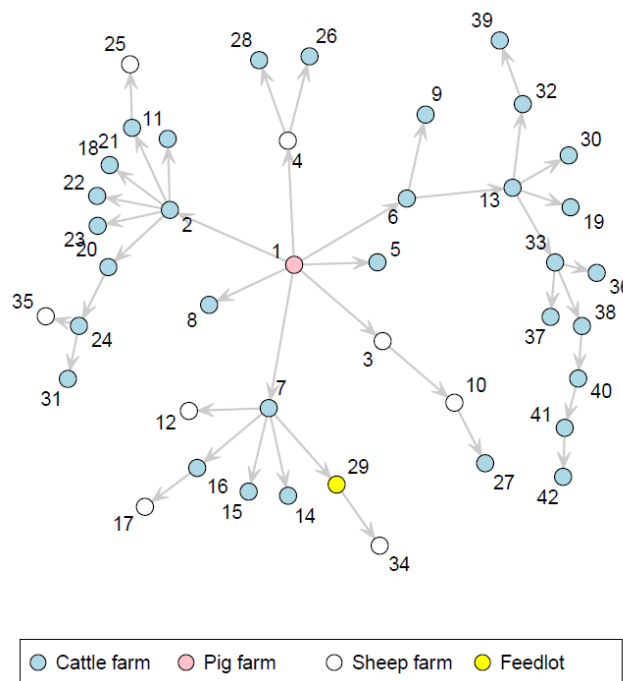# Exercise 1: Summary

The outbreak you analysed was adapted from *Reconstructing foot-and-mouth disease outbreaks: a methods comparison of transmission network models, Firestone et al,* https://www.nature.com/articles/s41598-019-41103-6 and was simulated using the Australian Animal Disease Spread (AADIS) hybrid model https://www.frontiersin.org/articles/10.3389/fenvs.2015.00017/full#:~:text=The%20Australian%20Animal%20Disease%20Spread,between%2Dherd%20spread%20and%20control.

The true transmission network for this outbreak was:

"The Australian Animal Disease Spread (AADIS) hybrid model was used to simulate 100 foot-and-mouth disease outbreaks using the baseline configuration, described in detail by Bradhurst et al., with movement restrictions and a stamping out only policy (i.e., no vaccination) from the point of outbreak detection fixed at 21 days after seeding on a large pig farm in central Victoria (infected premises 1, IP1) ... The origin of the outbreak was designated with the 7667 nucleotide whole genome consensus sequence (O/ JPN/2010-6/1 S) sampled from the first farm presumed to be infected in the 2010 outbreak of foot-and-mouth disease in Miyazaki Prefecture of Japan. Based on AADIS model outputs (date of exposure, date of diagnosis and the edge-list of the known transmission network), we simulated a sequence to seed the primary infected premises (IP1) assumed to have been infected 30 days after sampling of the sequence O/JPN/2010-6/1 S, then forward simulated sequences for each of the subsequent infected premises (IP2, …, IPn) based on the known transmission trees for these simulated outbreaks and these premises' simulated days of exposure and sampling"

This paper compares 9 published transmission reconstruction methods, by applying them to this and 5 other simulated foot-and-mouth outbreaks. We will be covering several of these methods in this course.