

3AM

8AM in London (GMT), 5PM in Tokyo (GMT+9)

3rd.1: Zoonotic Web

Moderator: Todd N. Theriault, *Indiana University*

Presentations:

- Liuhuaying Yang, *Complexity Science Hub, Vienna, Austria*
- Amélie Desvars-Larrive, *University of Veterinary Medicine Vienna, Vienna, Austria*



Liuhuaying Yang

Liuhuaying Yang is a data visualization specialist and faculty member at the Complexity Science Hub in Vienna. She creates interactive visualizations that transform complex scientific research and societal data into engaging, accessible experiences. Her expertise spans design and front-end development for interactive data projects at the interface of academic research and real-world applications. She has worked with organizations including the Massachusetts Bay Transportation Authority, MIT Senseable City Lab and SMART Future Mobility in Singapore, and SPH Lianhe Zaobao, producing interactive data journalism and research visualizations.

Her work has received first prize in the 2019 TRB Innovations in Transit Performance Measurement Challenge, first place in the interactive category of the 2023 World Dataviz Prize, two Gold awards in the 2024 Information is Beautiful Awards (one in the Science, Technology & Health category and one as Impressive Individual), and most recently the City of Vienna's Promotion Prize in STEM for her contributions to making complex science accessible and understandable.



Amélie Desvars-Larrive



Amélie Desvars-Larrive is a faculty member of the Complexity Science Hub.

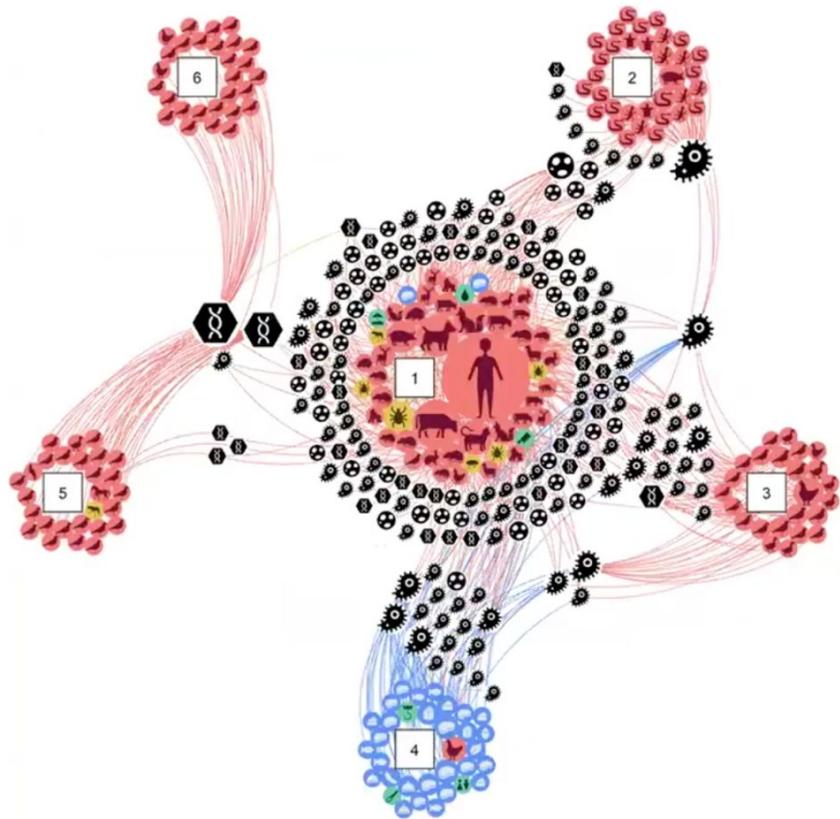
She graduated in 2004 as a doctor in veterinary medicine from the National Veterinary School of Toulouse, in France, with a specialisation in tropical diseases of livestock and epidemiology. Amélie worked for eight years in the Indian ocean as a field epidemiologist and veterinary research engineer, dealing with livestock and wildlife, especially rodents and bats. In 2013 she received a PhD in epidemiology from the University of Saint-Denis, La Réunion.

Amélie did her first PostDoc in the Department of Mathematics and Mathematical Statistics at Umeå University, in Sweden, where her research aimed to better understand the epidemiology and ecology of the zoonotic disease tularemia. Her second PostDoc was at the University of Veterinary Medicine Vienna in Conservation Medicine. Her project focused on urban brown rats (*Rattus norvegicus*) and their role in the epidemiology of (emerging) zoonotic diseases and as a source of antimicrobial resistance in the city.

Amélie's research interests include infectious disease epidemiology, including zoonotic and emerging diseases, veterinary epidemiology and public health, modelling of infectious diseases, the One Health approach, and rat-borne diseases.

Amélie is also an associate professor in infection epidemiology at the University of Veterinary Medicine Vienna.





24-hour event on
Envisioning Intelligences

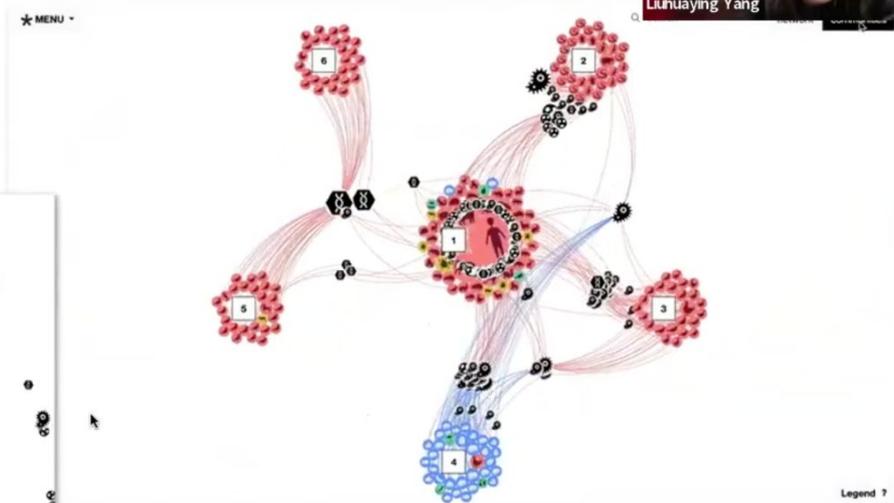
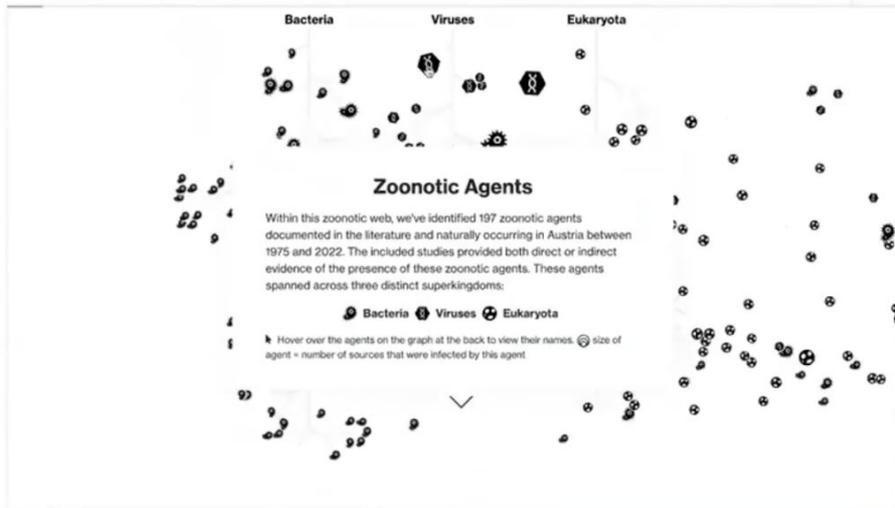


Liuhuaying Yang

How we created Zoonotic Web

Liuhuaying Yang
Complexity Science Hub, Vienna

Amélie Desvars-Larrive
University of Veterinary Medicine, Vienna



Gold award
Science,
Technology
and Health



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museum**

KNOWLEDGE FOR ALL
ISOTYPE – the Picture Language from Vienna

6.11.2025 – 5.4.2026

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Stadt Wien





Article

<https://doi.org/10.1038/s41467-024-48847-7>

A One Health framework for exploring zoonotic interactions demonstrated through a case study

Received: 29 February 2024

Amélie Desvars-Larrive^{1,2}, Anna Elisabeth Vogl¹,

Accepted: 24 June 2024

Gavriela Anadea Puspitarani^{1,2}, Lihuiyang Yang¹, Anja Joachim¹ & Annemarie Kaesbohrer¹

Published online: 15 July 2024

Check for updates

The eco-epidemiology of zoonoses is often oversimplified to host pathogen interactions while findings derived from global datasets are rarely directly transferable to smaller-scale contexts. Through a systematic literature search, we compiled a dataset of naturally occurring zoonotic interactions in Austria, spanning 1975–2022. We introduce the concept of zoonotic web to describe the complex relationships between zoonotic agents, their hosts, vectors, food, and environmental sources. The zoonotic web was explored through network analysis. After controlling for research effort, we demonstrate that, within the projected tripartite source source network of zoonotic agent sharing, the most influential zoonotic sources are human, cattle, chicken, and some meat products. Analysis of the One Health 3-cliques (triangular sets of nodes representing human, animal, and environment) confirms the increased probability of zoonotic spillover at human-cattle and human-food interfaces. We characterise six communities of zoonotic agent sharing, which assembly patterns are likely driven by highly connected infectious agents in the zoonotic web, proximity to human, and anthropogenic activities. Additionally, we report a frequency of emerging zoonotic diseases in Austria of one every six years. Here, we present a flexible network-based approach that offers insights into zoonotic transmission chains, facilitating the development of locally-relevant One Health strategies against zoonoses.

Zoonoses are caused by pathogens naturally transmissible between humans and wild or domestic animals. Events where humans and animal products meet create interfaces that facilitate zoonotic agent transmission. Notably, approximately 99% of endemic zoonotic infections in humans originate from domestic animals within anthropogenic environments, either directly or indirectly through contaminated food or vectors. Mansueti, et al. provided theoretical evidence supporting the positive relationship between the duration of domestication and the diversity of zoonotic agents that

humans share with each domestic species, which was initially hypothesised by McNeill³ as follows: “over 40% of human emerging infectious diseases (EIDs) are zoonotic”. Although direct zoonotic spillover from wildlife is rare and wildlife-to-human transmission typically occurs through indirect transmission, more than 70% of these zoonotic emergences are caused by pathogens with a wildlife origin⁴. However, the full host breadth of endemic and emerging zoonotic agents, as well as their animal and environmental reservoirs are rarely identified nor mapped.

¹Centre for Food Science and Veterinary Public Health, Clinical Department for Farm Animals and Food System Science, University of Veterinary Medicine Vienna, Vienna, Austria. ²Complexity Science Hub, Vienna, Austria. ³Department of Biological Sciences and Entomology, University of Veterinary Medicine Vienna, Vienna, Austria. ✉ email: amelie.desvars.larrive@vetmeduni.ac.at

Collaboration work



Research
Amélie Desvars-Larrive

Anna Vogl

Gavriela Puspitarani

Anja Joachim

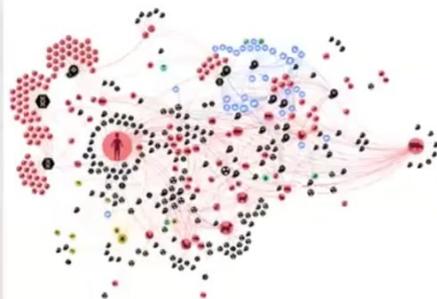
Annemarie Kaesbohrer



Visualization

Lihuiyang Yang

Institution
Complexity Science x Hub
vetmeduni



Visual

Zoonotic Web

Explore Austria's zoonotic interactions with an interactive visualization, introducing the 'zoonotic web' concept to describe animal-human-environment relationships.

Health Across Species

Lihuiyang Yang



Complexity Science*Hub

80+ researchers
14 topics in
complex systems

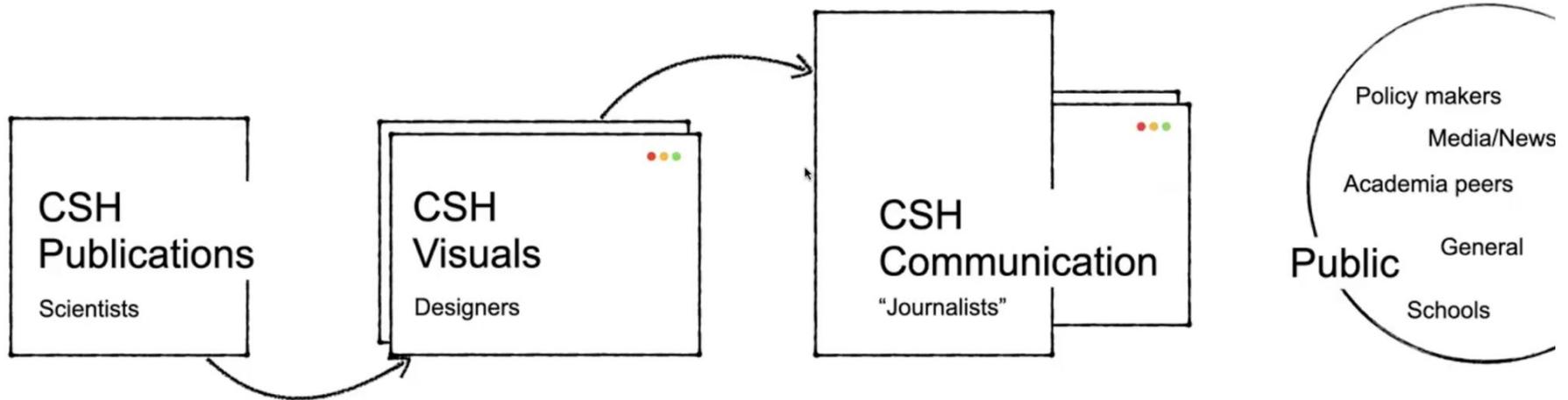


<https://csh.ac.at/>



CSH Workflow

Communicating Scientific Results via Visuals



Transforming Economies

Collective Minds, Algorithmic Fairness

Supply Chain Science

Lihuiyang Yang



👁 Visual

Antibiotics Shortage

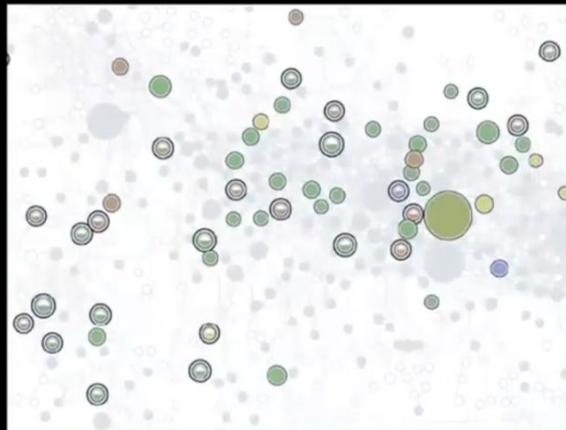
Explore how vulnerable the antibiotics supply in more than 100 countries is with respect to production disruptions in any of the other countries.



👁 Visual

Poverty Maps

Explore the inferred wealth in Sierra Leone and Uganda from multiple machine learning models.



👁 Visual

Economic Complexity and Green Transformation Opportunities

Explore the potential green products in Austria in product space.





Amélie Desvars-Larrive

Veterinarian, epidemiologist

Associate Professor, Infectious
Disease Epidemiology, University
of Veterinary Medicine Vienna

Faculty, Complexity Science Hub

Area of work

At the interface of field epidem
network science, and “One He



Core scientific interests

Zoonotic and emerging infectious diseases.

Spillover interfaces

where and how pathogens jump between
species.

One Health approach

trans-/interdisciplinary, cross-sectoral.

**Epidemiological modelling, data-driven
surveillance and public health**

Key focus

**Transform scattered, unstructured animal
health data into readily usable datasets to
enable robust analysis.**



One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems. It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent

—One Health High Level Expert Panel (OHHLEP)

<https://doi.org/10.1371/journal.ppat.1010537>

Zoonotic systems

Interfaces



Source image: <https://www.rp-pcp.org/about-the-platform>

System-thinking

Systems thinking is a way of making sense of the complexity of the world by looking at it in terms of wholes and relationships rather than by splitting it down into its parts.



Systems-based approach to zoonotic interfaces?



Conceptual

One Health

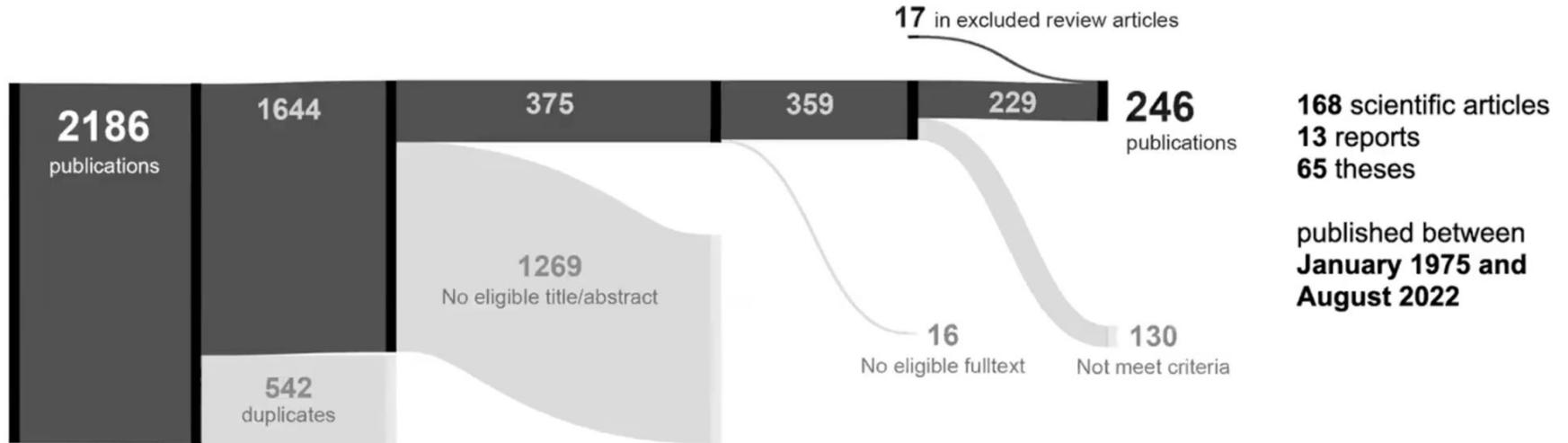
Technical

Network analysis

Quantitative, reproducible.

Dataset of zoonotic interactions in Austria, 1975

Systematic literature search (PRISMA guidelines)



Dataset of zoonotic interactions in Austria, 1975

246 publications → *.csv data file



2128 rows 48 data fields

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	pf_it	doi	pern	ISSN	pmid	reference	author	type_pul	year_j	type_study	locatic	year_data_c	type_pathog	pathogen_1	pathogen_2
29	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
30	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
31	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
32	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
33	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
34	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
35	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	parasite	Babesia microti	Babesia microti
36	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Rickettsia helvet	Rickettsia helve
37	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Bartonella	Bartonella
38	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
39	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
40	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
41	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
42	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
43	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
44	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	parasite	Babesia microti	Babesia microti
45	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Rickettsia helvet	Rickettsia helve
46	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Bartonella	Bartonella
47	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
48	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
49	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Borrelia	Borrelia afzelii, I
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53	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	parasite	Babesia microti	Babesia microti
54	8	10.3390/pathog	NA	NA	NA	Vector Surveill	Sonnberger, Ber	article	2022	original research	B	2019-2020	bacteria	Rickettsia helvet	Rickettsia helve

Zoonotic Web: node types

396 nodes by categories (representing actors)



199
sources

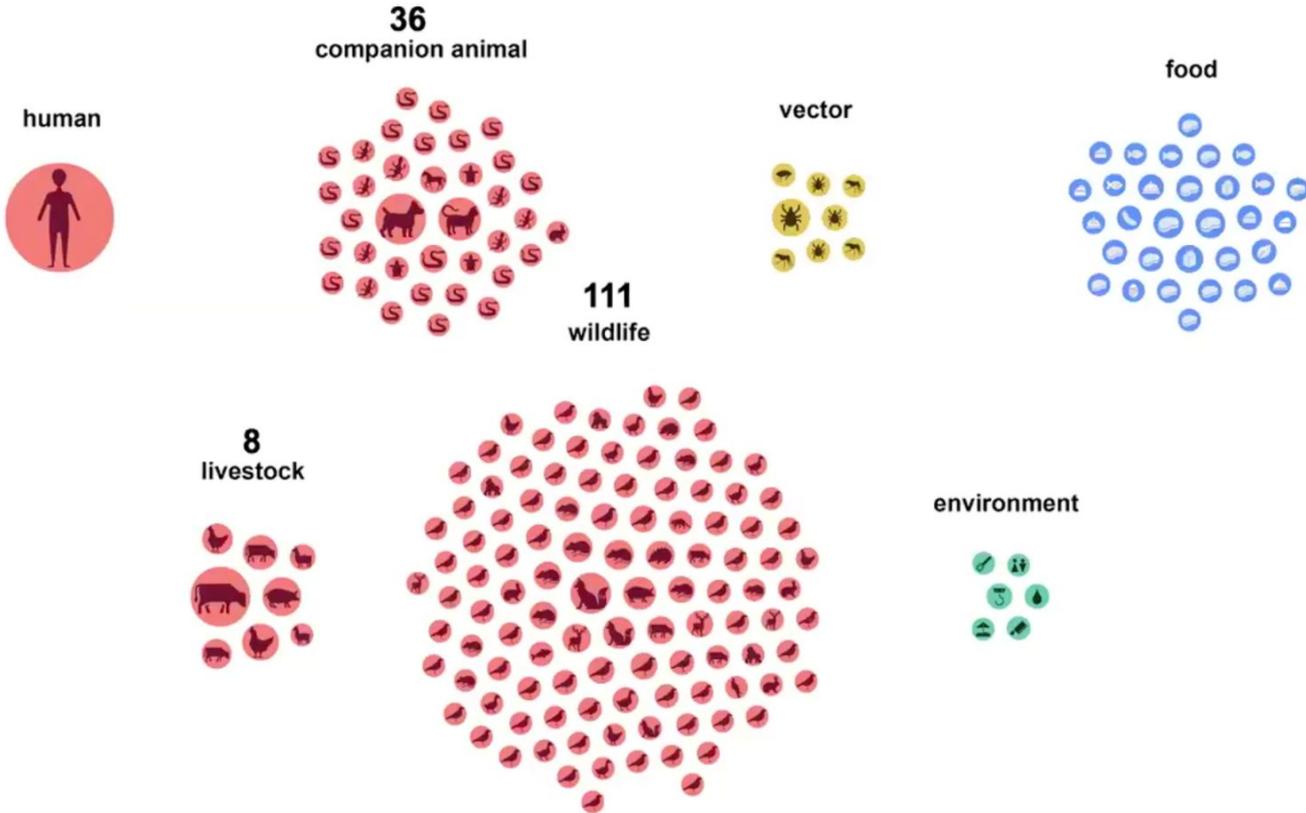
-  hosts
-  vectors
-  environment
-  food

197
zoonotic agents

-  bacteria
-  viruses
-  eukaryotes

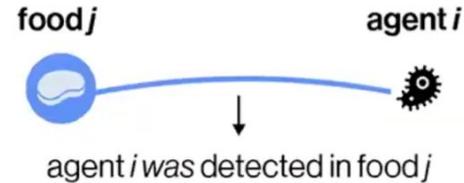
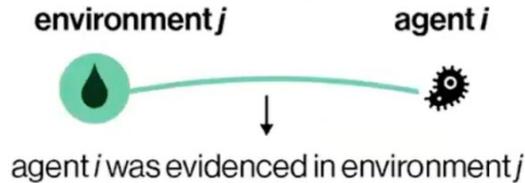
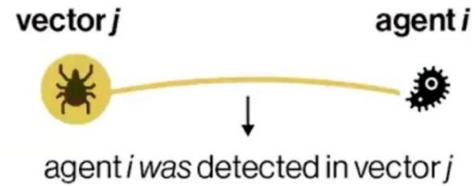
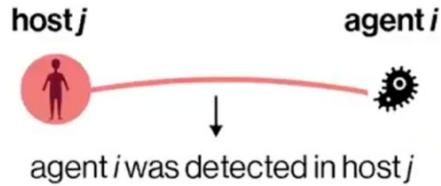
Zoonotic Web: node types

Sources

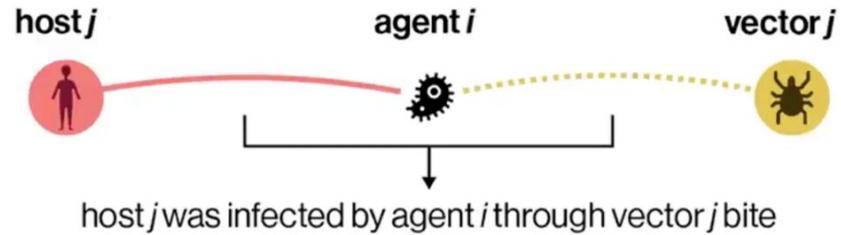


Zoonotic Web: direct links

658 edges (representing infections)

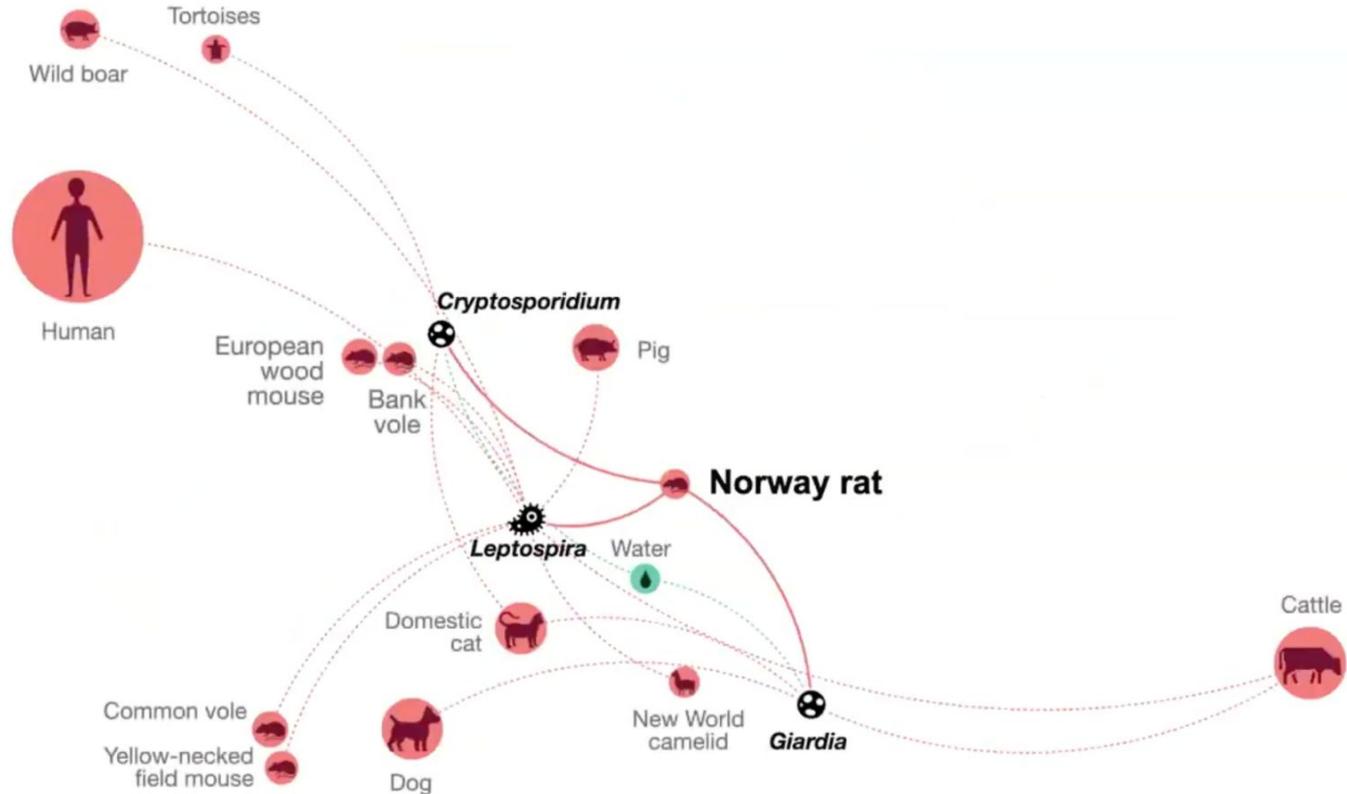


Zoonotic Web: potential chains



Zoonotic Web: potential chains

Example: subsystems rat-borne zoonoses



Network analysis: metrics



Node / Degree centrality

Node / Strength centrality

Node / Betweenness centrality

Node / Closeness centrality

Projected graph of source-source interactions

- Degree centrality
- Strength centrality
- Betweenness centrality
- Closeness centrality

Network analysis: metrics



Node / Degree centrality	Node / Strength centrality	Node / Betweenness centrality	Node / Closeness centrality
1. <i>Homo sapiens</i> (human) ¹ / 149	1. <i>Homo sapiens</i> (human) ¹ / 993.3	1. <i>Homo sapiens</i> (human) ¹ / 0.732	1. <i>Homo sapiens</i> (human) ¹ / 3.92
2. <i>Bos taurus</i> (cattle) ¹ / 79	2. <i>Bos taurus</i> (cattle) ¹ / 457.3	2. <i>Sus scrofa</i> (wild boar) ¹ / 0.212	2. <i>Bos taurus</i> (cattle) ¹ / 3.70
3. <i>Gallus gallus</i> (chicken) ¹ / 78	3. <i>Gallus gallus</i> (chicken) ¹ / 387.2	3. <i>Bos taurus</i> (cattle) ¹ / 0.122	3. <i>Gallus gallus</i> (chicken) ¹ / 3.61
4. <i>Sus scrofa</i> (wild boar) ¹ , Animal (unspecified) meat and meat product ³ / 59	4. Animal (unspecified) meat and meat product ² / 383.7	4. <i>Gallus gallus</i> (chicken) ¹ / 0.100	4. Animal (unspecified) meat and meat product ² / 3.54
5. <i>Equus caballus</i> (horse) ¹ / 57	5. Cattle meat and meat product ² / 281.0	5. Testudines (turtles) ¹ / 0.025	5. <i>Sus scrofa</i> (pig) ¹ / 3.51
6. <i>Asio otus</i> (long-eared owl), <i>Bubo bubo</i> (Eurasian eagle-owl), <i>Bubo scandiacus</i> (snowy owl), <i>Ciconia Ciconia</i> (white stork), <i>Circus aeruginosus</i> (western marsh harrier), <i>Coloeus monedula</i> (jackdaw), <i>Corvus cornix</i> (hooded crow), <i>Gypaetus barbatus</i> (lammergeier), <i>Strix uralensis</i> (Ural owl) ¹ , animal (unspecified) dairy ² / 56	6. <i>Ovis aries</i> (sheep) ¹ / 270.4	6. <i>Canis lupus familiaris</i> (dog) ¹ / 0.018	6. <i>Ovis aries</i> (sheep) ¹ / 3.46
7. Serpentes, Testudines, lizard (unspecified) ¹ / 53	7. Animal (unspecified) dairy ² / 265.1	7. <i>Felis catus</i> (domestic cat) ¹ / 0.016	7. Cattle meat and meat product ² / 3.42
8. <i>Ovis aries</i> (sheep) ¹ / 51	8. <i>Gypaetus barbatus</i> (lammergeier) ¹ / 259.7	8. Animal (unspecified) meat and meat product ² / 0.013	8. Animal (unspecified) ready to eat product ² / 3.39
9. <i>Sus scrofa</i> (pig) ¹ , cattle meat and meat product ² / 50	9. <i>Bubo scandiacus</i> (snowy owl), <i>Circus aeruginosus</i> (western marsh harrier), <i>Coloeus monedula</i> (jackdaw), ¹ / 256.6	9. <i>Apodemus flavicollis</i> (yellow-necked field mouse), <i>Nyctereutes procyonoides</i> (raccoon dog) ¹ / 0.0103	9. Pig meat and meat product ² / 3.38
10. Game meat and meat product ² / 44	10. <i>Strix uralensis</i> (Ural owl) ¹ / 256.3	10. <i>Ixodes</i> ³ / 0.101	10. <i>Canis lupus familiaris</i> (dog) ¹ / 3.32

The NCBI-resolved scientific and common names of the hosts are specified. Edge weights were adjusted to take into account the scientific research effort. The normalised values of the weighted betweenness and closeness are presented.

¹ Zoonotic source category: host; ² Zoonotic source category: food; ³ Zoonotic source category: invertebrate vector.

Network analysis: community detection

Zoonotic agent sharing communities



- Clusters of zoonotic sources sharing similar agents
- Leiden algorithm

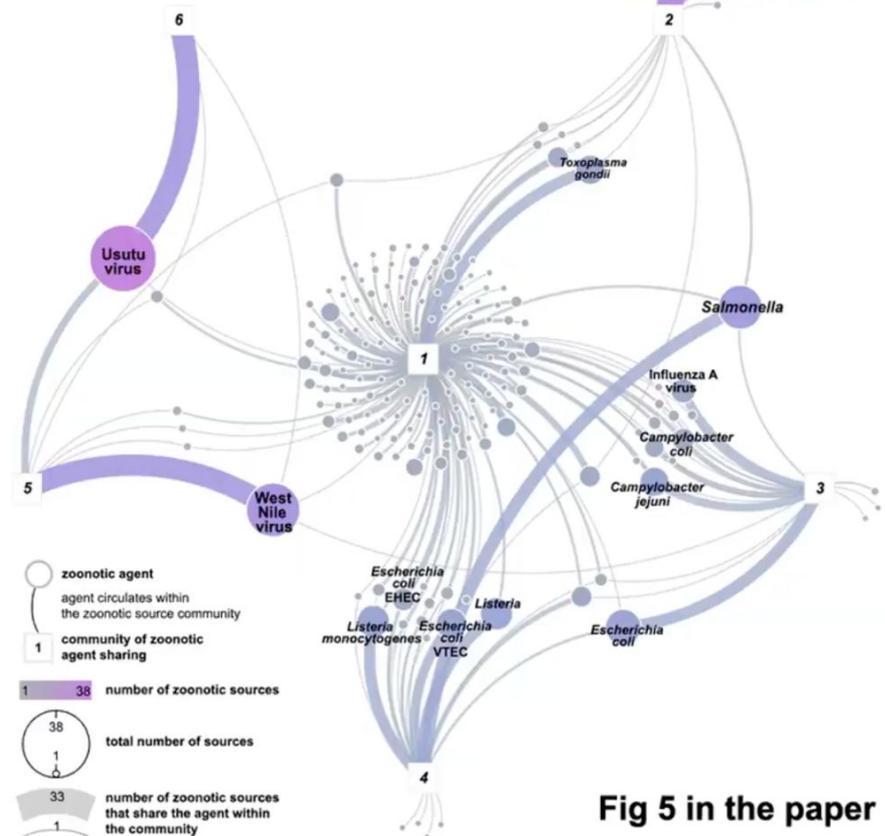


Fig 5 in the paper



How did we design interactive visuals?

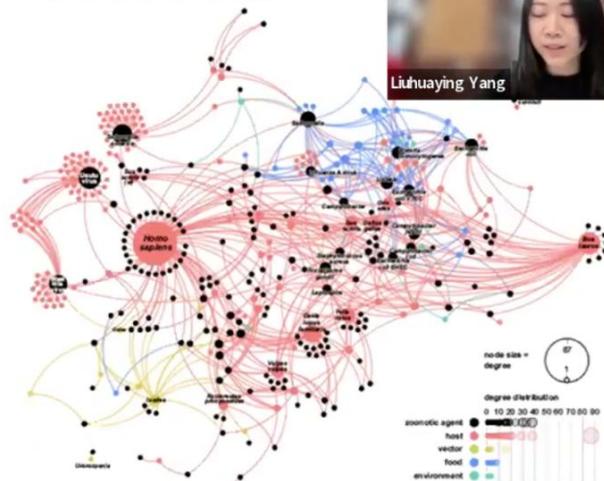
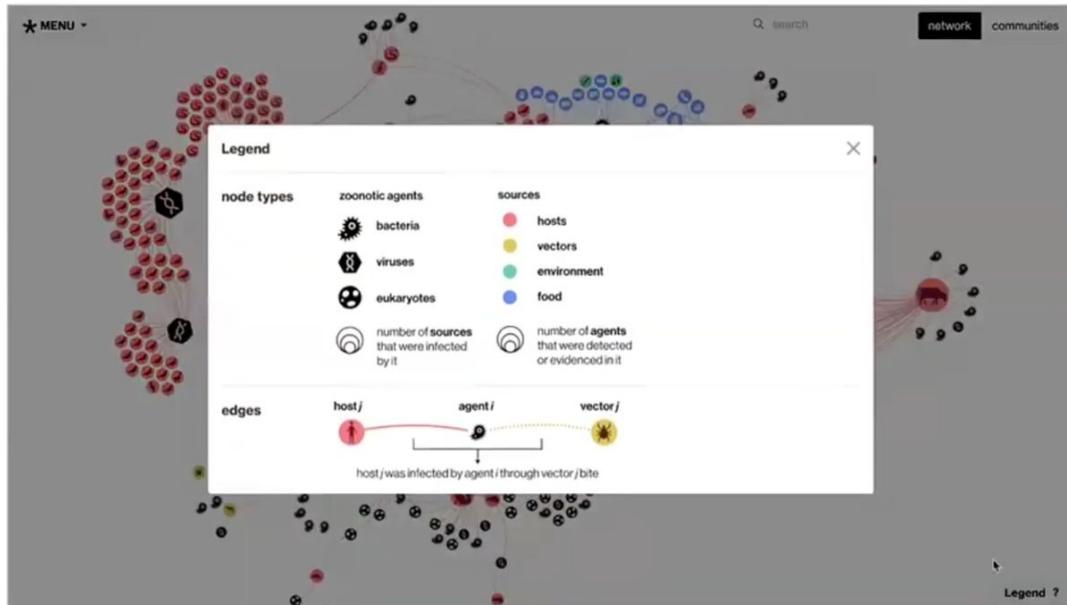


Fig. 3 | Network representation of the zoonotic web in Austria, 1975–2022. This representation uses the G3 force-link layout, providing a detailed visualization and offering epidemiological insights into naturally occurring zoonotic interactions in Austria. The zoonotic web is a bipartite network, where each node (circle) represents an actor in the zoonotic web, with one set of nodes representing zoonotic agents (black nodes) and the second set representing zoonotic sources that belong to different categories: vertebrate hosts (red nodes), vectors (yellow nodes), foodstuffs (blue nodes), and environmental matrices (green nodes). A link between a zoonotic agent i and a vertebrate host j indicates that agent i was directly or indirectly detected in host j ; a link between a zoonotic agent i and a vector j signifies that agent i was identified in vector j , implying that vector j may transmit agent i to a vertebrate host through a bite or mechanically; a link between a zoonotic agent i and an environmental matrix j indicates the presence of agent i in environment j , potentially leading to infection of a vertebrate host upon contact; and a link between a zoonotic agent i and a food matrix j indicates that agent i was detected in food j , which may result in the infection of a vertebrate host through ingestion. Node size represents the actor's degree centrality. The node degree centrality for each zoonotic source corresponds to the zoonotic agent richness, i.e., the number of (a) directly or indirectly evidenced from the zoonotic source. The node degree centrality for each zoonotic agent corresponds to the zoonotic source single, i.e., the number of sources from which the agent has been directly or indirectly evidenced, reflecting its "host" or "zoonotic source" plasticity. The bottom right graph illustrates the degree distribution for the "zoonotic agents" and "zoonotic sources" positions, the latter being disaggregated based on source categories. Interactive version: <https://nu.ubn.ac.at/zoonotic-web-dashboard.html>.

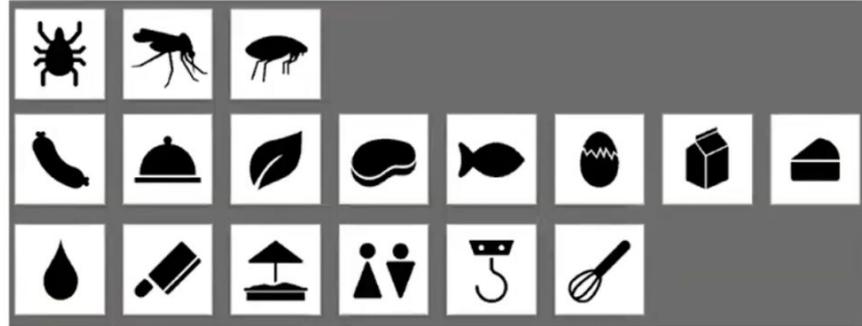
Network of zoonotic agent sharing

We generated a unipartite scientific research effort-adjusted network of zoonotic sources (i.e., accounting for research biases), based on zoonotic agent sharing. This network depicts patterns of zoonotic transmission potential between sources, with edges representing the likelihood that a given zoonotic source will transmit one or more zoonotic agents to another source relative to other sources in the network³⁵. Thus, for one zoonotic agent, connected sources belong to the same potential transmission chain^{35–38} (Fig. 4a). In this network, node rankings using the four centrality metrics (degree; strength, i.e., the sum of the weights of edges to/from a node; betweenness, i.e., the number of shortest paths that go through a node; and closeness, i.e., the average distance to all other nodes³⁹) showed positive correlation (0.26 < Kendall's Tau < 0.77, $p < 0.001$ in all cases, Supplementary

Table 5). Degree and strength centrality reflect co-occurrence patterns of zoonotic agents among sources³⁹. In contrast, betweenness and closeness centrality provide insights into indirect interactions through other sources³⁹. The nodes *Homo sapiens* (human), *Gallus gallus* (chicken), *Bos taurus* (cattle), and *animal (unguiculated) meat and meat product* were the most influential nodes in the network, appearing in the top 10 actors by the four centrality metrics. In addition, the nodes *Ovis aries* (sheep) and *ostrich meat and meat product* could also be considered influential, ranking in the top 10 actors by three (out of four) centrality metrics (Table 3). Notably, the nodes *Equus caballus* (horse) and various nodes representing bird species exhibited high degree and strength centrality, attributable to their shared interactions with the two Orthoflaviviruses, WNV and LSUV. Interestingly, the nodes *Sus scrofa* (wild boar), *Festuca* (tardis), *Canis lupus familiaris*

Icon system

Creating icons as needed



Identify needed icons



Icon rule: ncbi_host_sci → family_host → order_host → class_host

type_host	<input checked="" type="checkbox"/> name_host	sci_name_anim_h	ncbi_host_sci	ncbi_host_c	family_host	order_host	class_host	genus_host
human	human	NA	Homo sapiens	human	Hominidae	Primates	Mammalia	Homo
companion anim	dog	NA	Canis lupus familiaris	dog	Canidae	Carnivora	Mammalia	Canis
wildlife	eurasian blackbi	Turdus merula	Turdus merula	blackbird	Turdidae	Passeriformes	Aves	Turdus
wildlife	song thrush	Turdus philomelos	Turdus philomelos	song thrush	Turdidae	Passeriformes	Aves	Turdus
wildlife	eurasian blackbi	Turdus merula	Turdus merula	blackbird	Turdidae	Passeriformes	Aves	Turdus
wildlife	song thrush	Turdus philomelos	Turdus philomelos	song thrush	Turdidae	Passeriformes	Aves	Turdus
wildlife	house sparrow	Passer domesticus	Passer domesticus	House sparrow	Passeridae	Passeriformes	Aves	Passer
wildlife	blue tit	Cyanistes caeruleus	Cyanistes caeruleus	blue tit	Paridae	Passeriformes	Aves	Cyanistes
wildlife	borreal owl	Aegolius funereus	Aegolius funereus	boreal owl	Strigidae	Strigiformes	Aves	Aegolius
wildlife	northern goshaw	Accipiter gentilis	Accipiter gentilis	Northern goshaw	Accipitridae	Accipitriformes	Aves	Accipiter
wildlife	bearded reedling	Panurus biarmicus	Panurus biarmicus	bearded reedling	Sylviidae	Passeriformes	Aves	Panurus
companion anim	amazon parrot	Amazona	Amazona	Amazona	Psittacidae	Psittaciformes	Aves	Amazona
companion anim	horse	NA	Equus caballus	horse	Equidae	Perissodactyla	Mammalia	Equus
human	human	NA	Homo sapiens	human	Hominidae	Primates	Mammalia	Homo
wildlife	brown rat	Rattus norvegicus	Rattus norvegicus	Norway rat	Muridae	Rodentia	Mammalia	Rattus
human	human	NA	Homo sapiens	human	Hominidae	Primates	Mammalia	Homo
wildlife	japanese macaq	Macaca fuscata	Macaca fuscata	Japanese macar	Cercopithecidae	Primates	Mammalia	Macaca

Identify needed icons

25 icons for 155 hosts



- ~Homo sapiens
- ~cat (*Felis catus*)
- ~dog (*Canis lupus familiaris*)
- ~Anseriformes: duck, goose
- ~Galliformes: chicken, guineafowl, turkey
- ~Struthioniformes: ostrich

- ~Bovidae: cattle, goat, sheep
- ~Camelidae: alpaca, llama
- ~Suidae: pig

- ~Lagomorpha: rabbit
- ~Perissodactyla: horse
- ~Psittaciformes: amazon parrot, parakeet
- ~Squamata: snake, NA
- ~Testudines: tortoise, turtle, NA

- ~Aves: birds
- ~Canidae: fox
- ~Procyonidae: racoon
- ~Mephitidae: 鼬
- ~Mustelidae: 狸
- ~Cervidae: deer
- ~Rodentia: mouse
- ~Actinopteri: fish
- ~Eulipotyphla: 刺猬
- ~Primates
- ~Lepidosauria

Identify needed icons

3 icons for vectors



order_vector

order_vecto	family_vecto	genus_vecto	ncbi_vector
Diptera	Culicidae	Culex	Culex pipiens
Diptera	Culicidae	Culex	Culex pipiens
Diptera	Culicidae	Culex	Culex pipiens
Ixodida	Ixodidae	Hyalomma	Hyalomma marginatum
Siphonaptera	Pulicidae	Ctenocephalides	Ctenocephalides felis
Siphonaptera	Pulicidae	Ctenocephalides	Ctenocephalides felis
Diptera	Culicidae	Culex	Culex
Diptera	Culicidae	Aedes	Aedes
Diptera	Culicidae	Culiseta	Culiseta
Diptera	Culicidae	Anopheles	Anopheles
Diptera	Culicidae	Ochlerotatus	Ochlerotatus
Diptera	Culicidae	Coquillettidia	Coquillettidia richiardii
Diptera	Culicidae	Culex	Culex
Diptera	Culicidae	Aedes	Aedes
Diptera	Culicidae	Culiseta	Culiseta
Diptera	Culicidae	Anopheles	Anopheles
Diptera	Culicidae	Ochlerotatus	Ochlerotatus
Diptera	Culicidae	Culex	Culex
Diptera	Culicidae	Culex	Culex



order_vector:

Ixodida: ticks

Diptera: flies

Siphonaptera: fleas

Icon system

45 icons

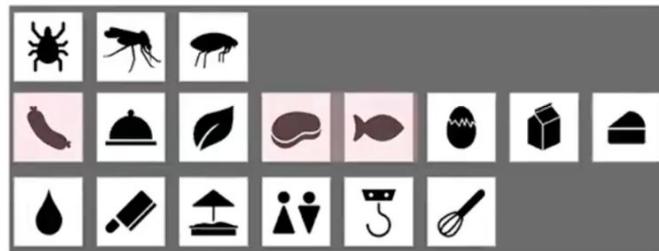


~Homo sapiens
~cat (Felis catus)
~dog (Canis lupus familiaris)
~Anseriformes: duck, goose
~Galliformes: chicken, guineafowl, turkey
~Struthioniformes: ostrich

~Bovidae: cattle, goat, sheep
~Camelidae: alpaca, llama
~Suidae: pig

~Lagomorpha: rabbit
~Perissodactyla: horse
~Psittaciformes: amazon parrot, parakeet
~Squamata: snake, NA
~Testudines: tortoise, turtle, NA

~Aves: birds
~Canidae: fox
~Procyonidae: racoon
~Mephitidae: 鼬
~Mustelidae: 狸
~Cervidae: deer
~Rodentia: mouse
~Actinopteri: fish
~Eulipotyphla: 刺猬
~Primates
~Lepidosauria



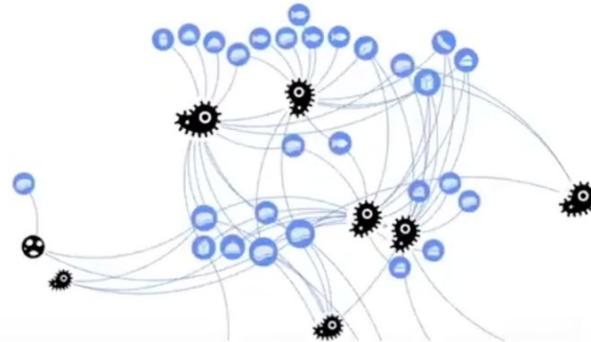
order_vector:
Ixodida: ticks
Diptera: flies
Siphonaptera: fleas

"sausage",
"ready to eat product",
"plant based food",
"meat and meat product",
"marine product",
"egg",
"dairy",
"cheese"

"water",
"slaughter knife",
"sandbox",
"public lavatory",
"meat processing plant",
"food processing plant"

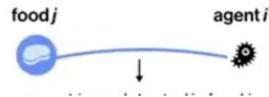


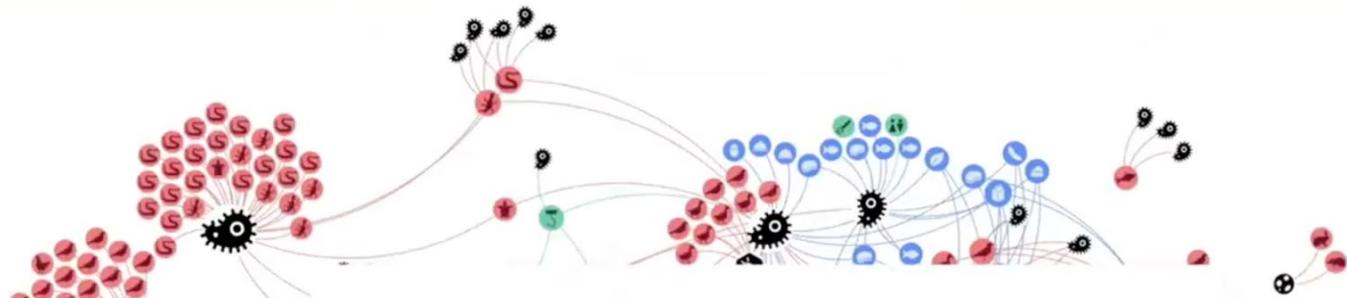
Narrative: scrollytelling



Food system-zoonotic agent interface

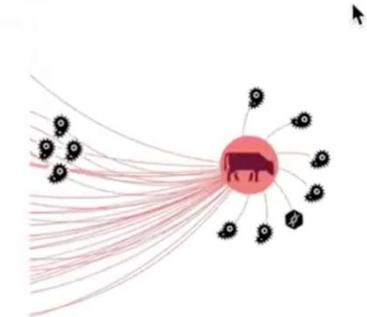
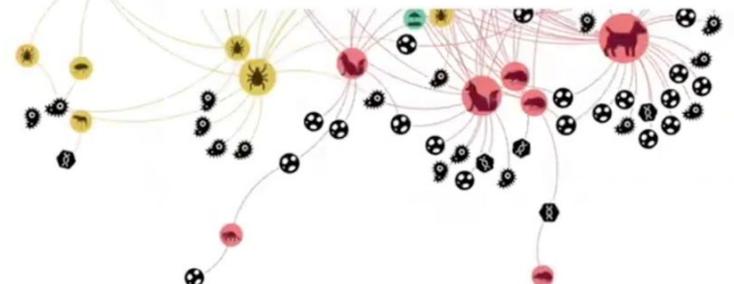
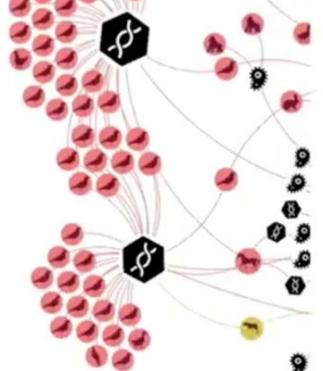
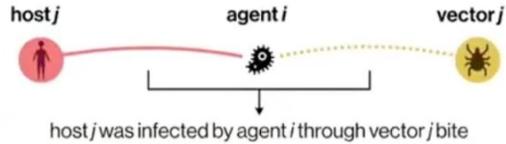
15 (7.6%) zoonotic agents were detected in food. Vertebrate hosts can be infected through ingestion of food. 🍖 Meat and meat products yielded the majority of positive results (55.8%), while 🌱 plant-based foods comprised only 2.5% of zoonotic agent-positive food products. Zoonotic agents identified in food were mainly of the genera *Listeria* (36.6% of positive foodstuffs), *Escherichia* (22.8%), and *Salmonella* (22.5%). Out of the 21 identified zoonotic agents in foodstuffs, all were 🦠 bacteria except for three 🦠 parasites (*Anisakis*, *Echinococcus*, and *Trichinella spiralis*)





Potential transmission chain

Some sources were identified as key actors in the transmission and spread of zoonotic agents in the zoonotic web, making them pivotal targets for disease control and prevention efforts. To illustrate this, we can draw dashed lines linking one source to another and observe the potential transmission chains, for example:





What's in the interactive visuals but not in the paper?

Zoonotic Agents

Definitions and examples

Bacteria are microscopic unicellular living organisms that can be found in every habitat: soil, rock, water, animals, plants, and even arctic ice. The majority of bacteria possess a genome consisting of a single chromosome, which is composed of a circular, double-stranded DNA molecule.

For instance, certain pathogenic variants of  *Escherichia coli* (*E. coli*) can contaminate various foods, potentially triggering zoonotic infections or outbreaks in humans upon ingestion of the contaminated food, particularly if inadequately cooked or pasteurized.



Viruses are microscopic agents that contain a small piece of genetic information (DNA or RNA) inside of a protective shell (capsid) and can replicate only inside living cells of an organism.

For instance,  West Nile virus (WNV) is a vector-borne zoonotic virus. It is transmitted from birds (the natural reservoirs of the virus) to humans through mosquito bites. About 1 out of 150 infected people develop a serious, sometimes fatal, illness (*source: CDC*).

Eukaryota (eukaryotes) are organisms whose cells have a membrane-bound nucleus. All animals, plants, fungi, and many unicellular organisms are eukaryotes. In our study, zoonotic eukaryotes refer to parasites, such as helminths (worms) and fungi.

For instance, the parasite  *Toxoplasma gondii* is the causative agent of toxoplasmosis. It can be contracted by ingesting undercooked, contaminated meat or shellfish. People can also get infected by accidentally ingesting the parasite's eggs found in cat feces, which can happen by eating contaminated vegetables or touching objects contaminated with cat feces and then putting hands in the mouth.

Zoonotic Agents

Data structure

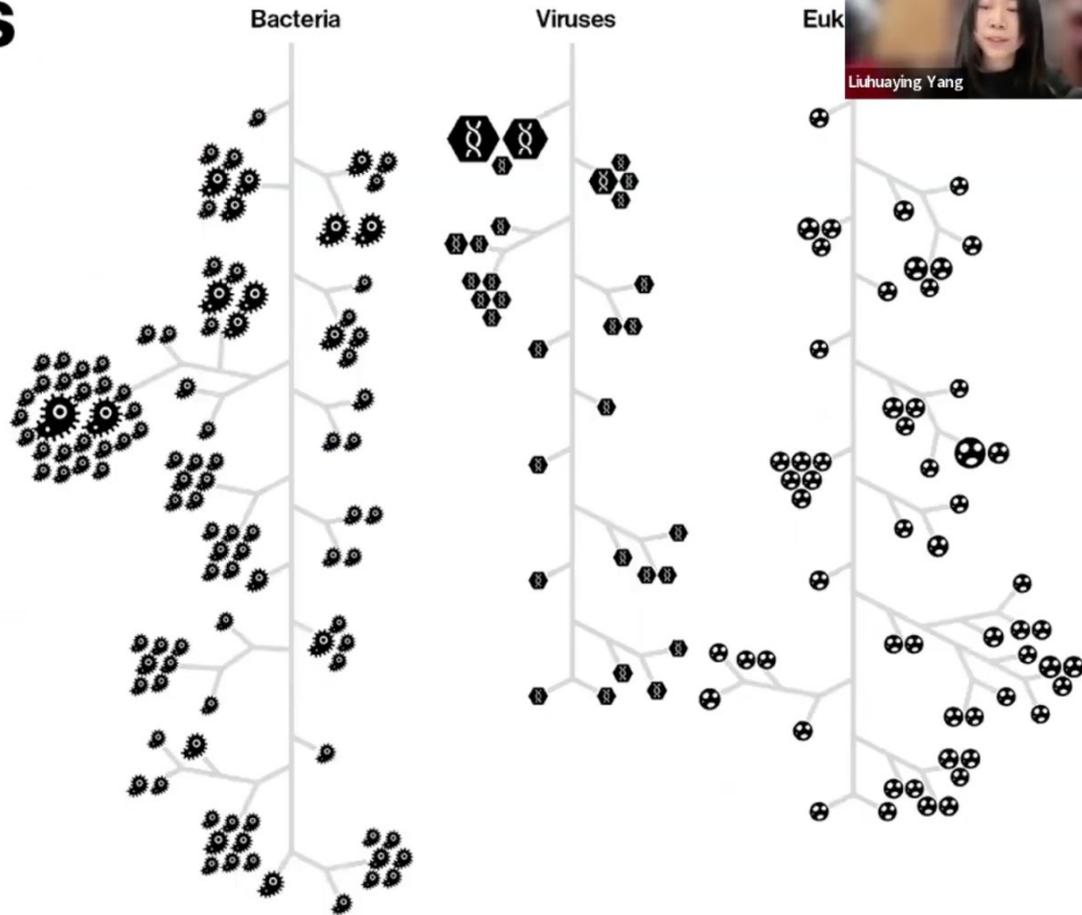


superkingdom_pathog	order_pathog	family_pathog	genus_pathog	ncbi_pathog
Viruses	Bunyavirales	Nairoviridae	Orthonairovirus	Orthonairovirus haemorrhag
Bacteria	Rickettsiales	Rickettsiaceae	Rickettsia	Rickettsia
Eukaryota	Piroplasmida	Babesiidae	Babesia	Babesia
Eukaryota	Rhabditida	Onchocercidae	Dirofilaria	Dirofilaria repens
Eukaryota	Rhabditida	Onchocercidae	Dirofilaria	Dirofilaria repens
Eukaryota	Rhabditida	Onchocercidae	Dirofilaria	Dirofilaria repens
Eukaryota	Rhabditida	Onchocercidae	Dirofilaria	Dirofilaria repens
Eukaryota	Rhabditida	Onchocercidae	Dirofilaria	Dirofilaria repens
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia afzelii
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia miyamotoi
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia garinii
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia burgdorferi
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia lusitaniae
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia valaisiana
Eukaryota	Piroplasmida	Babesiidae	Babesia	Babesia microti
Bacteria	Rickettsiales	Rickettsiaceae	Rickettsia	Rickettsia helvetica
Bacteria	Hyphomicrobiales	Bartonellaceae	Bartonella	Bartonella
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia afzelii
Bacteria	Spirochaetales	Borreliaceae	Borrelia	Borrelia miyamotoi

Zoonotic Agents

Design for Interactive Visuals

-  Bacteria
-  Viruses
-  Eukaryota

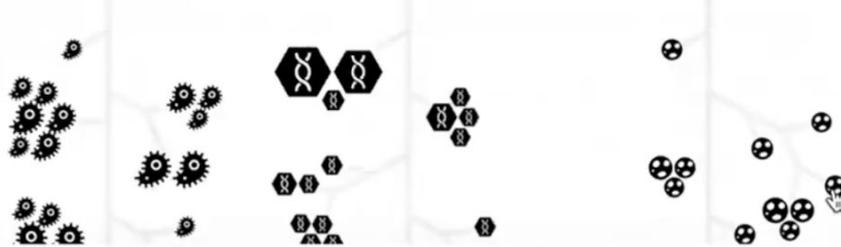




Bacteria

Viruses

Eukaryota



Taenia

Eukaryota / Cyclophyllidea /
Taeniidae / Taenia



Zoonotic Agents

Within this zoonotic web, we've identified 197 zoonotic agents documented in the literature and naturally occurring in Austria between 1975 and 2022. The included studies provided both direct or indirect evidence of the presence of these zoonotic agents. These agents spanned across three distinct superkingdoms:

 **Bacteria**  **Viruses**  **Eukaryota**

🖱️ Hover over the agents on the graph at the back to view their names. 🗪 size of agent = number of sources that were infected by this agent





**What's in the paper but not in
the interactive visuals?**

A One Health framework for exploring zoonotic interactions demonstrated through a case study

Received: 26 February 2024

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Check for updates

The eco-epidemiology of zoonoses is often oversimplified to linear pathogen transmission where findings derived from global datasets are rarely difficult to translate to smaller scale systems. Through a systematic literature search, we compiled a dataset of naturally occurring zoonotic interactions in Asia, spanning 1970–2022. We introduce the concept of zoonotic arcs to describe the complex relationships between zoonotic agents, food/beast, vectors, food, and environmental sources. The zoonotic web was explored through network analysis. After controlling for zoonotic effect, we demonstrate that within the projected zoonotic source sources network of zoonotic agent sharing, the most influential zoonotic sources are human, cattle, chicken, and some other products. Analysis of the One Health 3-Diagon (integrable with studies representing human, animal, and environment) confirms the increased probability of zoonotic zoonosis as human-cattle and human-chicken interactions. We illustrate the complexities of zoonotic agent sharing, which usually pathogen arcs are likely driven by higher complexity interactions agents in the zoonotic web, possibly to human and environmental sources. Additionally, we report a frequency of emerging zoonotic diseases in Asia of one every six years. Thus, we present a flexible network-based approach that offers insights into zoonotic transmission chains, facilitating the development of locally relevant One Health zoonotic agent sharing.

Zoonoses are caused by pathogens naturally transmissible between humans and/or domestic animals. While viruses are well understood, other zoonotic agents, such as bacteria, fungi, and protozoa, are less understood. Zoonotic agents are often transmitted across wildlife, environmental, and other reservoirs, and are often difficult to control. Zoonotic agents are often transmitted through contaminated food to humans. However, it is possible to control zoonotic agents by preventing the spread of zoonotic agents through the zoonotic web.

Research shows that zoonotic diseases, which are widely being studied by scholars, are difficult to control due to their complex nature. Zoonotic diseases are often transmitted through contaminated food to humans. However, it is possible to control zoonotic agents by preventing the spread of zoonotic agents through the zoonotic web.

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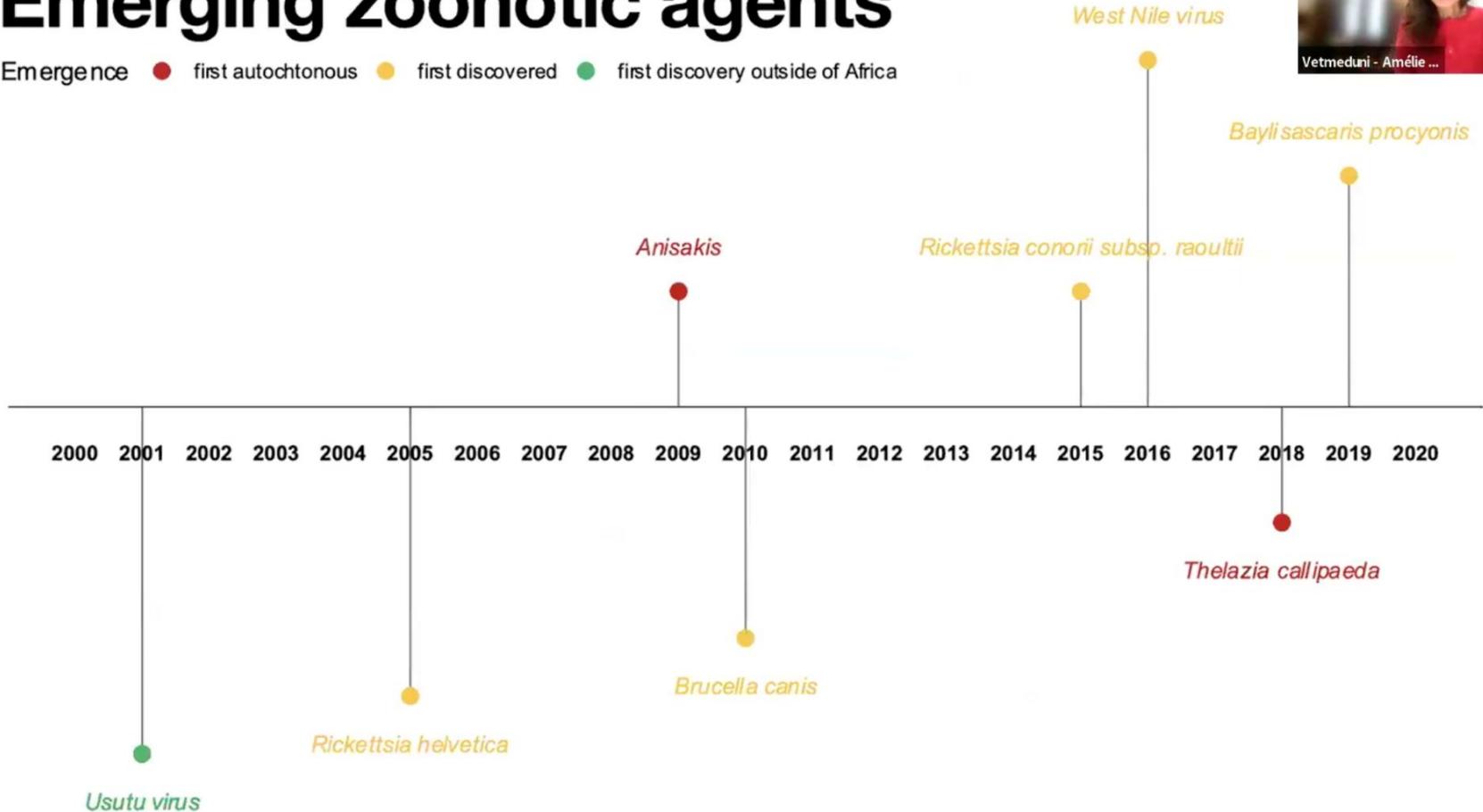
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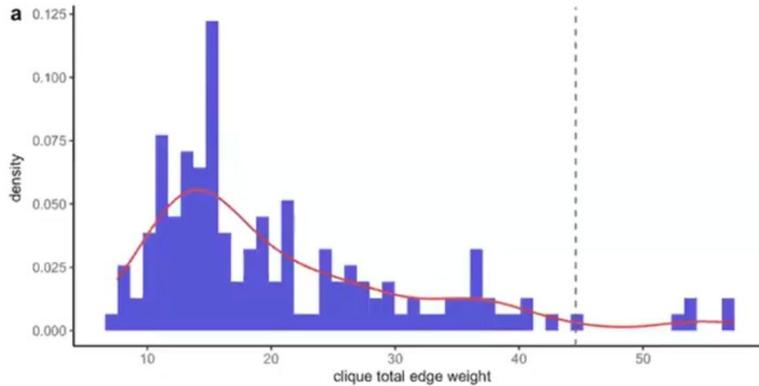
Emerging zoonotic agents

Emergence ● first autochthonous ● first discovered ● first discovery outside of Africa

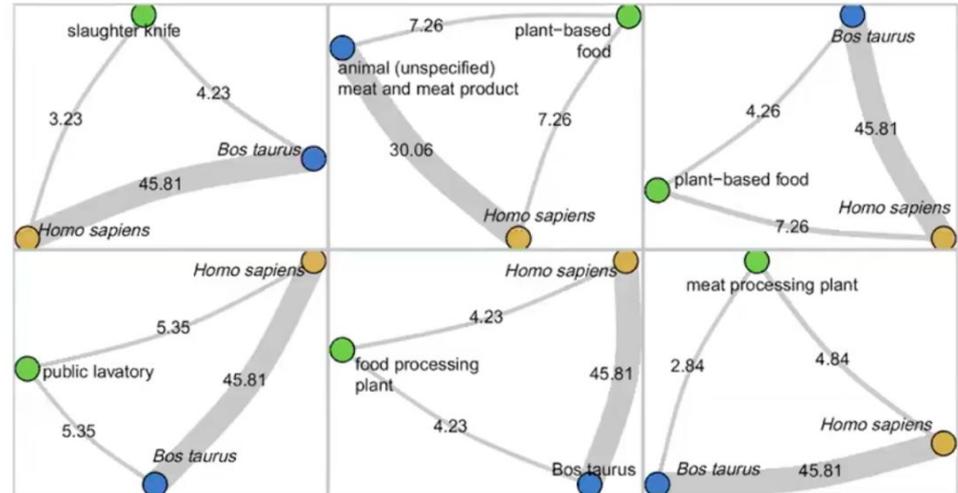


One health interfaces: 3-cliques

Quantifying spillover risk at human-animal-environment interfaces



The distribution of the research effort-adjusted number of zoonotic agents shared at human-animal-environment interfaces (=sum of the edge weights within One Health cliques) displayed a right-skewed pattern.



Six One Health cliques that ranked the highest based on the number of zoonotic agents shared.

Future work



- Expand the analysis to Brazil and France, and globally
- Moving from manual data extraction to automated data extraction (using LLM)
- Deeper in the methods
- Beyond a static, country-specific model



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