be utilised and exploited greater to increase our understanding of the immune system, and develop faster and more precise diagnostics.

Animal models are powerful tools in biomedicine; beyond the obvious greater experimental versatility they provide more experimental consistency than humans due to living in more controlled environments and being bred to provide a flatter genetic background. In the context of infection and immunity, human studies are often limited to pathogens which are commonly seen in the healthcare industry; animal studies are not so limited and can include more controlled and invasive measurements.

Although animals share biological similarities with us, there are significant and complex differences which lead to animal studies having a less than perfect predictive capability for humans. However, *in vitro* studies using human tissues still mostly fall far shorter from the mark than animal studies despite being biologically human, largely as they simply do not include the complexity of a whole organism and can be influenced by very artificial culture methods.

Modern biomedical science extensively takes advantage of both systems, but ultimately it is once human studies are performed that a gold standard can be set (where ethical and possible). Thus the problem lies in how we move from animal models to human models when undertaking an analysis of historical data. Through understanding the differences in the data is there a method of better adjusting animal transcriptomic data to make human predictions without having to initiate new studies? Perhaps a multitude of similar, high-content studies of infection from animal and human models side-by-side could provide some insights into this problem, even if limited in its scope to infection and immunity. Alternatively can a coefficient be found that gives confidence in the findings of animal models that can provide assurance that it worth trialling in a human model?