

NIHR Health Protection Research Unit in Emerging and Zoonotic Infections

Centrality as a means to identify potential risk in networks of shared pathogens

Maya Wardeh^{*1,2}, K. Marie McIntyre^{1,2} and Matthew Baylis^{1,2}

1. Department of Epidemiology and Population Health, Institute of Infection and Global Health, University of Liverpool.

2. Health Protection Research Unit in Emerging and Zoonotic Infections, University of Liverpool. (maya.wardeh@liverpool.ac.uk)

Introduction

We focused on 47 mammalian and avian hosts, including humans and animals commonly used in Europe as food or kept as pets [1]. We identified the 157 high impact pathogens [2] which cause infectious diseases in these species, and determined possible transmission routes for each pathogen. Interactions between these hosts and pathogens were extracted from the EID2 database [3] (eid2.liverpool.ac.uk).

Methods & Results

Viewing hosts as connected via the pathogens they share, we applied network analysis tools to investigate the risk of humans contracting diseases from their domesticated animals via each of the identified routes. In each network, hosts were linked if they shared at least one of the high impact pathogens. Links were weighted by the number of pathogens shared as well as Cohen's Kappa agreement measures.

We studied the characteristics and architecture of each network, and used eight centrality measures to identify the most central hosts in each network (*degree, strength, closeness, eigenvector, Opsahl degree, Opsahl closeness, Kappa strength, and Opsahl Kappa weighted degree*). We investigated whether central hosts pose most risk in transmitting high impact pathogens in each of the networks, as well as being at most risk of infection by these pathogens (Figure 1). Finally, we expanded the analysis to include all vertebrates and explored whether the high centrality hosts identified in the initial networks maintain similar levels in the expanded networks (Figure 2).

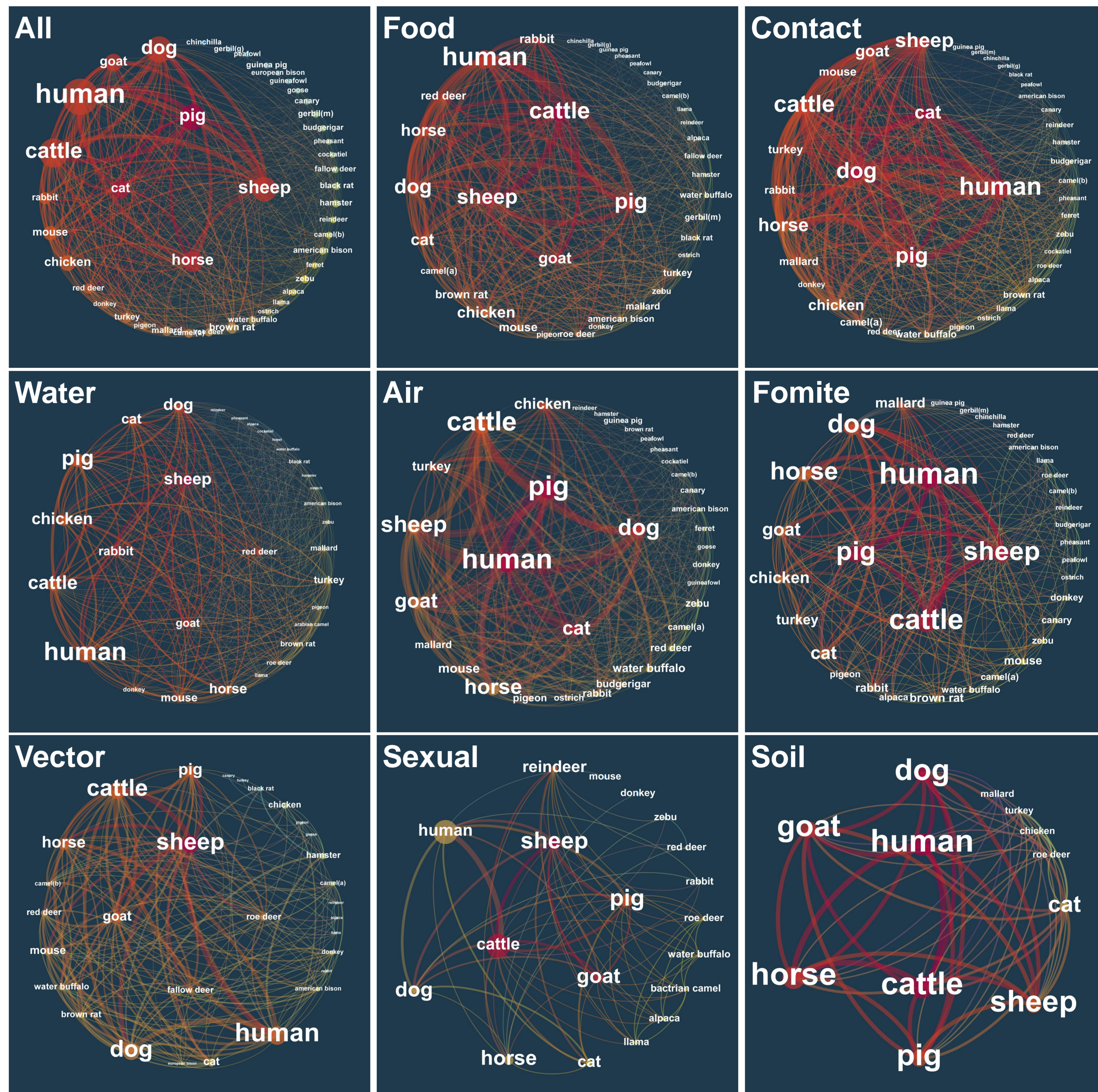
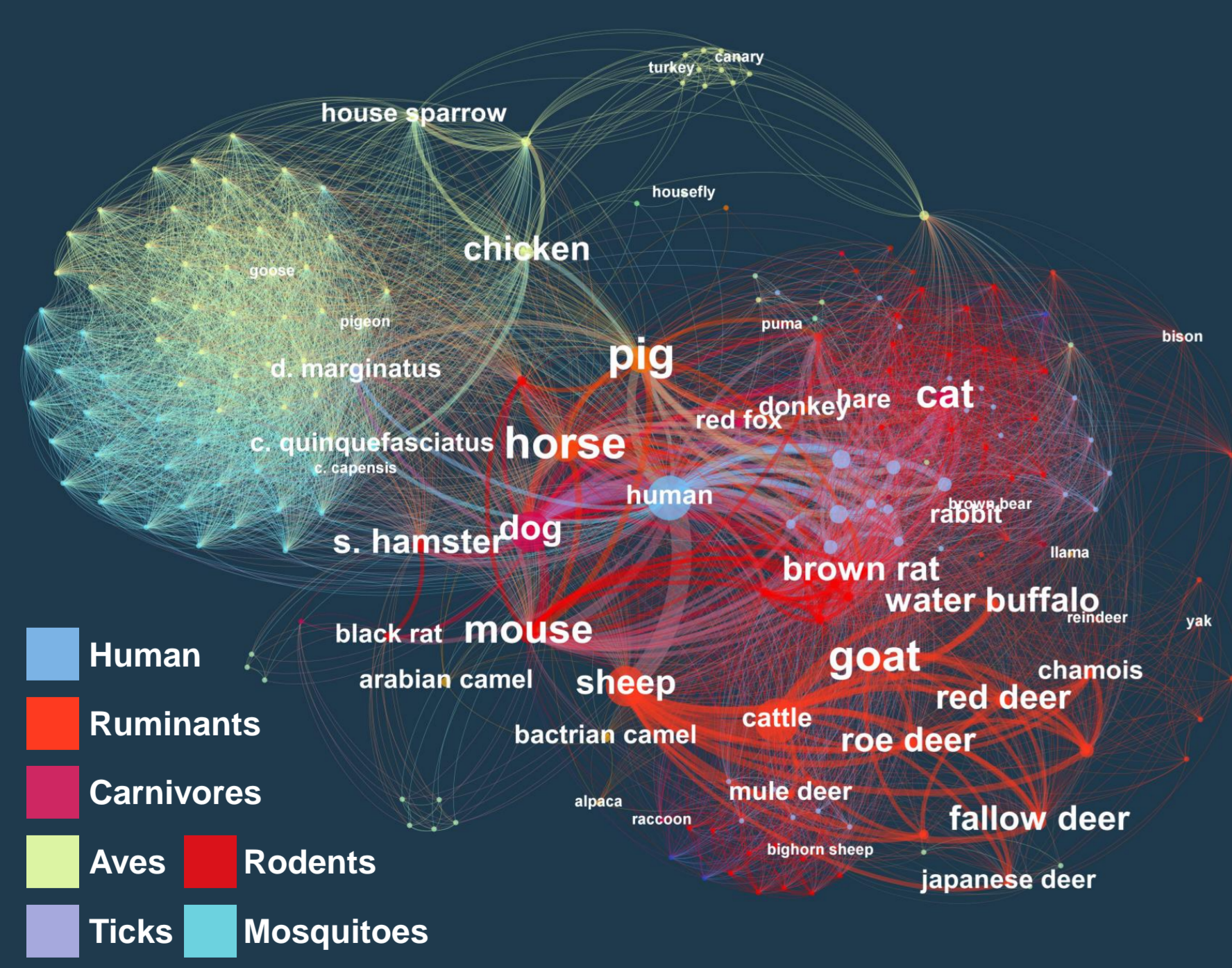
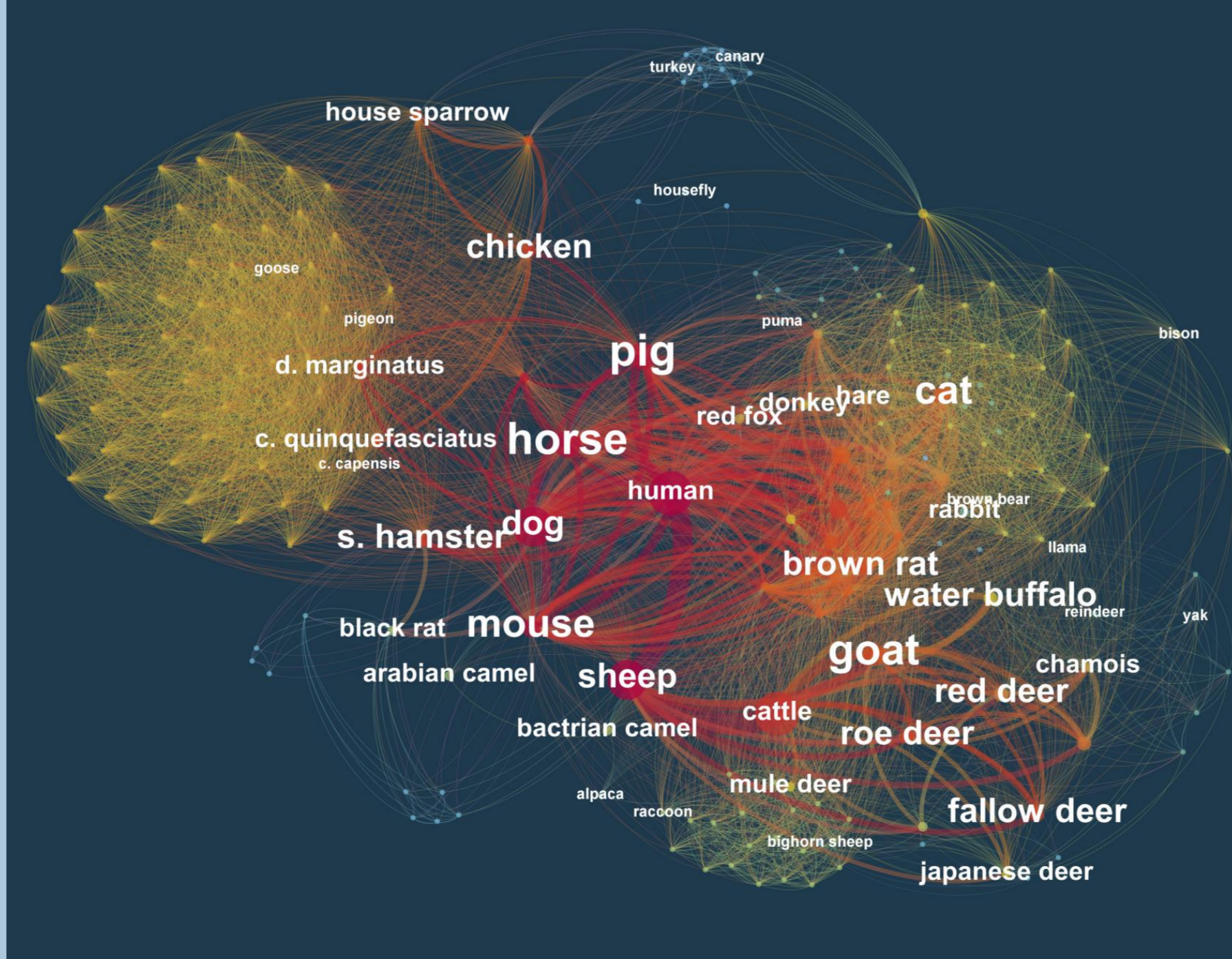


Figure 1 – The nine networks of humans and their domesticated animals, ordered by number of nodes. All refers to all routes. The colour of nodes corresponds to average centrality across the measures (from red, more central to blue, less central). The nodes within each circle are the most central across all eight measures. The size of nodes represents the number of pathogens infecting the host node

Classification



Centrality



Expanded analysis network measurements

- All Hosts: 1,093 nodes & 63,685 edges
- Food: 636 nodes & 35,141 edges
- Air: 545 nodes & 29,461 edges
- Contact: 498 nodes & 18,442 edges
- Water: 636 nodes & 35,141 edges
- Fomite: 345 nodes & 9,401 edges
- Vector: 231 nodes & 6,800 edges
- Sexual: 74 nodes & 506 edges
- Soil: 70 nodes & 1,245 edges

Figure 2 – Networks of all hosts sharing pathogens in the vector network

References

- (1) Using open-access taxonomic and spatial information to create a comprehensive database for the study of mammalian and avian livestock and pet infections. K.M. McIntyre et al. In Prev. Vet. Med. DOI:10.1016/j.(2013)
- (2) A Quantitative prioritisation of human and domestic animal pathogens in Europe. K.M. McIntyre et al. PLoS ONE 19(8), e103529. doi:10.1371/journal.pone.0103529 (2014).
- (3) Database of host-pathogen and related species interactions, and their global distribution. M. Wardeh et al. In Sci. Data. 09/2015; 2:150049. DOI:10.1038/sdata.2015.49. (2015)