

# FAIR data to understand fungal epidemics

## A look at *Asperillus fumigatus*

Sibbe Bakker

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Fungi are an increasing concern for public health; for the first time the world health organisation (WHO) included fungi in their ‘critical priority pathogens’ list [1, 2]. These pathogenic fungi, such as *Aspergillus fumigatus*, *Candida albicans* &c. exhibit increasing resistance to anti-fungal medicines, complicating treatment of these infections [3]. There is evidence that the increase in fungal resistance is driven by climate change and changes in trade. One important tool to understand where microbes come from is *phylogeography*, the study of how genotypes vary across geographical patterns [4]. For viruses, such as the flu, tools, like nextstrain [5] are available to record the phylogeography observed by different researchers. With better phylogeographic data, pathways of resistance may be better understood [3].

For fungal priority pathogens, the geophylogeny is hard to determine, because the metadata that is needed to put the genomes in a place and time is not recorded well by researchers. To develop a pipeline for fungal phylogeography, the case of *A. fumigatus* will be examined first, since me and my collaborators have expertise on this fungus. Public whole genome data from *A. fumigatus* will be compiled and the metadata will be extracted and made standard. Next, the annotated WGS data be placed on epidemiology sites like nextstrain. After this is completed, the pipeline for *A. fumigatus* can be generalised to other fungi.

Besides the obvious benefit of re-using data from the literature, which saves money, a frame work will be developed to better understand the epidemiology of fungi. Such understanding will be able to directly pave the way to finding paths of anti-fungal resistance, and being able to mitigate them [3]. Besides the human pathogens, the system described here may also be adapted to collect data from plant pathogens.

## References

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