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UNIVERSITÄT
BERN

Annual Event 2024
Multidisciplinary Center for Infectious Diseases (MCID)

MCID Annual Event 2024

"We look forward to welcoming you to the Multidisciplinary Center for Infectious Diseases (MCID) Annual Event 2024. As a management team, we are excited to host a truly multidisciplinary event, showcasing MCID-funded research and other exciting investigations on the 'study and mitigation of health, healthcare, societal, ethical, and economic risks from infectious diseases'.

We take this opportunity to thank the Stiftung Vinetum for their generous funding of the MCID, not only for financing much of the research to be presented at the meeting, but for providing a platform for multidisciplinary interaction and collaboration on the critical topic of infectious diseases."

Prof. Dr. Carmen Faso
(MCID / Vetsuisse / IZB / IFIK)
MCID Co-Chair

Prof. Dr. Volker Thiel
(IVI / Vetsuisse)
MCID Co-Chair

Dr. Rebecca Limenitakis
Managing Director

Dr. Anita Hochuli
Teaching and Outreach
Coordinator

STIFTUNG
vinetum

Program

Location: UniS (room S003), Schanzeneckstrasse 1, Bern

08.45-09.45 Annual Assembly of MCID Members

09.45-10.15 Registration and welcome coffee

10.15-10.30 Welcome and Introduction
MCID Co-Chairs, Carmen Faso and Volker Thiel

10.30-12.00 Research presentations: session 1
Session Chairs: Caroline Brall and Alban Ramette

10.30-10.45 "Enhancing wildlife health monitoring: An evaluation of an integrated participatory approach of syndromic surveillance in Swiss wild birds"
Isabelle Wethli ⚲

10.45-11.00 "Intestinal cross-reactive Immunoglobulin A to *Klebsiella pneumoniae* glycan antigens"
Tim Rollenske ⚲

11.00-11.15 "Transition to 'Honest Brokers'? Reviewing the Swiss National COVID-19 Science Task Force's roles"
Bettina Zimmermann ⚲

11.15-11.30 "Emerging zoonotic Wesselsbron flavivirus causes severe hepatitis and is transmitted directly to suckling lambs"
Obdulio García-Nicolás ⚲

11.30-12.00 Flash talks

"Human neural organoids beading it: neurons in 3D culture display signs of injury following monkeypox virus infection"
Isabel Schultz-Pernice ⚲

"Public Acceptance of Disease Measures on Companion Animals"
Michelle Wyler ⚲

"Influenza A viruses circulating in the human and pig population of Switzerland"
Jonas Steiner ⚲

"Novel interspecies peptide inhibits growth and colonization of *S. pneumoniae*"
Janine Lux ⚲

"*Aedes*-borne diseases risk modeling with regards to climate change in Switzerland"
Lilian Goepp ⚲

"Covid: Science, Narratives, and Policy"
Jule Ksinsik ⚲

12.00-13.45 Poster session (see abstracts, pages 10-20)

12.45-13.45 Lunch (provided)

13.45-15.15 Research presentations: session 2
Session Chairs: Lucy Hathaway and Martin Wohlfender

13.45-14.00 "African Swine Fever disease control areas for wild boar"
Beatriz Vidondo ⌕

14.00-14.15 "A marriage of exposure and predispositions? A field study combining panel and webtracking data to understand the emergence of Covid-19 conspiracy beliefs"
Mykola Makhortykh ⌕

14.15-14.30 "ICD-10 code embedding for patient matching: a first step for causal inference from hospital discharge data"
Judith Bouman ⌕

14.30-14.45 "Characterisation of phylogenetically distinct temperate *Mammaliicoccus sciuri* phages from Africa"
Jérémy Cherbuin ⌕

14.45-15.00 "Decoupling Nsp1-mediated mRNA Translation Inhibition and Degradation in, SARS-CoV-2"
Emilie Bäumlin ⌕

15.00-15.15 "Divided society: Affective polarization of views about preventive measures during the COVID-19"
Mert Ipecki ⌕

15.15-15.45 Coffee break

15.45-17.00 Panel discussion: "Science-policy interface post-pandemic"

Moderator:

Katrin Zöfel, Science Editor, SRF (Schweizer Radio und Fernsehen)

Panelists to include:

Barbara Wieland, Institute of Virology and Immunology

Caroline Schlaufer, Ethics and Policy Lab, Multidisciplinary Center for Infectious Diseases & KPM Center for Public Management, University of Bern

Martin Ackermann, Department of Environmental Systems Science, ETH Zürich

Parham Sendi, Communicable Diseases Division, Federal Office for Public Health & Institute for Infectious Diseases, University of Bern

17.00-17.15 Closing of event
MCID Co-Chairs, Carmen Faso and Volker Thiel

17.15 Apéro (all attendees welcome)

Abstracts, oral presentations

Decoupling Nsp1-mediated mRNA Translation Inhibition and Degradation in, SARS-CoV-2

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[2] Department of Chemistry, Biochemistry and Pharmaceutical Sciences, University of Bern

Non-structural protein 1 (Nsp1) of SARS-CoV-2 is an early-produced protein during infection and serves as a host shutoff factor essential for viral replication. Nsp1 inhibits the translation of host mRNAs and induces their decay. A signature 5′UTR sequence can render viral RNAs immune to these activities [1]. Here, we show that by using translation-competent cell lysates, we can monitor, Nsp1 translation inhibition of non-viral mRNAs and mRNA degradation. We observe that mutations of amino acid residues that are crucial for Nsp1 to bind the 40S subunit abolish both Nsp1 activities, whereas N-terminal residues that have a minor impact on translation inhibition predominantly influence mRNA decay. This observation suggests that these functions may operate separately, although ribosomal association for both processes is required. Interestingly, mRNA degradation persists in the presence of various translation inhibitors, and we further investigate the features of Nsp1-mediated RNA degradation in different translation steps. By employing translation-competent cell lysates, we gain a comprehensive understanding of Nsp1's role in translation inhibition, mRNA degradation, and evolution among different Coronaviruses.

ICD-10 code embedding for patient matching: a first step for causal inference from hospital discharge data

Bouman J.A.[1,2], Moser A.[3], Wohlfender M.[1,2,4], Leichtle A.B.[2,5,6], Beldi G.[2,7], Endrich O.[2,8,9], Riou J.[2,10,+], Althaus C.L.[1,2,+]

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[10] Department of Epidemiology and Health Systems, Unisanté, Center for Primary Care and Public Health & University of Lausanne
+ Equal contribution

To study the long-term effects of severe COVID-19 infections, a longitudinal cohort study is required. However, while such studies are expensive to perform on a large scale, observational data in the form of medical health records or hospital discharge data can provide a welcome alternative. To be able to exploit such routinely collected medical data, specialised statistical methods are required, such as methods to match "treated" patients to patients that are similar except from the treatment, i.e. "control" patients. In this study, we evaluate the performance of a Word2vec-Enhanced ICD-10 code-based Matching (WEMatch) approach compared to traditional, gold-standard Propensity Score Matching (PSM) algorithms within a null effect matched cohort design. For this analysis, we rely on hospital discharge data from the Insel Gruppe in Bern, Switzerland, from 2014 to 2023, which included ICD-10 medical coding information, age, sex, and body mass index. We find that WEMatch outperforms PSM across several types of treatment (primary ICD-10 code for hospitalisation). While there is still potential for further improvement of natural language enhanced patient matching algorithms, this study establishes a robust framework for systematically comparing patient matching algorithms. Moreover, the groundwork is set for applying WEMatch to clinically relevant questions.

Characterisation of phylogenetically distinct temperate *Mammaliicoccus sciuri* phages from Africa

Cherbuin J.[1,2,3], Llodrá J.[5], Borcard L.[2,4], Kaessmeyer S.[5], Ramette A.[2,4], Labroussaa F.[1,2], Jores J.[1,2].

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This study investigated the prophages of 26 African *Mammalicoccus sciuri* genomes isolated from camels and dogs. We identified 36 complete prophages *in silico* in 24 genomes. We induced and isolated eight functional phages and characterised them phenotypically and genetically. Transmission electron microscopy analysis revealed that all phages have a Siphovirus morphotype with minor variations. Five phages showed broad host range while the three other phages had narrower host range. The phylogenetically related broad host range phages had genomes ranging from 133 to 138 kbp. The closest known phage, a SPbeta-like phage, had only 3% similarity at the DNA level, supporting the fact that the four phages represent a new family. The other phages had genomes around 45 kbp and are phylogenetically related to known phages reported for plasmid and SCCmec transduction events. The *M. sciuri* phages characterized in this study were the first isolated from African strains, which highlights a knowledge gap with respect to sub-Saharan phages. Altogether our study identified phylogenetically distinct and large M. sciuri prophages that are likely to form a new phage genus. This is in line with the origin of the host species, since East African Staphylococcaceae strains are by and large an untapped resource.

Emerging zoonotic Wesselsbron flavivirus causes severe hepatitis and is transmitted directly to suckling lambs

Zimoch M.[1,2], Grau-Roma L.[3], Liniger M.[1], Donzé N.[1], Godel A.[1,4], Escribano D.[5], Trueb B.[4,6], Pramateftaki P.[6], Torres-Puig S.[6], Cerón J.J.[7], Jores J.[2,6], Summerfield A.[1,2,4], Ruggli N[1,4]., Benarafa C.[1,2,4], García-Nicolás O.[1,2,4]

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[6] Institute of Veterinary Bacteriology, Vetsuisse Faculty, University of Bern
[7] Department of Animal Medicine and Surgery, Faculty of Veterinary Medicine, Regional Campus of International Excellence "Campus Mare Nostrum", University of Murcia, Spain.

Wesselsbron virus (WSLV) is a mosquito-borne flavivirus endemic to sub-Saharan Africa, circulating in several mammalian species. Direct infection has been described in humans. WSLV SA999 strain was reconstructed using reverse genetics with the YAC system. Lactating ewes were intravenously inoculated with 105 TCID50/animal of clade I or II strains (SA999 or SAH177 strain, respectively). Ewes developed clinical signs of the disease, including high body temperature and viremia; viral shedding was detected in milk and in nasal, oral, ocular, and rectal swabs. Importantly, direct transmission to lambs was detected in 40% of the ewes from both clades. At 12 days post-infection, viral levels remained very high in organs, especially in the liver, of all infected animals, despite the presence of high levels of neutralizing antibodies. The SA999 strain caused more pronounced lesions in the livers of infected animals, while only animals infected with the SAH1777 strain had mild neurological lesions. The serological biochemistry analysis revealed that WSLV causes significant hepatitis, which was more severe in SA999-infected animals. Our results could have a significant impact on the ecology of WLSV in endemic areas where it is overlooked and it might be confused with RVFV in animals and YFV in humans.

Divided society: Affective polarization of views about preventive measures during the COVID-19 pandemic

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Background: During the COVID-19 pandemic, researchers observed variations in attitudes and responses to public health advice about mask-wearing and vaccination. Affective polarization - feelings of dislike and/or hostility towards those with opposite views - could play a role.
Methods: We used data from an online cross-sectional survey conducted in 2022 as part of a feasibility study for the BEready ("Bern, get ready") pandemic preparedness cohort which invited 15,000 private households from the canton of Bern, Switzerland. The survey included questions about participants' feelings towards vaccination/mask supporters and opponents using a feeling thermometer. We calculated affective polarization levels ranging from 0 (not polarized) to 10 (heavily polarized).
Results: The overall response rate was 22.8% (n=3425). Preliminary results show that the mean weighted mask-related affective polarization score in mask supporters was 6.20 (standard error, SE=0.08) and 3.68 (SE=0.15) in those opposed to mask-wearing. The vaccination-related affective polarization score was 5.82 in vaccination supporters (SE=0.08) and 2.56 (SE=0.16) in those opposed to vaccination.
Conclusions: We found affective polarization about mask-wearing and vaccination as COVID-19 prevention measures, which was stronger among supporters than opponents of the measures. More information about affective polarization could help to develop effective public health communication messages for future pandemics.

A marriage of exposure and predispositions? A field study combining panel and webtracking data to understand the emergence of Covid-19 conspiracy beliefs

Adam S.[1,2]_, Rohrbach T._[1]_, Keller F._[1]_, Makhortykh M._[1]_, de León E._[3]_, Valli C._[3]_, Baghumyan A._[1]_, Sydorova M._[1]

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As COVID-19 escalated into a global health crisis, pandemic-related conspiracy theories emerged rapidly. Based on the idea of motivated reasoning, this study combines original data from multi-wave survey panels in Germany and Switzerland with online tracking during the pandemic's onset to explore how individuals' predispositions and exposure to conspiracy content impact the formation of pandemic-related conspiracy beliefs. Our findings reveal widespread exposure to conspiracy-related content across various online media platforms, which is partly driven by predispositions. Individuals with strong populist or nativist views avoid mainstream media when looking for conspiracy narratives, while those with political mistrust gravitate towards alternative sources. Both predispositions and exposure significantly shape conspiracy beliefs: Political mistrust, populism, nativism, and alternative media exposure drive belief formation, while exposure to quality media mitigates it.

Intestinal cross-reactive Immunoglobulin A to *Klebsiella pneumoniae* glycan antigens

Burkhalter S.[1,2,3], Gemici I.[1,2], Schreiber J.[3], Lukasiewisz J.[4], Macpherson A.[1,2], Rollenske T.[1,2,3]

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4 Wilhelm University, Bonn, Germany Laboratory of Microbial Immunochemistry and Vaccines, Ludwik Hirszfeld Institute of Immunology and Experimental Therapy, Wroclaw, Poland,

The human gut microbiota is a highly diverse bacterial community which is constrained by intestinal secretory Immunoglobulin A (SIgA) antibodies. Individual intestinal IgA antibodies have been identified that can cross-react and -protect against multiple different microbial species and serotypes. Here we use structure-guided defined bacterial colonizations of germ-free mice to generate and isolate cross-protective antibodies to defined glycan surface epitopes of *Klebsiella pneumoniae* (Kp), a gram-negative encapsulated opportunistic pathogen and a major cause of antibiotic-resistant nosocomial infections. We show that long-term defined Kp bi-colonization leads to SIgA reactivity to the desired glycan epitope. Bi-colonizations of mouse knock-out models suggest that antibody affinity maturation is required to obtain the desired SIgA cross-re-activity. Single cell antibody repertoire sequencing and analysis of intestinal plasma cells identifies an Ig gene repertoire bias in bi-colonized mice. Recombinant monoclonal antibodies (mAbs) from mice showing the desired SIgA reactivity have been selected and are currently produced to perform further binding assays to determine their cross-reactive and -protective capacity. The data may define bacterial cross-reactivity as a driving force of intestinal B cell responses and identify protective cross-reactive mAbs for the prevention or treatment of Kp infections.

Disease control areas for African Swine fever on wild boar

*Fischer, C.[1], Villard, L.[1], Huber, L.[1], Pisano, S.[2], Martinuzzi, R.[1], De Harlé, T.[1], Waroquier, F.[1], Vidondo, B.[3]**

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Control measures against African Swine Fever outbreaks in wild boar involve complete closing of infected forests, banning of all activities (recreation, hunting and forest work) and depopulation. Since hunting is known to affect wild boar movements, our study focused on how non-lethal leisure activities and forest work affect the movement of wild boar. We captured and collared with GPS sensors 9 adult female wild boar and performed 119 disturbance experiments that simulated human leisure activities and forestry work. Monthly home range estimates varied from 30-450 Ha in Spring/Summer to 700-3600 Ha in Autumn/Winter during hunting season. A typical escape reaction lasted 40min and covered 500-800m distance, with return times of 24 days on average. Out of the trails, the presence of dogs triggered the more intense reactions, followed by silent activities (due to a surprise reaction) and very loud activities. Forestry work shows high variability. Our results confirm that 1) foreseen control areas of 3 to 15km radius are adequate for wild boar in Swiss Central Plateau, and 2) banning of off-path activities and forestry work is essential in emergency situations of disease control to protect other populations of wild and domestic pigs.

Enhancing wildlife health monitoring: An evaluation of an integrated participatory approach of syndromic surveillance in Swiss wild birds

Wethli I.[1,2], *Pewsner M.*[1], *Dürr S.*[2,3], *Vancauwenberghe L.*[4], *Vivar Rios C.*[5], *Adrian-Kalchhauser I.*[1], *Keller S.*[1,2]

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Wildlife health surveillance (WHS) programs are crucial for safeguarding biodiversity, domestic animal, and human health. Spikes in wildlife mortality and morbidity events can serve as the initial indicators of disease emergence. The Swiss WHS lacks baseline biological data and exhibits notable gaps in the monitoring of smaller garden wildlife species such as songbirds, hedgehogs, and squirrels. This poses a major challenge for species conservation and early detection of infectious diseases. Our project aim is to evaluate a syndrome-based, participatory approach to improve surveillance. Our approach focuses on free-ranging birds as a well-defined study group with extensive long-term population data availability and a settled citizen engagement. We define field-recognizable syndromes based on distinct pathological categories by analysing necropsy reports of birds submitted to the Institute of Fish and Wildlife Health, Switzerland in the framework of general WHS during the last two decades. These syndromes will be included in the development of an online reporting system (ORS) of diseased and dead birds. Also, we are engaging stakeholders to implement the ORS and foster interdisciplinary collaboration between wild bird health experts. Our goal is to create a use case for a syndromic surveillance system in which population-relevant health trends become visible timely.

Transition to "Honest Brokers"? Reviewing the Swiss National COVID-19 Science Task Force's roles

Zimmermann B.M.[1,2,3]

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In his renowned book "The Honest Broker: Making Sense of Science in Policy and Politics" (2007), Roger Pielke suggested four idealized roles of scientific policy advice. These roles range from (1) "pure scientists" and (2) "science arbiters" who provide scientific knowledge to policymakers to (3) "issue advocates" and (4) "honest brokers" who translate scientific knowledge into policy recommendations. Pielke suggested that roles (3) and (4) were more appropriate in contexts of high uncertainty and/or lack of value consensus. This contribution presents preliminary findings from my MCID-funded research project "ESPRIM". It aims to investigate what role(s) would have been most appropriate for the Swiss National COVID-19 Science Task Force, taking into account reflections of task force members in semi-structured interviews, a content analysis of policy briefs published by the task force, and media debate analyses. I will then show findings illustrating what roles were actually taken and how and why they changed over time. I will critically discuss the advantages and disadvantages of each of the taken roles and their appropriateness in a multi-faceted, long-lasting, existential crisis as represented by the COVID-19 pandemic.

Abstracts, poster presentations with flash talks

Aedes-borne diseases risk modeling with regards to climate change in Switzerland (Poster #7)

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Mosquito-borne diseases such as dengue, Zika and chikungunya are emerging in Europe, and vector-competent *Aedes* mosquito species have been spreading in Switzerland. Our project aims to study the future risk of diseases transmitted by these invasive mosquitoes for the Swiss population by 2060, accounting for climate change scenarios. We will employ a compartmental epidemiological model integrating the thermal dependency of parameters associated with the mosquito life cycle and host-vector interactions. A key parameter to this approach is the mosquito-to-human ratio, which will be estimated using a model accounting for temperature and precipitation patterns while incorporating demographic projections for human populations. We will calibrate and validate mosquito abundance models using ovitrap data. The sensitivity to climate change scenarios will be addressed by using 68 regional climate model simulations. Bayesian analysis of controlled laboratory experiments will provide uncertainty intervals of parameters associated with vector survival and behaviour. Outputs will consist of daily 2x2km grid maps of basic reproduction number estimates over Switzerland, informing about the local potential for disease transmission. These results will provide valuable insights into the evolving dynamics of mosquito-borne diseases in a changing climate, contributing to public health planning and disease prevention strategies.

Covid: Science, Narratives, and Policy (Poster #14)

Ksinsik J.[1,2], Schlaufer, C[1,2].

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This poster showcases the ongoing research of the MCID-funded project, "Covid-19: Science, Narratives, and Policy." The primary goal of this research is to investigate the involvement of scientists in policy debates during the Covid-19 pandemic, their interactions with other policy actors, their perceptions of their roles, and the narratives they constructed. Effective collaboration between science and policymaking is crucial for addressing future infectious disease threats. By participating in public debates, scientists can enhance the understanding of infectious disease threats among the public and policymakers, thereby influencing public trust in policies. Unlike similar studies that concentrate on institutionalized scientific policy advice, our project examines public discourse in the media. This presentation will cover initial findings, ongoing analyses, and the future directions of the project.

Novel interspecies peptide inhibits growth and colonization of _S. pneumoniae_ (Poster #16)

Lux J.[1,2], _Portmann H._[1], _Sánchez García L._[1], _Erhardt M._[1], _Holivololona L._[1], _Laloli L._[1], _Licheri M.F._[1], _Gallay C._[3], _Hoepner R._[4], _Croucher N.J._[5], _Straume D._[6], _Veening J.W._[3], _Dijkman R._[1,7], _Heller M._[8], _Grandgirard D._[1], _Leib S.L._[1,7], _Hathaway L.J._[1,7]

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[4] Department of Neurology, Bern University Hospital and University of Bern
[5] MRC Centre for Global Infectious Disease Analysis, Sir Michael Uren Hub, Imperial College London, UK
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[7] Multidisciplinary Center for Infectious Diseases, University of Bern
[8] Proteomics and Mass Spectrometry Core Facility, Department for BioMedical Research (DBMR), University of Bern

We identified a peptide released by _Klebsiella pneumoniae_ and analyzed its effect on _Streptococcus pneumoniae_ (pneumococcus) with a view to investigating its potential as a therapeutic for pneumococcal diseases. The secretome peptide was identified by mass spectrometry and we analyzed its effects on _S. pneumoniae_ by growth measurements, transformation assays, microscopy, RNA-Seq and colonization assays using primary human airway epithelial cells and an infant rat model. We assessed peptide toxicity using primary human airway epithelial cells and zebrafish larvae. The peptide suppressed growth of genetically diverse clinical pneumococcal isolates, including antibiotic-resistant strains, in defined medium and human cerebrospinal fluid. Bacteriostatic growth inhibition was dependent on uptake via a functional ABC transporter and caused downregulation of genes involved in amino acid and protein metabolism. The peptide caused irregular bacterial shapes, decreased chain length and decreased genetic transformation. Pneumococcal adherence to primary human airway epithelial cells and colonization of rat nasopharynx were also decreased. We did not detect toxicity of the peptide. Thus, we identified a _K. pneumoniae_ peptide which inhibits pneumococcal growth and colonization. The peptide has potential as a therapeutic for pneumococcal diseases, including treatment of antibiotic resistant strains, while avoiding bacterial lysis and dysbiosis.

Human neural organoids beading it: neurons in 3D culture display signs of injury following monkeypox virus infection (Poster #20)

Schultz-Pernice I.[1,2,3], _Fahmi A._[1,2,3], _Chiu Y._[4,5], _Oliveira Esteves B.I._[1,2], _David T._[1,2], _Golomingi A._[1,2], _Zumkehr B._[6], _Jandrasits D._[7], _Züst R._[7], _Steiner S._[8], _Wotzkow C._[8], _Blank F._[8,9], _Engler O._[7], _Baud D._[4,5], _Alves M.P._[1,2,10]

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In 2022-23 the world experienced the largest recorded monkeypox virus (MPXV) outbreak outside of endemic regions. Remarkably, cases of neurological manifestations were reported, some of which fatal. MPXV DNA and MPXV-specific IgM antibodies were detected in the cerebrospinal fluid of encephalitis-affected patients, suggesting neuroinvasive potential. We explored the susceptibility of neural tissue to MPXV infection using human neural organoids (hNOs). The virus efficiently replicates in hNOs as indicated by the exponential increase of infectious viral loads and the elevated frequency of MPXV-positive cells over time. Electron microscopy imaging confirmed the presence of viral particles and perinuclear viral factories within the tissue. We observed susceptibility of several cell types to MPXV, including neural progenitor cells and neurons. Furthermore, we detected the presence of viral antigens in neurites and cell foci. In line with this, we observed significantly more cell-associated than released infectious virus, suggesting viral spread by cell-to-cell contact. While hNOs displayed no evident outer morphological changes upon infection, we detected the formation of varicosities in neurites, pointing to viral manipulation of axonal transport and neuronal injury. In accordance, the apoptosis marker cleaved caspase-3 was detected within neurite swellings. Our findings identify a mechanism potentially contributing to MPXV-mediated neuropathology.

Influenza A viruses circulating in the human and pig population of Switzerland (Poster #22)

Steiner J.[1,4], Licheri M.[3,4], Mwanga M.[3,4], Licheri M.[3,4], Dijkman R.[3,4], Kelly J.[2,4], Nathues H.[1,4]

[1] Clinic for Swine, Department of Clinical Veterinary Medicine, Vetsuisse Faculty, University of Bern
[2] Institute of Virology and Immunology (IVI), Bern and Mittelhäusern
[3] Institute for Infectious Diseases, University of Bern
[4] Multidisciplinary Center for Infectious Diseases, University of Bern

Influenza A viruses (IAV)s dominate the ongoing discussion on candidates for the next human pandemic. They contribute to a disease burden which is assumed to be responsible for up to 700`000 human deaths every year worldwide. Novel IAVs with pandemic potential can evolve in pigs that serve as mixing vessel for pig-, human- and poultry-adapted strains. Therefore, IAVs in pigs require increased attention. In Switzerland, IAVs circulating in pigs are barely known but may still play a role in future pandemics. Here, a case of zoonotic transmission and sequencing data retrieved through IAV surveillance in the Swiss human and pig population are presented.
In our interdisciplinary project, healthy and infected herds are examined by using questionnaire data and laboratory results from nasal swabs obtained from pigs and their care takers. Laboratory results are derived from an IAV-qPCR followed by full genome sequencing.
IAVs were identified in pigs in 3 farms including a farmer on one of the farms. In all the pigs and the farmer swine IAV, subtype H1N1, clade 1C.2.2, was identified. The farmer and the pigs were infected with a virus with >99% nucleotide sequence similarity. This indicates a potential zoonotic transmission. By further viral and epidemiologic characterization this project contributes to prioritize IAVs for evaluation of human pandemic potential.

Public Acceptance of Disease Measures on Companion Animals (Poster #24)

Wyler M.K.[1,2], Schlaufer C[1,2].

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The control over zoonotic disease outbreaks is an important factor to ensure global public health. But while zoonotic diseases in connection with livestock already draw considerable attention in policymaking, a gap can be identified in the area of household pets. The Covid-19 pandemic, in which also cats and dogs have been carrier of the disease, has highlighted the importance of research and policy actions to address the risks of zoonotic diseases in connection with pets. , This raises the question of the extent to which policy measures for companion animals must differ from those for livestock and wild animals. Pets have a higher emotional value in society compared to other animals. Since public policy literature states that acceptance of policy measures is essential to ensure effective implementation, pets' special status in society requires great sensitivity when developing socially acceptable measures for them in the area of epidemics. , Hence, it is crucial to attain insights into which measures are perceived as acceptable in order to design suitable policy measures. For this purpose, the present poster provides an overview of existing research on stakeholder acceptance of disease control measures for pets, and maps existing knowledge in the form of a systematic literature review.

Abstracts, poster presentations

Ethical challenges in policy making during the COVID-19 pandemic: results from an interview study with Swiss policy makers and scientists (Poster #1)

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Policy making and science were deeply intertwined during the COVID-19 pandemic, particularly in justifying health policy measures and ethical considerations being at the core of decision-making trade-offs. However, not much is known about the actual ethical challenges encountered by policy makers and scientists involved in policy advice. This study aims to explore the ethical challenges in COVID-19-related political decision-making as perceived by Swiss policy makers and scientists involved in policy making, the role of ethics advice, and what can be learned for future public health crises. Thirteen qualitative expert interviews were conducted with policy makers and scientists involved in COVID-19 policy decisions in Switzerland. We used inductive thematic content analysis to analyse the interviews. Key ethical challenges included making trade-offs between common vs. individual good and economic welfare vs. health of the population, proportionality of policy measures, and public capacity to handle uncertainty. Opinions varied on the sufficiency of ethical considerations on the policy level. Constraints included a lack of time in the fast-paced dynamic of the pandemic, ethics as a complex subject area, its overlap with law, too much focus on few topics such as vaccination-related questions, and individual character traits. There were strong calls for more ethics training, involvement of the public in the discourse, and for accompanying communication to build trust.

Certificate of Advanced Studies (CAS) in One Health (Poster #2)

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In October 2022, the Quadripartite (FAO, UNEP, WHO, WOAH) adopted a Joint Action Plan, which calls on its member countries to take priority actions in implementing the One Health approach. One of the axes is the training of professionals in the environment, human health, animal health, agriculture, and administration to equip them with the knowledge, competencies and tools for applying the One Health approach in their daily activities. To respond to this need, the Veterinary Public Health Institute is developing a Certificate of Advanced Studies (CAS) in One Health with the support of the University of Bern, the Vetsuisse Faculty and the MCID. Registration opening is planned for 2025.

BioPreparedness Biobank: Operation and Services (Poster #3)

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The BioPreparedness Biobank is now fully operational, serving as a state-of-the-art repository for high-risk pathogens within a Biosafety Level 3 (BSL-3) environment. Equipped with an advanced automated freezer systems and dedicated information management system, the biobank offers a comprehensive suite of services related to the requirements of pathogen management. These services include standardized deposit and retrieval processes and specialized support for regulatory compliance, inventory management and transfer processes. The collection in the biobank is growing with the integration of partner collections (Spiez Labor, VetSuisse) and especially through the production of synthetic viral genomes in yeast hosts. The Synthetic Genome platform is an essential and innovative part of the Biobank Core Activity providing access to modified or previously inaccessible strains. The BioPreparedness Biobank is fully operational, providing biobanking services meeting the high standards of pathogen management and enabling significant advancements in the research on high-risk pathogens.

Privacy-preserving synthetic data generation using Gaussian mixture copulas with an application to medicine (Poster #4)

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Synthetic data are used in various fields such as medicine to protect privacy, facilitate open research and for data augmentation. It aims to reproduce statistical characteristics of real-world data without revealing patient information at an individual level. In the recent years, deep generative networks have been used extensively for this task but they lack of interpretability and can overfit., In this work, we developed an interpretable statistical method to generate confidential synthetic data with a limited sample size. Our method based on copulas can model a broad class of continuous multivariate distributions, which gives us a very flexible approach to synthetic data generation. More specifically, we focus on the Gaussian mixture copula allowing to model data with a multi-modal dependence structure and arbitrary marginals. We assess the efficiency of our method both in terms of statistical utility and privacy. An application to a dataset collected on menopausal women patients at Inselspital in Bern is presented.

Assessing the role of prolonged close contact in the spread of respiratory viral infections in schools (AirChecker Study Phase 3) (Poster #5)

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Background: Crowded indoor settings play an essential role in the transmission of respiratory infections. We studied the transmission in schools and the importance of close contact.
Methods: We conducted a six-week longitudinal study from January-March 2024 in four school classes in Bern. We monitored daily close contact <1.5m) between students with wearable sensors and ventilation conditions (CO_2). We collected saliva samples three times a week and analysed them by qPCR. We also recorded reasons for absence and symptoms, and used questionnaires on students' well-being and social contacts.
Results: We included 69 students aged 13-15 years (participation rate: 82%); 26 (38%) were female, 41 (62%) male. The median daily maximum CO_2 level was 828 ppm (interquartile range 709-972) across classes. The social contact network documented mainly contacts within classes, and few intensive contacts. A total of 42 (60%) students tested positive for at least one virus. Rhinovirus (13, 19%), influenza A (13, 19%) and RSV (12, 17%) were the most common respiratory infections.
Conclusions: A wide range of non-SARS-CoV-2 respiratory viruses were detected in students, but no SARS-CoV-2. In future analyses, we will integrate the genomic and the social contact network into a probabilistic model to determine transmission in schools and its relationship to close contact.

BEready pilot study – zoonotic risk, closeness of human-animal contact and preventative health measures in household pets (Poster #6)

Gasser L.[1]; Hodel E.M.[2,3]; Iff F.[2]; Wegmüller S.[4]; Lim E.J.[2]; Grimm K.[2,5]; Wandeler G.[3,5]; Low N.[2,3]; Schuller S.[1,3]

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Background: BEready ("Bern get ready") is a longitudinal household cohort study to foster pandemic preparedness. Because many emerging diseases are zoonotic, the BEready cohort also includes dogs and cats of participating households.
Methods: In the pilot study, 29 cats and 15 dogs, belonging to 28 of 108 households, were enrolled. Participants completed an online questionnaire about their pets and the extent of their contact. We produced summary statistics of responses provided.
Results: Most of the animals lived in close contact with their owners, with 26/43 (60.5%) having access to their owner's bed and 38/43 (88.4%) to the sofa. Six/42 (14.3%) pets licked their owners face. Feeding raw meet was reported for 21/44 (47.7%) pets. Contact with livestock was noted for 15/43 (34.9%) pets. Thirty-nine/43 pets (90.7%) were vaccinated at least once and for 34/43 (79.1%) pets regular antiparasitic treatments were reported.
Conclusions: Dogs and cats in the pilot study are generally well cared for and have close physical contact with their owners. Therefore, there is a potential for zoonotic transmission of pathogens. There are also some behaviours which might elevate the risk for infectious diseases, such as feeding of raw meat, contact to livestock and not deworming the animals.

BEready – a population based cohort study to assess viral respiratory infections within households (Poster #8)

Grimm K.[1,2], _Hodel E.M._[1,3], _Gasser L._[4], _Wegmüller S._[5], _Schuller S._[3,4], _Magyar U._[6], _Iff F._[1], _Lim E._[1], _Furrer L._[7], _Bittel P._[3,7], _Low N._[1,3], _Wandeler G._[2,3]_

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During the COVID-19 pandemic, many countries lacked an appropriate research infrastructure to study emerging pathogens. We established BEready, a population-based cohort to study respiratory infections epidemiology in the canton of Bern, Switzerland.
Methods: We enrolled 108 households (pilot study: 161 adults, 32 children, 29 cats, 15 dogs). Self-sampling via nasal swabs was triggered by one of the following symptoms > 48h: cough, runny nose, sore throat, shortness of breath. Household members took swabs a week later to detect secondary cases. Samples were analysed for respiratory viruses using CE-IVD certified multiplex PCR panels.
Results: From May 2023 to April 2024, we observed 140 disease events among 79 households. 117 participants (mean age 45 (SD 21), 54% women) developed symptoms, most frequently runny nose (n = 132), cough (97), sore throat (89). We received 283 samples from 140 index cases, 119 family contacts, 21 cats and 3 dogs. Of 181 samples analysed, the following pathogens could be identified (index/family contact): 43 rhinovirus (30/13), 21 SARS-CoV2 (19/2), 4 human parainfluenza virus (2/2), 3 seasonal coronavirus OC43 (3/0), 2 influenza A virus (2/0), 2 RSV (2/0) and 1 bocavirus (1/0).
Conclusions: Self-sampling in households is feasible and will be extended to the full BEready cohort.

Governing under pressure and navigating blame and credit in times of crisis (Poster #9)

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This project sheds light on officeholders' blame deflection and credit claiming strategies when facing crisis-related pressure and simultaneously electoral politics. In the backdrop of transboundary crises, governments face the challenge of managing complex problems and coordinating tasks among different government levels. At the same time, such multi-level governance structures allow officeholders to shift blame to different actors. By combining qualitative and quantitative methods, this project examines media conferences by the Swiss and German Federal Ministers of Health throughout the COVID-19 pandemic. The findings reveal that, despite crisis-related pressure and electoral politics, Ministers of Health in consensus oriented political systems employ rather subtle and implicit forms of blame deflection, even praise other actors and claim credit particularly before elections in Germany. This project contributes to a better understanding of governments' communication strategies in times of crisis and during elections in federal systems and offers insights into the dynamics of complex governance structures, crisis management and policymaking.

Parasite infection and host resource acquisition drive the evolution of senescence (Poster #10)

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The evolution of senescence, one of the best-studied life-history traits, has received little attention in the context of parasite infection. The mortality of mosquitoes and other disease vectors is a critical parameter determining parasite transmission. We expect parasites to contribute to senescence in at least two ways. Firstly, they deplete their host's energy, which can gradually increase the host's rate of mortality. Secondly, infected hosts need energy for their defence. This increase in energy allocation can increase oxidative stress, which damages macromolecules and thus increases senescence. The host's life-history also feeds back to influence resource allocation and risk of parasite infection through epidemiological dynamics. To understand quantitatively the impact of these interactions on infection dynamics and on the evolution of senescence, we developed a multiscale model that describes within-host and among-host dynamics. We found that infection prevalence is maximised at intermediate levels of resource acquisition, but only when senescence depends on both oxidative stress and energy depletion. Furthermore, we found that for a single environmental condition, there are two evolutionary equilibria for the parasites' replication rate, and therefore senescence. More generally, the model's predictions are qualitatively similar to empirical observations, which indicate there is no one-way impact of host resource acquisition on infection dynamics and virulence evolution.

The "Bern, get ready" (BEready) pilot study about participation and feasibility: what have we learned? (Poster #11)

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Background: The lack of data at the start of the COVID-19 pandemic hampered evidence-based decision making. The objective of this study was to test the feasibility of BEready ("Bern, get ready", a population-based household cohort for pandemic preparedness.
Methods: In 2023, we enrolled households, sampled at random, in the canton of Bern. Adults, children and pets were eligible. The initial in-person (or animal) visit included blood sampling. The baseline questionnaire was completed online. Participants took nasal swabs during episodes of respiratory symptoms. At 12 months, they completed online questionnaires and provided a dried blood spot. Using logistic regression, we described the agreement to participate according to demographic and socio-economic variables.
Results: Of 1,338 households invited, 9% agreed to participate. 108 households were enrolled (193 people, 29 cats and 15 dogs). In multivariable analysis, participation was lower in households with 3+ people (adjusted odds ratio, aOR 0.3, 95% confidence interval, CI 0.19–0.46, p<0.001) and higher in households with upper secondary or higher education (aOR 2.83, 95%CI 1.15–9.37, p=0.046).
Conclusions: Online questionnaires and self-sampling are feasible methods for household cohort studies on pandemic preparedness. Community engagement could be a way to increase enrolment.

Vaccination status amongst human and animal participants of the BEready population-based household cohort study for pandemic preparedness in the canton of Bern, Switzerland (Poster #12)

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Background: The COVID-19 pandemic underscored the critical importance of vaccination to reduce severe illness and death. The "Bern, get ready" (BEready) cohort study is collecting vaccination data from households in the canton of Bern.
Methods: We enrolled 108 households (161 adults, 32 children, 29 cats, 15 dogs) in our pilot study. At enrolment in 2023, participants provided information about their and their pets' vaccination history. We extracted data from questionnaires and immunisation cards.
Results: Of 161 adults / 32 children, 158 (98.1%) / 30 (93.8%) reported having ever received any vaccine. Of 125 (77.6%) / 28 (87.5 %) with an immunisation card, 95 (76%) / 24 (92.85%) provided a copy of it. For COVID-19, 152 (94.4%) / 22 (68.8%) had received at least one dose of vaccine, >99% with an mRNA vaccine. In 82.8% of cats and 33.3% of dogs a full vaccination record was available. Of those, 37.5% of cats and 100% of dogs were vaccinated according to current recommendations.
Conclusions: Data about vaccination status were easy to collect. Vaccination data will be used to support future studies in BEready. Available data from pets suggests that for cats current vaccination recommendations are often not followed.

Navigating Uncertainty: From pandemic experiences to future imaginaries beyond marginalization (Poster #13)

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Intersections between sociocultural contexts, emotions, embodiment, and beliefs shaped the diversity of Covid-19 pandemic experiences. In this social anthropological study, we retrospectively explored how marginalized communities experienced the pandemic in the canton of Bern. We trained peer researchers to co-lead 7 semi-structured focus group discussions with n=53 undocumented migrants, LGBTQ+, and other marginalized community members from 05-09/2023. We used reflexive thematic analysis, supported by MAXQDA software. We will provide insights into people's perceptions of the past, present, and an imagined future: The sudden shift from normality to crisis disproportionately affected people in transitional life phases, such as recent migration, sexual identity development, unemployment, or lack of access to medication. Angst was often linked to information overload and uncertainty about COVID-19 and its progression. The concept of "in-betweenness" emerged, where individuals experienced the pandemic both personally and through the perspectives of others. Spatial-material changes such as mask use, vaccines and other measures influenced embodied pandemic experiences. Despite angst and uncertainty, the crisis offered a chance for agency and empowerment. Issues that remain unsolved in the present, including distrust in biomedical paradigms, and taboos surrounding violence and societal division, shape communities' imagined futures within the 'new normalcy'.

In Vitro and *Ex Vivo* Characterization Studies of Tick-Borne Encephalitis Virus (Poster #15)

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Climate change and urbanization heighten the threat of tick-borne encephalitis virus (TBEV), particularly in the Eurasian region. Our study addresses the escalating public health concern by investigating the European TBEV subtype and its severe neurological complications. To address this issue, nine different strains of TBEV, mainly originating from Switzerland, were selected and compared using in vivo and ex vivo models, including cell cultures and brain organotypic slice cultures. The results from both models revealed discernible differences among the strains in terms of virulence, highlighting the suitability of these models for quantitative experiments. Moreover, employing confocal imaging on full-thickness ex vivo slices provided higher resolution insights, uncovering variations in the neurotropism of the different strains.

Network Biological Risk - a "one health" network for the detection, prevention and management of biological risk in Switzerland (Poster #17)

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The Network Biological Risk was founded in 2023 to consolidate and optimise existing infrastructures and expertise in the field of biological risks. The aim is to establish and operate an effective national network with international reach for the management of biological events and infectious diseases with epidemic and pandemic potential. The network follows a "one health" approach and includes public institutions, private companies, non-profit organizations and authorities in the fields of research, diagnostics, vaccine and therapeutics development, biosafety and human and animal healthcare. By bringing together these different actors, the network promotes knowledge exchange across disciplines and sectors, strengthens synergies and develops strategies to fill gaps in the management of biological events. Emphasis is placed on the detection and prevention of biological risks and the development of corresponding technology platforms, in particular for diagnostics and vaccines.

Efficient horizontal antibiotic resistance gene transfer from *Escherichia coli* to *Enterococcus in vivo* independently of a discernible selective pressure (Poster #18)

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The transfer of antibiotic resistance (ABX) genes from *Escherichia coli* to other Gram-negative bacteria is a critical public health concern. In Gram-positive species such as *Enterococcus* rapid acquisition of ABX resistance genes is also well recognized. Horizontal gene transfer (HGT) between intestinal *E. coli* and *Enterococcus spp. in vivo* is less well studied. However, within the intestines, *E. coli* and *Enterococcus* coexist in a densely populated and interactive microbial ecosystem, providing abundant opportunities for HGT., Remarkably, we could show the uptake of ABX resistance genes from *E. coli* in *Enterococcus* even in the absence of direct antibiotic pressure in an *in vivo* setting. To date, the underlying selective forces remain unknown. The observed efficient and seemingly selection-independent ABX resistance gene acquisition by *Enterococcus* points toward a novel genetic mechanism. Understanding these mechanisms and dynamics holds enormous potential for developing strategies to mitigate the spread of antibiotic resistance and safeguard public health.

Interplay between the Malaria Parasite and the Host Microbiota (Poster #19)

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Traditionally, the narrative surrounding malaria has centered on the interactions between the parasite and the human host. However, recent scientific research has shown that although symptomatic _Plasmodium_ infection occurs exclusively in the bloodstream, pathophysiological changes such as increase in pro-inflammatory cell infiltration in the lamina propria, increased intestinal permeability and dysbiosis occur. This in turn revealed specific gut bacterial communities associated with both susceptibility and severity of malaria disease and humoral response following infection, acting as unexpected players in a tripartite interaction with the parasite and the host. But whether and to what extent the altered composition of the gut microbiome contributes to the antibody response and the repertoire of _Plasmodium_-specific antibodies is unknown. In this project, we aim to investigate the impact of the humoral immune response during _Plasmodium_ infection in the context of the presence or absence of the microbiome. Our studies revealed significant differences in mice's ability to control parasite proliferation based on their colonization status. Current analysis of spleen, mesenteric lymph node and intestine samples to assess the IgM, IgG2b and IgA antibody response together with flow cytometry of immune cell populations will provide us with qualitative and quantitative insight into the dynamics of these immune repertoires under the joint influence of the microbiota and the parasite.

The use of bacterial lysates as adjuvant in an influenza vaccine leads to neutrophil infiltration and increased adaptive immune responses in the lung (Poster #21)

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Current influenza vaccine formulations are suboptimal in inducing protective immune responses in vulnerable populations. We hypothesize that influenza vaccines can be improved by including adjuvants, which trigger innate immunity and boost adaptive responses. The bacterial lysate BronchoVaxom (BV) was shown to protect from respiratory infections through unspecific innate stimulation, but its adjuvant potential has not been investigated so far. We immunized mice twice intranasally with saline, BV, inactivated A/Brisbane/59/2007 (H1N1) virus, or both. Lung, bronchoalveolar lavage fluid (BAL), nasal associated lymphoid tissue (NALT), lung draining lymph nodes (dLN) and serum were harvested one week post boost. In lung and BAL, the frequencies of total CD4+ and CD8+ T cells and the frequency of IL-17-secreting CD4+ T cells were increased following BV+H1N1 immunization compared to H1N1 alone. In dLNs and NALT, these frequencies were unchanged, indicating a local lung response. Anti-H1N1 IgA titers in BAL and serum were higher in mice immunized with BV+H1N1 compared to H1N1 alone. Furthermore, neutrophils were massively recruited in BAL and lung 6 hours post BV immunization, resulting in an increased production of IL-1β in BAL. These results indicate the probable important role of neutrophils in the mechanisms of action of BV and the potential of BV as a mucosal adjuvant.

Machine learning-based short-term forecasting of COVID-19 hospital admissions using routine hospital data (Poster #23)

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Background and aims of study: The COVID-19 pandemic has highlighted the need for real-time infectious disease surveillance and forecasting systems to identify trends in transmission. In this study, we present a comparison of short-term forecasting models of hospital admissions due to COVID-19 based on routine hospital data from the canton of Bern.
Methods and Results: We compare the ability of various machine learning algorithms, e.g., tree-based models and neural networks, to forecast COVID-19 hospital admissions 1 to 4 weeks ahead based on retrospective electronic health record data from the Insel Group hospitals between 25 February 2020 and 30 June 2023. We will evaluate the algorithms on leave-future-out training time series with multiple cutting points and select the best-performing subset of features among the variables in the data set, e.g., the number of hospital admissions with specific diagnoses, laboratory results and measurements such as body temperature.
Implications: This study presents an innovative approach to use routine hospital data to forecast increases in hospital demand related to epidemic waves. With the increasing availability of electronic health records, tools such as our best-performing model will increasingly provide more precise information, which may improve evidence-based public health decision-making during future disease outbreaks.

Preparation of a 6-month prospective observational study to compare and predict respiratory tract infections in postmenopausal women with and without hormone replacement therapy (Poster #25)

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Aim: To conduct a 6-month prospective observational study in 400 postmenopausal women to assess the effect of hormone replacement therapy (HRT) on the frequency and severity of respiratory tract infections (RTIs) («MenoFlu») (target launch 9-2024).
Methods: In preparation for MenoFlu we have conducted a cross-sectional study in 253 apparently healthy women aged 40-69 years («Frauenherzen») aiming to assess whether data from a wearable device and questionnaires can be used to reduce the uncertainty of cardiovascular disease (CVD) risk prediction in the absence of blood lipid and/or blood pressure data benchmarked to the validated CVD risk calculator SCORE2.
Results: The «Frauenherzen» cohort is representative of the population that will be recruited for the «MenoFlu» study. 30.3% of women were current HRT user. 60% of women had at least one RTI in the previous 12 months. We will present preliminary results from the «Frauenherzen» study, e.g. the distribution of 1) reported RTI within the last 12 months, 2) RTI risk factors, 3) psychometric profiles. Furthermore, we will explore the associations between HRT (non-)use and participant characteristics and the number of past RTIs.
Conclusion: The «Frauenherzen» data will provide insights into the underlying factors that may influence the risk and severity of RTI.