Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) complete genome

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Abstract: Coronavirus disease 2019 (COVID-19) is a contagious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The first known case was identified in December 2019. The disease has since spread worldwide, leading to an ongoing pandemic. Symptoms of COVID-19 are variable, but often include fever, cough, headache, fatigue, breathing difficulties, and loss of smell and taste. Symptoms begin 1 - 14 days after exposure to the coronavirus. The standard diagnostic method is by detection of the virus' nucleic acid by real-time reverse transcription polymerase chain reaction (rRT-PCR), transcription-mediated amplification (TMA), or by reverse transcription loop-mediated isothermal amplification (RT-LAMP) from a nasopharyngeal swab. (https://en.wikipedia.org/wiki/COVID-19). Upto 12/1/2021 in USA, Total Cases are 48,377,531, Total accines Administered are 460,773,508, Total Deaths 778,489 (https://www.cdc.gov/coronavirus/2019-ncov/index.html). Here gives the gives **SARS-CoV-2** complete genome sequenced by China in 1/13/2020, as a reference for readers (https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3).

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Key words: COVID-19; SARS-CoV-2; genome; sequence; life; research; literature; cell

https://bmcresnotes.biomedcentral.com/articles/10.1186/1756-0500-5-52
https://www.youtube.com/watch?v=i66Lf2a_Pa8
https://journals.sagepub.com/doi/full/10.1177/2054358120938573

40 articles, meta appares 90 times in the abstract.

1. Introduction

Coronavirus disease 2019 (COVID-19) is a contagious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The first known case was identified in December 2019. The disease has since spread worldwide, leading to an ongoing pandemic. Symptoms of COVID-19 are variable, but often include fever, cough, headache, fatigue, breathing difficulties, and loss of smell and taste. Symptoms begin 1 - 14 days after exposure to the coronavirus. At least 30% of people who are infected do not develop noticeable symptoms. Of those people who develop symptoms noticeable enough to be classed as patients, around 80% develop mild to moderate symptoms, while 14% develop severe, and 5% suffer critical symptoms. Some people continue to experience a range of effects for months after recovery, and damage to organs has been observed. Multi-year studies are underway to further investigate the long-term effects of the disease. COVID-19 transmits when people breathe in air contaminated by droplets and small airborne particles containing the virus. People remain contagious for up to 20 days, and can spread the virus even if they do not develop symptoms. The standard diagnostic method is by detection of the virus' nucleic acid by real-time reverse transcription polymerase chain reaction (rRT-PCR), transcription-mediated amplification (TMA), or by reverse transcription loop-mediated isothermal amplification (RT-LAMP) from a nasopharyngeal swab. Several COVID-19 vaccines have been approved and distributed in various countries, which have initiated mass vaccination campaigns. Other preventive measures include physical or social distancing, quarantining, ventilation of indoor spaces, covering coughs and sneezes, hand washing, and keeping unwashed hands away from the face. The use of face masks or coverings has been recommended in public settings to minimize the risk of transmissions. Management involves the treatment of symptoms, supportive care, isolation, and experimental measures. (https://en.wikipedia.org/wiki/COVID-19). Upto 12/1/2021 in USA, Total Cases are 48,377,531, Total accines Administered are 460,773,508, Total Deaths 778,489 (https://www.cdc.gov/coronavirus/2019-ncov/index.html).

Here gives the gives **SARS-CoV-2** complete genome sequenced by China in 1/13/2020, as a reference for readers (https://www.ncbi.nlm.nih.gov/nuccore/MN908947.3).

Adeiza, S. S., et al. (2020). "Random effects meta-analysis of COVID-19/S. aureus partnership in co-infection." GMS Hyg Infect Control **15**: Doc29.

Aim: To assess the hypothesis that coinfection with SARS-CoV-2 and S. aureus exacerbates morbidity and mortality among patients, the study aims to report the pooled burden of S. aureus co-infections in patients hospitalized with COVID-19. Methods: We searched electronic databases and the bibliographies of pertinent papers for articles. We considered studies in which the core result was the number of patients with bacterial (S. aureus) co-infection. We performed random effects meta-analysis (REM) because the studies included were sampled from a universe of different populations and high heterogeneity was anticipated. Using the Cochran's Q statistic, the observed dispersion (heterogeneity) among effect sizes was assessed. The percentage of total variability in the estimates of the effect size was calculated with the I(2) index. To check for publication bias, the Egger weighted regression, Begg rank correlation and meta-funnel plot were used. We conducted meta-regression analysis to evaluate the variability between our outcomes and the covariates using computational options such as "methods of moments" and then "maximum likelihood" ratio. Results: We included 18 studies and retrieved data for 63,370 patients hospitalized with influenza-like illness, of which about 14,369 (22.67%) tested positive for COVID-19 by rRT-PCR. Of this number, 8,249 (57.4%) patient samples were analyzed. Bacterial, fungal and viral agents were detected in 3,038 (36.8%); S. aureus in 1,192 (39.2%). Five studies reported MRSA co-infection. Study quality ranged from 6 to 9 (median 7.1) on a JBI scale. From the meta-analysis, 33.1% patients were found to be coinfected (95%, CI 18.0 to 52.6%, Q=3473: df=17, I(2)=99.48%, p=0.00). The rate of S. aureus /COVID-19 co-infection was 25.6% (95% CI: 15.6 to 39.0, Q=783.4, df=17, I(2)=97.702%, p=0.003).The proportion of COVID-19/S. aureus co-infected patients with MRSA was 53.9% (95% CI, 24.5 to 80.9, n=66, 5 studies, Q=29.32, df=4, I(2)=86.369%, p=0.000). With the multivariate meta-regression model, study type (p=0.029), quality (p=0.000) and country (p=0.000) were significantly associated with heterogeneity. Conclusions: The pooled rates of S. aureus among COVID-19 patients documented in this study support the concern of clinicians about the presence of S. aureus in co-infections. Improved antibiotic stewardship can be accomplished through rapid diagnosis by longitudinal sampling of patients.

Amadori, D. and M. Maltoni (2004). "[Production and diffusion of scientific results in oncology]." Ann Ist Super Sanita **40**(3): 357-362.

The production of data from oncological research must follow specific steps linked to the type of research carried out. Research can be subdivided into the following areas: translational research, clinical research (Phases I, II and III), pharmacoutilization research, meta-analysis, and guidelines. A topic for discussion is represented by levels of evidence (LOE) of research, considered necessary for the transferral of therapeutic approaches to clinical practice. These involve production times of scientific research, and, in particular, the end-points deemed necessary by the appropriate regulatory bodies to permit the commercialization of drugs (problem of surrogate end-points). The interrelation between researchers and pharmaceutical companies has also recently become an object of reflection and research to find solutions that will guarantee both the independence of research and the legitimate needs of companies. A particularly important issue is the correct transmission of scientifically relevant data to the public by mass media sources. The communication of therapeutic advances obtained through research and scientific innovations should not lead to unrealistic expectations in the general population, which rather serve to weaken the already fragile relationship between the official world of oncology and the diverse universe of patients and their families.

Asarnow, D. and R. Singh (2013). "The impact of structural diversity and parameterization on maps of the protein universe." BMC Proc **7**(Suppl 7): S1.

BACKGROUND: Low dimensional maps of protein structure space (MPSS) provide a powerful global representation of all proteins. In such mappings structural relationships are depicted through spatial adjacency of points, each of which represents a molecule. MPSS can help in understanding the local and global topological characteristics of the structure space, as well as elucidate structure-function relationships within and between sets of proteins. A number of meta- and method-dependent parameters are involved in creating MPSS. However, at the state-of-the-art, a systematic investigation of the influence of these parameters on MPSS construction has yet to be carried out. Further, while specific cases in which MPSS out-perform pairwise distances for prediction of functional annotations have been noted, no general explanation for this phenomenon has yet been advanced. METHODS: We address the above questions within the technical context of creating MPSS by utilizing multidimensional scaling (MDS) for obtaining low-dimensional projections of structure alignment distances. RESULTS AND CONCLUSION: MDS is demonstrated as an effective method for construction of MPSS where related structures are co-located, even when their functional and evolutionary proximity cannot be deduced from distributions of pairwise comparisons alone. In particular, we show that MPSS exceed pairwise distance distributions in predictive capability for those annotations of shared function or origin which are characterized by a high level of structural diversity. We also determine the impact of the choice of structure alignment and MDS algorithms on the accuracy of such predictions.

Barnden, J. A. (2020). "The Meta-Dynamic Nature of Consciousness." Entropy (Basel) **22**(12).

How, if at all, consciousness can be part of the physical universe remains a baffling problem. This article outlines a new, developing philosophical theory of how it could do so, and offers a preliminary mathematical formulation of a physical grounding for key aspects of the theory. Because the philosophical side has radical elements, so does the physical-theory side. The philosophical side is radical, first, in proposing that the productivity or dynamism in the universe that many believe to be responsible for its systematic regularities is actually itself a physical constituent of the universe, along with more familiar entities. Indeed, it proposes that instances of dynamism can themselves take part in physical interactions with other entities, this interaction then being "meta-dynamism" (a type of meta-causation). Secondly, the theory is radical, and unique, in arguing that consciousness is necessarily partly constituted of meta-dynamic auto-sensitivity, in other words it must react via meta-dynamism to its own dynamism, and also in conjecturing that some specific form of this sensitivity is sufficient for and indeed constitutive of consciousness. The article proposes a way for physical laws to be modified to accommodate meta-dynamism, via the radical step of including elements that explicitly refer to dynamism itself. Additionally, laws become, explicitly, temporally non-local in referring directly to quantity values holding at times prior to a given instant of application of the law. The approach therefore implicitly brings in considerations about what information determines states. Because of the temporal non-locality, and also because of the deep connections between dynamism and time-flow, the approach also implicitly connects to the topic of entropy insofar as this is related to time.

Chisholm-Burns, M. A., et al. (2010). "US pharmacists' effect as team members on patient care: systematic review and meta-analyses." Med Care **48**(10): 923-933.

BACKGROUND: One approach postulated to improve the provision of health care is effective utilization of team-based care including pharmacists. OBJECTIVE: The objective of this study was to conduct a comprehensive systematic review with focused meta-analyses to examine the effects of pharmacist-provided direct patient care on therapeutic, safety, and humanistic outcomes. METHODS: The following databases were searched from inception to January 2009: NLM PubMed; Ovid/MEDLINE; ABI/INFORM; Health Business Fulltext Elite; Academic Search Complete; International Pharmaceutical Abstracts; PsycINFO; Cochrane Database of Systematic Reviews; National Guideline Clearinghouse; Database of Abstracts of Reviews of Effects; ClinicalTrials.gov; LexisNexis Academic Universe; and Google Scholar. Studies selected included those reporting pharmacist-provided care, comparison groups, and patient-related outcomes. Of these, 56,573 citations were considered. Data were extracted by multidisciplinary study review teams. Variables examined included study characteristics, pharmacists' interventions/services, patient characteristics, and study outcomes. Data for meta-analyses were extracted from randomized controlled trials meeting meta-analysis criteria. RESULTS: A total of 298 studies were included. Favorable results were found in therapeutic and safety outcomes, and meta-analyses conducted for hemoglobin A1c, LDL cholesterol, blood pressure, and adverse drug events were significant ($P < 0.05$), favoring pharmacists' direct patient care over comparative services. Results for humanistic outcomes were favorable with variability. Medication adherence, patient knowledge, and quality of life-general health meta-analyses were significant ($P < 0.05$), favoring pharmacists' direct patient care. CONCLUSIONS: Pharmacist-provided direct patient care has favorable effects across various patient outcomes, health care settings, and disease states. Incorporating pharmacists as health care team members in direct patient care is a viable solution to help improve US health care.

Corrao, S., et al. (2004). "[Biomedical information on the internet using search engines. A one-year trial]." Recenti Prog Med **95**(1): 22-26.

The internet is a communication medium and content distributor that provide information in the general sense but it could be of great utility regarding as the search and retrieval of biomedical information.

Search engines represent a great deal to rapidly find information on the net. However, we do not know whether general search engines and meta-search ones are reliable in order to find useful and validated biomedical information. The aim of our study was to verify the reproducibility of a search by key-words (pediatric or evidence) using 9 international search engines and 1 meta-search engine at the baseline and after a one year period. We analysed the first 20 citations as output of each searching. We evaluated the formal quality of Web-sites and their domain extensions. Moreover, we compared the output of each search at the start of this study and after a one year period and we considered as a criterion of reliability the number of Web-sites cited again. We found some interesting results that are reported throughout the text. Our findings point out an extreme dynamicity of the information on the Web and, for this reason, we advice a great caution when someone want to use search and meta-search engines as a tool for searching and retrieve reliable biomedical information. On the other hand, some search and meta-search engines could be very useful as a first step searching for defining better a search and, moreover, for finding institutional Web-sites too. This paper allows to know a more conscious approach to the internet biomedical information universe.

Cunalata-Paredes, A. V. and E. Gea-Izquierdo (2021). "COPD in the major nonsmoking adult: A systematic review and meta-analysis." Arch Environ Occup Health **76**(6): 319-329.

Chronic Obstructive Pulmonary Disease (COPD) main cause is attributed to active smokers, but there's a small percentage that comes from risk factors that have been less considered. The aim of this research was to identify the risk factors and the clinical presentation of the population over 64 years of age that lead to the development of COPD. A systematic review and a meta-analysis was performed. From the 92 studies interpreted, we identified seven studies on the presence of COPD in nonsmokers older adults, having a universe of 14,920 patients. The primary risk factor to trigger the development of COPD was secondhand smoking. The study defined the most common risk factors that currently trigger COPD development among nonsmokers and provided an insight into the potential clinical differences between nonsmokers and smokers.

Dubois, C. A., et al. (2017). "Which priority indicators to use to evaluate nursing care performance? A discussion paper." J Adv Nurs **73**(12): 3154-3167.

AIMS: A discussion of an optimal set of indicators that can be used on a priority basis to assess the performance of nursing care. BACKGROUND: Recent advances in conceptualization of nursing care performance, exemplified by the Nursing Care Performance Framework, have revealed a broad universe of potentially nursing-sensitive indicators. Organizations now face the challenge of selecting, from this universe, a realistic subset of indicators that can form a balanced and common scorecard. DESIGN: Discussion paper drawing on a systematic assessment of selected performance indicators. DATA SOURCES: Previous works, based on systematic reviews of the literature published between 1990 - 2014, have contributed to the development of the Nursing Care Performance Framework. These works confirmed a robust set of indicators that capture the universe of content currently supported by the scientific literature and cover all major areas of nursing care performance. Building on these previous works, this study consisted in gathering the specific evidence supporting 25 selected indicators, focusing on systematic syntheses, meta-analyses and integrative reviews. IMPLICATIONS FOR NURSING: This study has identified a set of 12 indicators that have sufficient breadth and depth to capture the whole spectrum of nursing care and that could be implemented on a priority basis. CONCLUSIONS: This study sets the stage for new initiatives aiming at filling current gaps in operationalization of nursing care performance. The next milestone is to set up the infrastructure required to collect data on these indicators and make effective use of them.

Evaristo, J. and J. J. McDonnell (2017). "Prevalence and magnitude of groundwater use by vegetation: a global stable isotope meta-analysis." Sci Rep **7**: 44110.

The role of groundwater as a resource in sustaining terrestrial vegetation is widely recognized. But the global prevalence and magnitude of groundwater use by vegetation is unknown. Here we perform a meta-analysis of plant xylem water stable isotope (delta(2)H and delta(18)O, n = 7367) information from 138 published papers - representing 251 genera, and 414 species of angiosperms (n = 376) and gymnosperms (n = 38). We show that the prevalence of groundwater use by vegetation (defined as the number of samples out of a universe of plant samples reported to have groundwater contribution to xylem water) is 37% (95% confidence interval, 28-46%). This is across 162 sites and 12 terrestrial biomes (89% of heterogeneity explained; Q-value = 1235; P < 0.0001). However, the magnitude of groundwater source contribution to the xylem water mixture (defined as the proportion of groundwater contribution in xylem water) is limited to 23% (95% CI, 20-26%; 95% prediction interval, 3-77%). Spatial analysis shows that the magnitude of groundwater source contribution increases with aridity. Our results suggest that while groundwater influence is globally prevalent, its proportional contribution to the total terrestrial transpiration is limited.

Fleiss, J. L. (1993). "The statistical basis of meta-analysis." Stat Methods Med Res **2**(2): 121-145.

Two models for study-to-study variation in a meta-analysis are presented, critiqued and illustrated. One, the fixed effects model, takes the studies being analysed as the universe of interest; the other, the random effects model, takes these studies as representing a sample from a larger population of possible studies. With emphasis on clinical trials, this paper illustrates in some detail the application of both models to three summary measures of the effect of an experimental intervention versus a control: the standardized difference for comparing two means, and the relative risk and odds ratio for comparing two proportions.

Furtado, G. E., et al. (2018). "Physical frailty and cognitive status over-60 age populations: A systematic review with meta-analysis." Arch Gerontol Geriatr **78**: 240-248.

The aim of this meta-analysis was to analyse the magnitude of the effect-size of the cognitive status of populations over 60 years of age, when comparing nonfrail versus pre-frail and nonfrail versus frail subgroups. A systematic review of prospective studies published from 2000 to 2017 was completed in Medline, B-on, Ebsco, Ebsco Health, Scielo, ERIC, LILACS and Sport discus databases and observational, cohort and cross-sectional studies were selected. The Mini-Mental State Examination to screening cognitive status and the Fried phenotype for assess physical frailty state was used as clinical outcomes. After applying additional search criteria, 14 manuscripts (26,798 old participants) were selected from an initial universe of 1681 identified. When comparing the scores of cognitive status of the participants who were non-frail (n=12,729, 47.4%) versus pre-frail (n=11,559, 43.2%) and non-frail versus frail (n=2452, 9.4%) subgroups, significant statistical differences were found for both comparisons (M+/-SD=0.60, 95%CI: 0.50-0.62, p<0.001 and M+/-SD=3.43, 95%CI: 2.26-4.60, p<0.001, respectively). It is clear that poor cognitive function is strongly closed associated with pre-frailty and frailty subgroups in older populations around the world.

Furtado, G. E., et al. (2019). "Physical Frailty and cognitive performance in older populations, part I: systematic review with meta-analysis." Cien Saude Colet **24**(1): 203-218.

The purpose of present study was to analyze the magnitude of the effect-size in the assessment of the cognitive status of populations over 60 years of age. The search strategy included PubMed, B-on, Ebsco, Ebsco Health, Scielo, Eric, Lilacs and Sportdiscus data bases. Only observational, cohort and cross-sectional studies were included in the meta-analysis. The central descriptors were elderly-frail, older adults, cognition and geriatric assessment and other additional terms. After applying the additional search criteria, 12 manuscripts were selected from an initial universe of 1,078 identified. When comparing the mean cognitive profile scores of the participants of the pre-frail (n =11,265) and frail (n = 2,460) groups, significant statistical differences were found (p<0,001), with lower mean scores emerging in frail-group. The results showed that cognitive decline is strongly associated with frailty, being a probable main clinical outcome. In this sense, any strategy aimed at mitigating or reversing the incidence of frailty with ageing should take into account that physical and cognitive frailty seem to have similar temporal trajectories.

Gambino, R. and G. Pulvirenti (2020). ""The Boundless Realm Where All Form Lies". Representing Imagination at the Crossway Between Literary and Neurocognitive Studies." Front Integr Neurosci **14**: 618605.

According to ancient texts on poetics, the concept of representation is deeply bound to that of "mimesis;" this last was intended in two main ways: as "imitation" and as "world construction." In Aristotle's Poetics, mimesis is theorized as the main form of "world simulation," giving rise to the complex universe of fiction. The concept of simulation plays a pivotal role in the neurocognitive theories on the embodied mind: within this frame, embodied simulation is intended as a functional prelinguistic activation of the human sensorimotor mechanism. This happens not only with regard to intercorporeality and intersubjectivity in the real world but also in relation to the process of imagination giving rise to literary imagery and to the reader's reception of the fictional world, since human beings share a common sensorimotor apparatus. Imagination is a central concept in the recent neurocognitive studies since it plays a core role in human life and in artistic production and reception. Imagination has been considered as a complex emergent cognitive faculty deeply intertwined with perception, memory, and consciousness, shaping human life and transforming the limited horizon of our perceptual affective understanding, being, and acting. Although there is an immense bulk of literature on this topic, imagination is still an elusive concept: its definition and understanding change according to different heuristic frames-mainly the philosophical, aesthetic, poetic, and cognitive ones-giving rise to debates about its modalities and effects, particularly in relation to the construction of aesthetic and symbolic constraints. In this paper, we claim that scientific research may take advantage from the literary representation of the imaginative faculties, which occurs in specific tests characterized by dynamic images and motion. In such meta-representation of the imagination, we witness the phenomenological emergence of endogenous dynamic processes involving a cluster of cognitive faculties, activated by triggering the reader's embodied simulation. One of the main German poets, Johann Wolfgang von Goethe, in the second part of his masterwork Faust II, intuitively represents the very process of the imagination and its responding to embodied simulation with regard both to the author's creative act and to its reception by the reader. At the crossway between literary and neurocognitive, this study aims to highlight the advantage offered to future transdisciplinary inquiries by the literary representation showing features and dynamics of the still mysterious phenomenon of the imagination.

Hardwicke, T. E. and J. P. A. Ioannidis (2018). "Mapping the universe of registered reports." Nat Hum Behav **2**(11): 793-796.

Heater, B. S., et al. (1988). "Nursing interventions and patient outcomes: a meta-analysis of studies." Nurs Res **37**(5): 303-307.

The 84 subject-studies and 4,146 individual subjects in this meta-analysis were obtained from nurse-conducted experimental research over an 8-year period. The entire universe of accessible subject-studies that met criteria was included. Although both published and unpublished research were included to protect the study from publication bias, there was no statistically significant difference in findings. The mean effect size for the sample of comparisons from the 84 studies was .59. The associated U3 value of 72.2 and r of .28 indicate that patients who receive research-based nursing interventions can expect 28% better outcomes than 72% of the patients who receive standard nursing care.

Hedges, L. V. and J. M. Schauer (2019). "Statistical analyses for studying replication: Meta-analytic perspectives." Psychol Methods **24**(5): 557-570.

Formal empirical assessments of replication have recently become more prominent in several areas of science, including psychology. These assessments have used different statistical approaches to determine if a finding has been replicated. The purpose of this article is to provide several alternative conceptual frameworks that lead to different statistical analyses to test hypotheses about replication. All of these analyses are based on statistical methods used in meta-analysis. The differences among the methods described involve whether the burden of proof is placed on replication or nonreplication, whether replication is exact or allows for a small amount of "negligible heterogeneity," and whether the studies observed are assumed to be fixed (constituting the entire body of relevant evidence) or are a sample from a universe of possibly relevant studies. The statistical power of each of these tests is computed and shown to be low in many cases, raising issues of the interpretability of tests for replication. (PsycINFO Database Record (c) 2019 APA, all rights reserved).

Hu, C., et al. (2016). "A Multi-Verse Optimizer with Levy Flights for Numerical Optimization and Its Application in Test Scheduling for Network-on-Chip." PLoS One **11**(12): e0167341.

We propose a new meta-heuristic algorithm named Levy flights multi-verse optimizer (LFMVO), which incorporates Levy flights into multi-verse optimizer (MVO) algorithm to solve numerical and engineering optimization problems. The Original MVO easily falls into stagnation when wormholes stochastically re-span a number of universes (solutions) around the best universe achieved over the course of iterations. Since Levy flights are superior in exploring unknown, large-scale search space, they are integrated into the previous best universe to force MVO out of stagnation. We test this method on three sets of 23 well-known benchmark test functions and an NP complete problem of test scheduling for Network-on-Chip (NoC). Experimental results prove that the proposed LFMVO is more competitive than its peers in both the quality of the resulting solutions and convergence speed.

Kibiki, G. S., et al. (2004). "Hepatosplenic schistosomiasis: a review." East Afr Med J **81**(9): 480-485.

BACKGROUND: Schistosomiasis is a granulomatous disease that is caused by infection with schistosomes. It is a major health threat in tropical and subtropical countries. Due to increased movement, all residents of the universe are at risk of contracting this infection. The infection goes through several stages, but the most life-threatening form and leading cause of mortality is hepatosplenic schistosomiasis (HSS). It is a chronic complication, which develops as a consequence of inflammatory response. This complication has not been adequately addressed or attended the and as a consequence most of patients presenting with this complication in our settings die. OBJECTIVES: To review literature on hepatosplenic schistosomiasis, to give the state-of-the-art management of HSS, to give our own experience on management of this complication and hence impart knowledge to medical personnel on HSS. DATA SOURCE: Literature is from Medline database and experience from gastroenterology clinics. Our own experience has been blended on top. STUDY SELECTION AND DATA EXTRACTION: We have selected material, which have been verified and can be applicable in resource poor-countries, where this problem is a major health threat. DATA SYNTHESIS: Based on published studies and meta-analyses and our own experience we have been able to draw conclusions on the current understanding of the subject. CONCLUSION: Hepatosplenic schistosomiasis is a deadly complication and occurs mainly in poor countries. Regular reviews and updates of our knowledge is important to enable stakeholders of health sector understand the problem and develop strategies on its management.

Lee, Y., et al. (2017). "Gih (Qi): Beyond Affordance." Front Psychol **8**: 556.

Ancient Eastern thought posited the ontological integration of the "mind-body world". The body-mind syncretism was a foundational precept in Eastern philosophy in which "Gih" ("Qi") was considered the basic entity of the universe and the human being. This study attempts to build a meta-theory and to demonstrate empirical designs for Gih, discussing the problems of the mind and body, or the subject and object, compared with the concept of "affordance" proposed by ecological approaches. The notion of Gih extends beyond that of affordance in that Gih activates a psychosomatic process between the physical condition and the mental state that facilitates the bi-directional interactions between subject and object. Therefore, the concept of Gih integrates mind and body, providing a means of comparing Eastern and Western philosophical systems.

Lukowski, J. K., et al. (2021). "Expanding Molecular Coverage in Mass Spectrometry Imaging of Microbial Systems Using Metal-Assisted Laser Desorption/Ionization." Microbiol Spectr **9**(1): e0052021.

Mass spectrometry imaging (MSI) is becoming an increasingly popular analytical technique to investigate microbial systems. However, differences in the ionization efficiencies of distinct MSI methods lead to biases in terms of what types and classes of molecules can be detected. Here, we sought to increase the molecular coverage of microbial colonies by employing metal-assisted laser desorption/ionization (MetA-LDI) MSI, and we compared our results to more commonly utilized matrix-assisted laser desorption/ionization MALDI MSI. We found substantial (approximately 67%) overlap in the molecules detected in our analysis of Bacillus subtilis colony biofilms using both methods, but each ionization technique did lead to the identification of a unique subset of molecular species. MetA-LDI MSI tended to identify more small molecules and neutral lipids, whereas MALDI MSI more readily detected other lipids and surfactin species. Putative annotations were made using METASPACE, Metlin, and the BsubCyc database. These annotations were then confirmed from analyses of replicate bacterial colonies using liquid extraction surface analysis tandem mass spectrometry. Additionally, we analyzed B. subtilis biofilms in a polymer-based emulated soil micromodel using MetA-LDI MSI to better understand bacterial processes and metabolism in a native, soil-like environment. We were able to detect different molecular signatures within the micropore regions of the micromodel. We also show that MetA-LDI MSI can be used to analyze microbial biofilms from electrically insulating material. Overall, this study expands the molecular universe of microbial metabolism that can be visualized by MSI. IMPORTANCE Matrix-assisted laser desorption/ionization mass spectrometry imaging is becoming an important technique to investigate molecular processes within microbial colonies and microbiomes under different environmental conditions. However, this method is limited in terms of the types and classes of molecules that can be detected. In this study, we utilized metal-assisted laser desorption/ionization mass spectrometry imaging, which expanded the range of molecules that could be imaged from microbial samples. One advantage of this technique is that the addition of a metal helps facilitate ionization from electrically nonconductive substrates, which allows for the investigation of biofilms grown in polymer-based devices, like soil-emulating micromodels.

Nelson, S. J., et al. (1993). "Recognizing new medical knowledge computationally." Proc Annu Symp Comput Appl Med Care: 409-413.

Can new medical knowledge be recognized computationally? We know knowledge is changing, and our knowledge-based systems will need to accommodate that change in knowledge on a regular basis if they are to stay successful. Computational recognition of these changes seems desirable. It is

unlikely that low level objects in the computational universe, bits and characters, will change much over time, higher level objects of language, where meaning begins to emerge, may show change. An analysis of ten arbitrarily selected paragraphs from the Medical Knowledge Self-Assessment Program of the American College of Physicians was used as a test bed for nominal phrase recognition. While there were words not known to Meta-1.2, only 8 of the 32 concepts new to the primary author were pointed to by new words. Use of a barrier word method was successful in identifying 23 of the 32 new concepts. Use of co-occurrence (in sentences) of putative nominal phrases may reduce the amount of human effort involved in recognizing the emergence of new relationships.

Nugent, W. R. (2011). "The (non)comparability of the correlation effect size across different measurement procedures: a challenge to meta-analysis as a tool for identifying "evidence based practices"." J Evid Based Soc Work **8**(3): 253-274.

Meta-analysis is becoming a principal tool for research synthesis and for the identification and justification of evidence based practices. A fundamental assumption in meta-analysis is that effect sizes based upon different measures are comparable. Recent work has challenged this assumption in the case of the standardized mean difference. In this article it is shown that population universe (true) score level correlation effect sizes, for the relationship between two constructs A and B, based upon different measures will be comparable only if construct validity invariance holds across the measures used to make inferences to A and the measures used to make inferences to B. The results of a simulation study are also reported which show that the results of a meta-analysis may be significantly and adversely affected by violations of construct validity invariance. Finally, it is concluded that the theoretical results obtained in this article, and the results of the simulation study, combine to suggest that the role of meta-analysis in the synthesis of social work research, and in the identification of evidence based practices, be de-emphasized until important questions about the sensitivity of meta-analysis to violations of construct validity invariance are answered.

Prabhu, S. and I. Pe'er (2012). "Ultrafast genome-wide scan for SNP-SNP interactions in common complex disease." Genome Res **22**(11): 2230-2240.

Long-range gene-gene interactions are biologically compelling models for disease genetics and can provide insights on relevant mechanisms and pathways. Despite considerable effort, rigorous interaction mapping in humans has remained prohibitively difficult due to computational and statistical limitations. We introduce a novel algorithmic approach to find long-range interactions in common diseases using a standard two-locus test that contrasts the linkage disequilibrium between SNPs in cases and controls. Our ultrafast method overcomes the computational burden of a genome x genome scan by using a novel randomization technique that requires 10x to 100x fewer tests than a brute-force approach. By sampling small groups of cases and highlighting combinations of alleles carried by all individuals in the group, this algorithm drastically trims the universe of combinations while simultaneously guaranteeing that all statistically significant pairs are reported. Our implementation can comprehensively scan large data sets (2K cases, 3K controls, 500K SNPs) to find all candidate pairwise interactions (LD-contrast) in a few hours-a task that typically took days or weeks to complete by methods running on equivalent desktop computers. We applied our method to the Wellcome Trust bipolar disorder data and found a significant interaction between SNPs located within genes encoding two calcium channel subunits: RYR2 on chr1q43 and CACNA2D4 on chr12p13 (LD-contrast test,). We replicated this pattern of interchromosomal LD between the genes in a separate bipolar data set from the GAIN project, demonstrating an example of gene-gene interaction that plays a role in the largely uncharted genetic landscape of bipolar disorder.

Rodriguez-Otero, L. M. (2020). "[Literature review on studies of women who have sex with women]." Medwave **20**(3): e7884.

Women who have sex with other women are a group that has been mostly invisible from public health policies. This category includes the group of lesbians, bisexual women, heterosexual behaviour, and homosexual practices, who have sexual relations with transsexual and transgender (trans) women and trans men who have sex with women. In the absence of a Spanish literature review of a study that addresses women who have sex with other women, a narrative bibliographic review was done using the PubMed/MEDLINE, Scopus, Dialnet, and Taylor and Francis databases. From a universe of 679 articles and after applying the inclusion criteria, 40 documents were analysed, from 1998 to 2019. Three meta-categories were identified (sexual education, the incidence of certain sexually transmitted infections, and aspects related to sexual practices), concerning prevention and risky behaviours. Women who have sex with other women are a particularly vulnerable group when it comes to sexually transmitted infections. These may include bacterial vaginitis, human

papillomavirus and acquired immunodeficiency virus. Likewise, there is a lack of specific training and information in health and education professionals, as well as in women who have sex with other women.

Sarazin, P., et al. (2016). "Trends in OSHA Compliance Monitoring Data 1979-2011: Statistical Modeling of Ancillary Information across 77 Chemicals." Ann Occup Hyg **60**(4): 432-452.

OBJECTIVES: The Integrated Management Information System (IMIS) is the largest multi-industry source of exposure measurements available in North America. However, many have suspected that the criteria through which worksites are selected for inspection are related to exposure levels. We investigated associations between exposure levels and ancillary variables in IMIS in order to understand the predictors of high exposure within an enforcement context. METHODS: We analyzed the association between nine variables (reason for inspection, establishment size, total amount of penalty, Occupational Safety and Health Administration (OSHA) plan, OSHA region, union status, inspection scope, year, and industry) and exposure levels in IMIS using multimodel inference for 77 agents. For each agent, we used two different types of models: (i) logistic models were used for the odds ratio (OR) of exposure being above the threshold limit value (TLV) and (ii) linear models were used for exposure concentrations restricted to detected results to estimate percent increase in exposure level, i.e. relative index of exposure (RIE). Meta-analytic methods were used to combine results for each variable across agents. RESULTS: A total of 511,047 exposure measurements were modeled for logistic models and 299,791 for linear models. Higher exposures were measured during follow-up inspections than planned inspections [meta-OR = 1.61, 95% confidence interval (CI): 1.44-1.81; meta-RIE = 1.06, 95% CI: 1.03-1.09]. Lower exposures were observed for measurements collected under state OSHA plans compared to measurements collected under federal OSHA (meta-OR = 0.82, 95% CI: 0.73-0.92; meta-RIE = 0.86, 95% CI: 0.81-0.91). A 'high' total historical amount of penalty relative to none was associated with higher exposures (meta-OR = 1.54, 95% CI: 1.40-1.71; meta-RIE = 1.18, 95% CI: 1.13-1.23). CONCLUSIONS: The relationships observed between exposure levels and ancillary variables across a vast majority of agents suggest that certain elements of OSHA's process of selecting worksites for inspection influence the exposure levels that OSHA inspectors encounter. Nonetheless, given the paucity of other sources of exposure data and the lack of a more demonstrably representative data source, our study considers the use of IMIS data for the estimation of exposures in the broader universe of worksites in the USA.

Schwimmer, J., et al. (2000). "A review of the literature for whole-body FDG PET in the management of patients with melanoma." Q J Nucl Med **44**(2): 153-167.

BACKGROUND: A review and meta-analysis of the literature on the use of 2-[18F]fluoro-2-deoxy-D-glucose (FDG) positron emission tomography (PET) in the detection of recurrent melanoma was conducted. The goals were to evaluate the quality of data reporting and to determine the overall values for the sensitivity and specificity of whole body FDG PET and management changes. METHODS: Guidelines to evaluate reporting within articles were formulated based on the United States medical payer source criteria for assessing studies reporting information on the utilization of new medical technology. A meta-analysis was conducted using methodology described in the peer reviewed literature. RESULTS: Our MEDLINE PLUS search resulted in a universe of 89 total articles. Within these 89, 19 were categorized in our targeted content area of which 13 were selected for analysis in our targeted subset, with the remaining 70 covering 24 different related content areas. Five of 13 (38%) articles in the target subset reported data which was adequate for incorporation into modeling objectives based on PET sensitivity and specificity values, with 1 of 13 (8%) in the same target subset reporting data adequate for modeling based on change-in-management data. Through a meta-analysis of the 13 target articles we determined, within a 95% confidence level, an overall sensitivity of 92% (95% confidence level 88.41%-95.82%) and an overall specificity of 90% (95% confidence level 83.26%-96.05%) as calculated by number of lesions, for FDG PET detecting recurrent melanoma throughout the whole body. Furthermore, limited data available for change-in-management suggests an overall FDG PET directed change-in-management value of 22%. CONCLUSIONS: Our review suggests that improvements can be made to more effectively report the results of these FDG PET studies. The overall values determined through the meta-analysis indicate the potential benefits of using FDG PET as a diagnostic/management tool. Furthermore, these values should prove useful to assessing the cost effectiveness of utilizing FDG PET in the management of recurrent melanoma.

Scott, T. A. and J. Piel (2019). "The hidden enzymology of bacterial natural product biosynthesis." Nat Rev Chem **3**(7): 404-425.

Bacterial natural products display astounding structural diversity, which, in turn, endows them with a remarkable range of biological activities that are of significant value to modern society. Such structural features are generated by biosynthetic enzymes that construct core scaffolds or perform peripheral modifications, and can thus define natural product families, introduce pharmacophores and permit metabolic diversification. Modern genomics approaches have greatly enhanced our ability to access and characterize natural product pathways via sequence-similarity-based bioinformatics discovery strategies. However, many biosynthetic enzymes catalyse exceptional, unprecedented transformations that continue to defy functional prediction and remain hidden from us in bacterial (meta)genomic sequence data. In this Review, we highlight exciting examples of unusual enzymology that have been uncovered recently in the context of natural product biosynthesis. These suggest that much of the natural product diversity, including entire substance classes, awaits discovery. New approaches to lift the veil on the cryptic chemistries of the natural product universe are also discussed.

Stout, N. and C. Bell (1991). "Effectiveness of source documents for identifying fatal occupational injuries: a synthesis of studies." Am J Public Health **81**(6): 725-728.

BACKGROUND: The complete and accurate identification of fatal occupational injuries among the US work force is an important first step in developing work injury prevention efforts. Numerous sources of information, such as death certificates, Workers' Compensation files, Occupational Safety and Health Administration (OSHA) files, medical examiner records, state health and labor department reports, and various combinations of these, have been used to identify cases of work-related fatal injuries. Recent studies have questioned the effectiveness of these sources for identifying such cases. METHODS: At least 10 studies have used multiple sources to define the universe of fatal work injuries within a state and to determine the capture rates, or proportion of the universe identified, by each source. Results of these studies, which are not all available in published literature, are summarized here in a format that allows researchers to readily compare the ascertainment capabilities of the sources. RESULTS: The overall average capture rates of sources were as follows: death certificates, 81%; medical examiner records, 61%; Workers' Compensation reports, 57%; and OSHA reports 32%. Variations by state and value added through the use of multiple sources are presented and discussed. CONCLUSIONS: This meta-analysis of 10 state-based studies summarizes the effectiveness of various source documents for capturing cases of fatal occupational injuries to help researchers make informed decisions when designing occupational injury surveillance systems.

Sun, X., et al. (2016). "MiR-548c impairs migration and invasion of endometrial and ovarian cancer cells via downregulation of Twist." J Exp Clin Cancer Res **35**: 10.

BACKGROUND: MicroRNAs (miRNAs) are a class of small non-coding RNAs, which post-transcriptionally repress the expression of genes involved in cancer initiation and progression. Although some miRNAs that target many signaling pathways (also called universe miRNAs) are supposed to play a global role in diverse human tumors, their regulatory functions in gynecological cancers remain largely unknown. We investigated the biological role and underlying mechanism of miR-548c (one universe miRNA) in endometrial and ovarian cancer. METHODS: The effects of miR-548c overexpression on cell proliferation, migration and invasion were studied in endometrial and ovarian cancer cells. TWIST1 (Twist) was identified as a direct miR-548c target by western blot analysis and luciferase activity assay. The expression of miR-548c and Twist were examined by qRT-PCR in endometrial and ovarian cancer tissues. RESULTS: Here, we report that miR-548c is down-regulated in endometrial and ovarian cancer tissues when compared to normal tissues, and our meta-analysis reveal that decreased miR-548c expression correlates with poor prognosis in endometrial cancer patients. We show that in endometrial and ovarian cancer cells, ectopic expression of miR-548c significantly inhibits whereas knockdown of miR-548c dramatically induces cancer cell proliferation, migration and invasion. By using luciferase reporter assay, we demonstrate that Twist, a known oncogene in endometrial and ovarian cancers, is a direct target of miR-548c. Furthermore, the expression of Twist partially abrogates the tumor suppressive effects of miR-548c on cell migration and invasion. CONCLUSION: These findings suggest that miR-548c directly downregulates Twist, and provide a novel mechanism for Twist upregulation in both endometrial and ovarian cancers. The use of miR-548c may hold therapeutic potential for the treatment of Twist-overexpressing tumors.

Tauber, S. and A. von Haeseler (2013). "Exploring the sampling universe of RNA-seq." Stat Appl Genet Mol Biol **12**(2): 175-188.

How deep is deep enough? While RNA-sequencing represents a well-established technology,

the required sequencing depth for detecting all expressed genes is not known. If we leave the entire biological overhead and meta-information behind we are dealing with a classical sampling process. Such sampling processes are well known from population genetics and thoroughly investigated. Here we use the Pitman Sampling Formula to model the sampling process of RNA-sequencing. By doing so we characterize the sampling by means of two parameters which grasp the conglomerate of different sequencing technologies, protocols and their associated biases. We differ between two levels of sampling: number of reads per gene and respectively, number of reads starting at each position of a specific gene. The latter approach allows us to evaluate the theoretical expectation of uniform coverage and the performance of sequencing protocols in that respect. Most importantly, given a pilot sequencing experiment we provide an estimate for the size of the underlying sampling universe and, based on these findings, evaluate an estimator for the number of newly detected genes when sequencing an additional sample of arbitrary size.

Van Ryzin, M. J., et al. (2016). "A component-centered meta-analysis of family-based prevention programs for adolescent substance use." Clin Psychol Rev **45**: 72-80.

Although research has documented the positive effects of family-based prevention programs, the field lacks specific information regarding why these programs are effective. The current study summarized the effects of family-based programs on adolescent substance use using a component-based approach to meta-analysis in which we decomposed programs into a set of key topics or components that were specifically addressed by program curricula (e.g., parental monitoring/behavior management, problem solving, positive family relations, etc.). Components were coded according to the amount of time spent on program services that targeted youth, parents, and the whole family; we also coded effect sizes across studies for each substance-related outcome. Given the nested nature of the data, we used hierarchical linear modeling to link program components (Level 2) with effect sizes (Level 1). The overall effect size across programs was .31, which did not differ by type of substance. Youth-focused components designed to encourage more positive family relationships and a positive orientation toward the future emerged as key factors predicting larger than average effect sizes. Our results suggest that, within the universe of family-based prevention, where components such as parental monitoring/behavior management are almost universal, adding or expanding certain youth-focused components may be able to enhance program efficacy.

Yang, K., et al. (2011). "Is CD133 a biomarker for cancer stem cells of colorectal cancer and brain tumors? A meta-analysis." Int J Biol Markers **26**(3): 173-180.

BACKGROUND: CD133 has been used to identify normal and cancer stem cells from several different tissues. Nowadays some researchers have reported that CD133 expression was not restricted to cancer stem cells (CSCs) of colorectal cancer and brain tumors, and CD133-negative subsets could also initiate tumors. We therefore performed a meta-analysis to assess the value of CD133 as a biomarker of CSCs for colorectal cancer and brain tumors. METHODS: A Medline search was performed to identify relevant studies for the analysis. The meta-analysis was done using RevMan 5.0 software. Outcome measures were colony formation rate and xenotransplanted tumor formation rate. RESULTS: Fifteen identified studies were available for analysis. For in vitro tests, there were no significant differences in the colony formation rates between CD133-positive and CD133-negative cells for colorectal cancer and brain tumors. For in vivo tests, the xenotransplanted tumor formation rate showed a significant difference between CD133-positive cells and CD133-negative cells in colorectal cancer only, corresponding to a risk difference of 0.40 (95%CI: 0.07, 0.73). Samples (cell lines versus tissues), applied biomarkers (combined versus single), and injection site were included as factors in sensitivity analyses, but the results were very inconsistent. CONCLUSIONS: CD133 may not be suitable as a universe biomarker in identifying CSCs of colorectal cancer and brain tumors. Additional studies are necessary to further delineate its role.

Zhu, M., et al. (2021). "Meta-Prism: Ultra-fast and highly accurate microbial community structure search utilizing dual indexing and parallel computation." Brief Bioinform **22**(1): 557-567.

Microbiome samples are accumulating at an unprecedented speed. As a result, a massive amount of samples have become available for the mining of the intrinsic patterns among them. However, due to the lack of advanced computational tools, fast yet accurate comparisons and searches among thousands to millions of samples are still in urgent need. In this work, we proposed the Meta-Prism method for comparing and searching the microbial community structures amongst tens of thousands of samples. Meta-Prism is at least 10 times faster than contemporary methods serving the same purpose and can provide very accurate search results. The method is based on three computational techniques: dual-

indexing approach for sample subgrouping, refined scoring function that could scrutinize the minute differences among samples, and parallel computation on CPU or GPU. The superiority of Meta-Prism on speed and accuracy for multiple sample searches is proven based on searching against ten thousand samples derived from both human and environments. Therefore, Meta-Prism could facilitate similarity search and in-depth understanding among massive number of heterogenous samples in the microbiome universe. The codes of Meta-Prism are available at: https://github.com/HUST-NingKang-Lab/metaPrism.

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