دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Population

1-Detection of mosaic and population-level structural variants with Sniffles2

By Smolka, M (Smolka, Moritz) [1] ; Paulin, LF (Paulin, Luis F.) [1] ; Grochowski, CM (Grochowski, Christopher M.) [2] ; Horner, DW (Horner, Dominic W.) [3] , [4] ; Mahmoud, M (Mahmoud, Medhat) [1] , [2] ; Behera, S (Behera, Sairam) [1] ; Kalef-Ezra, E (Kalef-Ezra, Ester) [3] , [4] ; Gandhi, M (Gandhi, Mira) [5] ; Hong, K (Hong, Karl) [6] ; Pehlivan, D (Pehlivan, Davut) [2] , [7] ;
(provided by Clarivate) Source NATURE BIOTECHNOLOGY Volume 42 Issue 10 Page 1571-+ DOI 10.1038/s41587-023-02024-y Published OCT 2024 Early Access JAN 2024 Indexed 2024-01-26 Document Type Article

Abstract

Calling structural variations (SVs) is technically challenging, but using long reads remains the most accurate way to identify complex genomic alterations. Here we present Sniffles2, which improves over current methods by implementing a repeat aware clustering coupled with a fast consensus sequence and coverage-adaptive filtering. Sniffles2 is 11.8 times faster and 29% more accurate than state-of-the-art SV callers across different coverages (5-50x), sequencing technologies (ONT and HiFi) and SV types. Furthermore, Sniffles2 solves the problem of family-level to population-level SV calling to produce fully genotyped VCF files. Across 11 probands, we accurately identified causative SVs around MECP2, including highly complex alleles with three overlapping SVs. Sniffles2 also enables the detection of mosaic SVs in bulk long-read data. As a result, we identified multiple mosaic SVs in brain tissue from a patient with multiple system atrophy. The identified SV showed a remarkable diversity within the cingulate cortex, impacting both genes involved in neuron function and repetitive elements. Sniffles2 detects mosaic structural variation from bulk long-read sequencing data.

Keywords

Keywords Plus

COPY NUMBERMECP2DUPLICATIONREARRANGEMENTSMECHANISMS

Population

2-Vitamin D: Evidence-Based Health Benefits and Recommendations for Population Guidelines

---

By Grant, WB (Grant, William B.) [1] ; Wimalawansa, SJ (Wimalawansa, Sunil J.) [2] ; Pludowski, P (Pludowski, Pawel) [3] ; Cheng, RZ (Cheng, Richard Z.) [4] , [5]

(provided by Clarivate) Source NUTRIENTS Volume 17 Issue 2 DOI 10.3390/nu17020277 Article Number 277 Published JAN 2025 Indexed 2025-02-01 Document Type Review

Abstract

Vitamin D offers numerous under-recognized health benefits beyond its well-known role in musculoskeletal health. It is vital for extra-renal tissues, prenatal health, brain function, immunity, pregnancy, cancer prevention, and cardiovascular health. Existing guidelines issued by governmental and health organizations are bone-centric and largely overlook the abovementioned extra-skeletal benefits and optimal thresholds for vitamin D. In addition, they rely on randomized controlled trials (RCTs), which seldom show benefits due to high baseline 25-hydroxyvitamin D [25(OH)D] concentrations, moderate supplementation doses, and flawed study designs. This review emphasizes the findings from prospective cohort studies showing that higher 25(OH)D concentrations reduce the risks of major diseases and mortality, including pregnancy and birth outcomes. Serum concentrations > 30 ng/mL (75 nmol/L) significantly lower disease and mortality risks compared to <20 ng/mL. With 25% of the U.S. population and 60% of Central Europeans having levels <20 ng/mL, concentrations should be raised above 30 ng/mL. This is achievable through daily supplementation with 2000 IU/day (50 mcg/day) of vitamin D3, which prevent diseases and deaths. Furthermore, a daily dose between 4000 and 6000 IU of vitamin D3 to achieve serum 25(OH)D levels between 40 and 70 ng/mL would provide greater protection against many adverse health outcomes. Future guidelines and recommendations should integrate the findings from observational perspective cohort studies and well-designed RCTs to improve public health and personalized care.

Keywords

Author Keywords

cancercardiovascular diseasechronic kidney diseasechronic lower respiratory diseasesCOVID-19dementiadiabetes mellitusEndocrine Societypregnancy

Keywords Plus

25-HYDROXYVITAMIN DD SUPPLEMENTATIONCARDIOVASCULAR-DISEASEMORTALITY-RATESD-RECEPTORCALCIUM SUPPLEMENTATIONUNITED-STATESD DEFICIENCYRISK-FACTORSCANCER-RISK

Population

3-APOE Genotype and Alzheimer Disease Risk Across Age, Sex, and Population Ancestry

---

By Belloy, ME (Belloy, Michael E.) [1] , [2] , [3] , [13] ; Andrews, SJ (Andrews, Shea J.) [4] ; Le Guen, Y (Le Guen, Yann) [1] ; Cuccaro, M (Cuccaro, Michael) [5] , [6] ; Farrer, LA (Farrer, Lindsay A.) [7] , [8] , [9] , [10] , [11] ; Napolioni, V (Napolioni, Valerio) [12] ; Greicius, MD (Greicius, Michael D.) [1] (provided by Clarivate) Source JAMA NEUROLOGY Volume 80 Issue 12 Page 1284-1294 DOI 10.1001/jamaneurol.2023.3599 Published DEC 2023 Early Access NOV 2023 Indexed 2024-04-18 Document Type Article

Abstract

ImportanceApolipoprotein E (APOE)*2 and APOE*4 are, respectively, the strongest protective and risk-increasing, common genetic variants for late-onset Alzheimer disease (AD), making APOE status highly relevant toward clinical trial design and AD research broadly. The associations of APOE genotypes with AD are modulated by age, sex, race and ethnicity, and ancestry, but these associations remain unclear, particularly among racial and ethnic groups understudied in the AD and genetics research fields. ObjectiveTo assess the stratified associations of APOE genotypes with AD risk across sex, age, race and ethnicity, and global population ancestry. Design, Setting, ParticipantsThis genetic association study included case-control, family-based, population-based, and longitudinal AD-related cohorts that recruited referred and volunteer participants. Data were analyzed between March 2022 and April 2023. Genetic data were available from high-density, single-nucleotide variant microarrays, exome microarrays, and whole-exome and whole-genome sequencing. Summary statistics were ascertained from published AD genetic studies. Main Outcomes and MeasuresThe main outcomes were risk for AD (odds ratios [ORs]) and risk of conversion to AD (hazard ratios [HRs]), with 95% CIs. Risk for AD was evaluated through case-control logistic regression analyses. Risk of conversion to AD was evaluated through Cox proportional hazards regression survival analyses. ResultsAmong 68 756 unique individuals, analyses included 21 852 East Asian (demographic data not available), 5738 Hispanic (68.2% female; mean [SD] age, 75.4 [8.8] years), 7145 non-Hispanic Black (hereafter referred to as Black) (70.8% female; mean [SD] age, 78.4 [8.2] years), and 34 021 non-Hispanic White (hereafter referred to as White) (59.3% female; mean [SD] age, 77.0 [9.1] years) individuals. There was a general, stepwise pattern of ORs for APOE*4 genotypes and AD risk across race and ethnicity groups. Odds ratios for APOE*34 and AD risk attenuated following East Asian (OR, 4.54; 95% CI, 3.99-5.17),White (OR, 3.46; 95% CI, 3.27-3.65), Black (OR, 2.18; 95% CI, 1.90-2.49) and Hispanic (OR, 1.90; 95% CI, 1.65-2.18) individuals. Similarly, ORs for APOE*22+23 and AD risk attenuated following White (OR, 0.53, 95% CI, 0.48-0.58), Black (OR, 0.69, 95% CI, 0.57-0.84), and Hispanic (OR, 0.89; 95% CI, 0.72-1.10) individuals, with no association for Hispanic individuals. Deviating from the global pattern of ORs, APOE*22+23 was not associated with AD risk in East Asian individuals (OR, 0.97; 95% CI, 0.77-1.23). Global population ancestry could not explain why Hispanic individuals showed APOE associations with less pronounced AD risk compared with Black and White individuals. Within Black individuals, decreased global African ancestry or increased global European ancestry showed a pattern of APOE*4 dosage associated with increasing AD risk, but no such pattern was apparent for APOE*2 dosage with AD risk. The sex-by-age-specific interaction effect of APOE*34 among White individuals (higher risk in women) was reproduced but shifted to ages 60 to 70 years (OR, 1.48; 95% CI, 1.10-2.01) and was additionally replicated in a meta-analysis of Black individuals and Hispanic individuals (OR, 1.72; 95% CI, 1.01-2.94). Conclusion and RelevanceThrough recent advances in AD-related genetic cohorts, this study provided the largest-to-date overview of the association of APOE with AD risk across age, sex, race and ethnicity, and population ancestry. These novel insights are critical to guide AD clinical trial design and research.

Keywords
Keywords Plus
APOLIPOPROTEIN-E GENOTYPEASSOCIATIONETHNICITY

دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Population

4-JADES: A large population of obscured, narrow-line active galactic nuclei at high redshift

---

By Scholtz, J (Scholtz, Jan) [1] , [2] ; Maiolino, R (Maiolino, Roberto) [1] , [2] , [3] ; D'Eugenio, F (D'Eugenio, Francesco) [1] , [2] ; Curtis-Lake, E (Curtis-Lake, Emma) [4] ; Carniani, S (Carniani, Stefano) [5] ; Charlot, S (Charlot, Stephane) [6] ; Curti, M (Curti, Mirko) [7] ; Silcock, MS (Silcock, Maddie S.) [4] ; Arribas, S (Arribas, Santiago) [8] ; Baker, W (Baker, William) [1] , [2] ; (provided by Clarivate) **Source ASTRONOMY & ASTROPHYSICS Volume 697 DOI 10.1051/0004-6361/202348804 Article Number A175 Published MAY 16 2025 Indexed 2025-05-23 Document Type Article**

Abstract

We present the identification of 41 narrow-line active galactic nuclei (type-2 AGN) candidates in the two deepest observations of the JADES spectroscopic survey with JWST/NIRSpec. The spectral coverage and the depth of our observations allowed us to select narrow-line AGN based on both rest-frame optical and UV emission lines up to z = 10. Due to the metallicity decrease of galaxies, at z > 3, the standard optical diagnostic diagrams (N2-BPT or S2-VO87) become unable to distinguish many AGN from other sources of photoionisation. Therefore, we also used high ionisation lines, such as He II lambda 4686, He II lambda 1640, [Ne IV] lambda 2422, [Ne V] lambda 3420, and N V lambda 1240, also in combination with other UV transitions, to trace the presence of AGN. Out of a parent sample of 209 galaxies, we identified 42 type-2 AGN (although ten of them are tentative), making the fraction of galaxies in JADES hosting type-2 AGN about 20 +/- 5%, which does not evolve significantly in the redshift range between 2 and 10. The selected type-2 AGN have estimated bolometric luminosities of 10(41.3 - 44.9) erg s(-1) and host-galaxy stellar masses of 10(7.2 - 9.3) M-circle dot. The star formation rates of the selected AGN host galaxies are consistent with those of the star-forming main sequence. The AGN host galaxies at z = 4 - 6 contribute similar to 18-30% to the UV luminosity function across different UV luminosity bins, increasing slightly with UV luminosity.

Keywords
Author Keywords
galaxies: evolutiongalaxies: high-redshiftgalaxies: ISMquasars: supermassive black holes

Keywords Plus
STAR-FORMING GALAXIESSUPERMASSIVE BLACK-HOLESSIMILAR-TO 5X-RAYDWARF GALAXIESHE IIINTERSTELLAR-MEDIUMSTELLAR POPULATIONNEBULAR EMISSIONHOST GALAXIES

Population

5-Association between Semaglutide and Nonarteritic Anterior Ischemic Optic Neuropathy A Multinational Population-Based Study

---

By Chou, CC (Chou, Chien-Chih) [1] , [2] , [3] ; Pan, SY (Pan, Ssu-Yu) [1] , [2] ; Sheen, YJ (Sheen, Yi-Jing) [1] , [3] , [4] , [5] ; Lin, JF (Lin, Jun-Fu) [6] ; Lin, CH (Lin, Ching-Heng) [6] , [7] , [8] , [9] ; Lin, HJ (Lin, Hui-Ju) [10] , [11] ; Wang, IJ (Wang, I-Jong) [12] , [13] ; Weng, CH (Weng, Chien-Hsiang) [14] , [15]

(provided by Clarivate) Source OPHTHALMOLOGY Volume 132 Issue 4 Page 381-388 DOI 10.1016/j.ophtha.2024.10.030 Published APR 2025 Early Access MAR 2025 Indexed 2025-04-27 Document Type Article

Abstract

Purpose: To investigate whether semaglutide increases the risk of nonarteritic anterior ischemic optic neuropathy (NAION) in the general population. Design: This retrospective cohort study used a deidentified global electronic medical records database. The enrollment period was extended from January 2017 to August 2023, with observations concluding in August 2024. Participants: This study included individuals with type 2 diabetes mellitus (T2DM) or obesity. They were further categorized into T2DM-only, obesity-only, and T2DM with obesity groups to assess the differences among these subgroups. The effects of semaglutide were compared with those of glucose-lowering or weight-loss medications other than glucagon-like peptide receptor agonists. Methods: Patient data were obtained from 160 health care organizations across 21 countries. Outcomes were evaluated at 1, 2, and 3 years of follow-up. A 1:1 propensity score matching was performed to balance age, sex, body mass index, hemoglobin A1C, medications, and underlying comorbidities. Cox regression models were used to compute hazard ratios (HRs) and 95% confidence intervals (CIs). Main Outcome Measures: The occurrence of NAION. Results: The final analysis included 37 314 participants with T2DM only, 129 690 participants with obesity only, and 130 216 participants with both T2DM and obesity. The results indicated that the administration of semaglutide was not associated with the development of NAION in the T2DM-only group (1-year follow-up: HR, 2.32; 95% CI, 0.60-8.97; 2 years: HR, 2.31; 95% CI, 0.86-6.17; 3 years: HR, 1.51; 95% CI, 0.71-3.25), the obesity-only group (1-year follow-up: HR, 0.41; 95% CI, 0.08-2.09; 2 years: HR, 0.67; 95% CI, 0.20-2.24; 3 years: HR, 0.72; 95% CI, 0.24-2.16), and the T2DM with obesity group (1 year follow-up: HR, 0.81; 95% CI, 0.42-1.57; 2 years: HR, 1.2; 95% CI, 0.74-1.94; 3 years: HR, 1.19; 95% CI, 0.78-1.82). Conclusions: The findings suggest that semaglutide may not be associated with an increased risk of NAION in the general population. Therefore, avoidance of semaglutide based solely on concerns regarding the risk of NAION may not be warranted because its potential benefits for blood glucose control and cardiovascular health likely outweigh its potential risks. Financial Disclosure(s): The author(s) have no proprietary or commercial interest in any materials discussed in this article. Ophthalmology 2025;132:381-388 (c) 2024 by the American Academy of Ophthalmology

Keywords
Author Keywords
Nonarteritic anterior ischemic optic neuropathySemaglutideStroke
Keywords Plus RATIORISK

Population

6-Individual-level risk factors for suicide mortality in the general population: an umbrella review

By Favril, L (Favril, Louis) [1] ; Yu, RQ (Yu, Rongqin) [2] ; Geddes, JR (Geddes, John R.) [2] ; Fazel, S (Fazel, Seena) [2] , [3] (provided by Clarivate) Source LANCET PUBLIC HEALTH Volume 8 Issue 11 Page E868-E877 DOI 10.1016/S2468-2667(23)00207-4 Published NOV 2023 Indexed 2023-11-26 Document Type Review

Abstract

Background Deaths by suicide remain a major public ealth hallenge worldwide. Identifying and targeting risk factors for suicide mortality is a potential approach to prevention. We aimed to summarise current knowledge on the range and magnitude of individual-level risk factors for suicide mortality in the general population and evaluate the quality of the evidence.Methods In this umbrella review, five bibliographic databases were systematically searched for articles published from database inception to Aug 31, 2022. We included meta-analyses of observational studies on individual-level risk factors for suicide mortality in the general population. Biological, genetic, perinatal, and ecological risk factors were beyond the scope of this study. Effect sizes were synthesised and compared across domains. To test robustness and consistency of the findings, evidence for small-study effects and excess significance bias (ie, the ratio between the overall meta-analysis effect size and that of its largest included study) was examined, and prediction intervals were calculated. Risk of bias was assessed by the Risk of Bias in Systematic Reviews instrument. The protocol was preregistered with PROSPERO (CRD42021230119). Findings We identified 33 meta-analyses on 38 risk factors for suicide mortality in the general population. 422 (93%) of the 454 primary studies included in the meta-analyses were from high-income countries. A previous suicide attempt and suicidal ideation emerged as strong risk factors (with effect sizes ranging from 6 to 16). Psychiatric disorders were associated with a greatly elevated risk of suicide mortality, with risk ratios in the range of 4-13. Suicide risk for physical illnesses (such as cancer and epilepsy) and sociodemographic factors (including unemployment and low education) were typically increased two-fold. Contact with the criminal justice system, state care in childhood, access to firearms, and parental death by suicide also increased the risk of suicide mortality. Among risk factors for which sex-stratified analyses were available, associations were generally similar for males and females. However, the quality of the evidence was limited by excess significance and high heterogeneity, and prediction intervals suggested poor replicability for almost two-thirds of identified risk factors.Interpretation A wide range of risk factors were identified across various domains, which underscores suicide mortality as a multifactorial phenomenon. Prevention strategies that span individual and population approaches should account for the identified factors and their relative strengths. Despite the large number of risk factors investigated, few associations were supported by robust evidence. Evidence of causal inference will need to be tested in high-quality study designs.Funding Wellcome Trust.Copyright (c) 2023 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY 4.0 license. Lancet 8: Institute Research Faculty Criminology, Ghent, Department University UK Prof Prof Correspondence Prof Psychiatry, Oxford seena.fazel@psych.ox.ac.uk

Keywords
Keywords Plus MENTAL-DISORDERSMETAANALYSISASSOCIATIONBEHAVIORSTHOUGHTSHEALTHBIAS

Population

7-Accelerating growth of human coastal populations at the global and continent levels: 2000-2018

By Cosby, AG (Cosby, A. G.) [1] ; Lebakula, V (Lebakula, V.) [2] ; Smith, CN (Smith, C. N.) [3] ; Wanik, DW (Wanik, D. W.) [4] ; Bergene, K (Bergene, K.) [1] , [5] ; Rose, AN (Rose, A. N.) [2] ; Swanson, D (Swanson, D.) [6] , [7] ; Bloom, DE (Bloom, D. E.) [8] Source SCIENTIFIC REPORTS Volume 14 Issue 1 DOI 10.1038/s41598-024-73287-x Article Number 22489 Published SEP 28 2024 Indexed 2024-10-11 Document Type Article

Abstract

Current human population growth along Earth's coasts is on a collision path with anticipated consequences of increasing natural and anthropogenic induced coastal hazards. Using recently-available ambient, dasymetric data, we developed methods to estimate annual continental and global coastal populations from (2000-2018) measured horizontally from the shoreline inward. We found: (1) large concentrations of population in relatively small bands and regions along the coast (similar to 2 billion within 50 km and similar to 1 billion within 10 km); (2) higher growth rates of coastal population than inland population (an addition of 463 million within 50 km and 233 million within 10 km); (3) strong influence of distance from the coast to predict population distribution; and (4) that macro population patterns and growth could be expressed and modeled as a power function at continental and global levels. Findings point to emerging macro population patterns along the coast as contributing to increasing anthropogenic effects on Earth systems and increasing human risks associated with sea-level rise, land subsidence, extreme weather, and public health. Reliable data tracking of the magnitude, spatial distribution and change of human populations in the coastal regions is essential for comprehensive coastal monitoring.

Keywords
Keywords Plus
CLIMATE-CHANGEGEOGRAPHYLANDSCANNIGHT

Population

8-Population genomics analyses reveal the role of hybridization in the rapid invasion of fall armyworm

---

By Wang, X (Wang, Xuan) [1] , [2] , [3] ; Du, ZY (Du, Zhenyong) [1] , [2] , [3] ; Duan, YE (Duan, Yuange) [1] , [2] , [3] ; Liu, SL (Liu, Shanlin) [1] , [2] , [3] ; Liu, J (Liu, Jie) [2] , [4] ; Li, BY (Li, Bingyan) [1] , [2] , [3] ; Ma, L (Ma, Ling) [1] , [2] , [3] ; Wu, YF (Wu, Yunfei) [5] ; Tian, L (Tian, Li) [1] , [2] , [3] ; Song, F (Song, Fan) [1] , [2] , [3] ; (provided by Clarivate) Source JOURNAL OF ADVANCED RESEARCH Volume 74 Page 43-55 DOI 10.1016/j.jare.2024.09.028 Published AUG 2025 Indexed 2025-08-26 Document Type Article

Abstract

Introduction: Invasive species pose a major threat to global biodiversity and agricultural productivity, yet the genomic mechanisms driving their rapid expansion into new habitats are not fully understood. The fall armyworm, Spodoptera frugiperda, originally from the Americas, has expanded its reach across the Old World, causing substantial reduction in crop yield. Although the hybridization between two genetically distinct strains has been well-documented, the role of such hybridization in enhancing the species' invasive capabilities remains largely unexplored. Objectives: This study aims to investigate the contributions of hybridization and natural selection to the rapid invasion of the fall armyworm. Methods: We analyzed the whole-genome resequencing data from 432 individuals spanning its global distribution. We identified the genomic signatures of selection associated with invasion and explored their linkage with the Tpi gene indicating strain differentiation. Furthermore, we detected signatures of balancing selection in native populations for candidate genes that underwent selective sweeps during the invasion process. Results: Our analysis revealed pronounced genomic differentiation between native and invasive populations. Invasive populations displayed a uniform genomic structure distinctly different from that of native populations, indicating hybridization between the strains during invasion. This hybridization likely contributes to maintaining high genetic diversity in invasive regions, which is crucial for survival and adaptation. Additionally, polymorphisms on genes under selection during invasion were possibly preserved through balancing selection in their native environments. Conclusion: Our findings reveal the genomic basis of the fall armyworm's successful invasion and rapid adaptation to new environments, highlighting the important role of hybridization in the dynamics of invasive species. (c) 2024 The Authors. Published by Elsevier B.V. on behalf of Cairo University. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Keywords
Author Keywords
Spodoptera frugiperdaFall armywormInvasionHybridizationBalancing selection

Keywords Plus
SPODOPTERA-FRUGIPERDAHOST STRAINSEVOLUTIONARY GENETICSLEPIDOPTERANOCTUIDAEHISTORYDIFFERENTIATIONIDENTIFICATIONSPECIATIONINFERENCE

Population

9-Global variations in lung cancer incidence by histological subtype in 2020: a population-based study

By Zhang, YT (Zhang, Yanting) [1] ; Vaccarella, S (Vaccarella, Salvatore) [2] ; Morgan, E (Morgan, Eileen) [2] ; Li, MM (Li, Mengmeng) [3] ; Etxeberria, J (Etxeberria, Jaione) [4] ; Chokunonga, E (Chokunonga, Eric) [5] ; Manraj, SS (Manraj, Shyam Shunker) [6] ; Kamate, B (Kamate, Bakarou) [7] ; Omonisi, A (Omonisi, Abidemi) [8] ; Bray, F (Bray, Freddie) [2]

(provided by Clarivate) Source LANCET ONCOLOGY Volume 24 Issue 11 Page 1206-1218 DOI 10.1016/S1470-2045(23)00444-8 Published NOV 2023 Early Access OCT 2023 Indexed 2023-11-30
Document Type Article

Abstract

Background Lung cancer is the second most common cancer worldwide, yet the distribution by histological subtype remains unknown. We aimed to quantify the global, regional, and national burden of lung cancer incidence for the four main subtypes in 185 countries and territories.Methods In this population-based study, we used data from Cancer Incidence in Five Continents Volume XI and the African Cancer Registry Network to assess the proportions of adenocarcinoma, squamous cell carcinoma, small-cell carcinoma, and large-cell carcinoma among all lung cancers by country, sex, and age group and subsequently applied these data to corresponding national (GLOBOCAN) estimates of lung cancer incidence in 2020. Unspecified morphologies were reallocated to specified subtypes. Age-standardised incidence rates were calculated using the world standard population to compare subtype risks worldwide, adjusted for differences in age composition between populations by country. Findings In 2020, there were an estimated 2 206 771 new cases of lung cancer, with 1 435 943 in males and 770 828 in females worldwide. In males, 560 108 (39%) of all lung cancer cases were adenocarcinoma, 351 807 (25%) were squamous cell carcinoma, 163 862 (11%) were small-cell carcinoma, and 115 322 (8%) were large-cell carcinoma cases. In females, 440 510 (57%) of all lung cancer cases were adenocarcinoma, 91 070 (12%) were squamous cell carcinoma, 68 224 (9%) were small-cell carcinoma, and 49 246 (6%) were large-cell carcinoma cases. Age-standardised incidence rates for adenocarcinoma, squamous cell carcinoma, small-cell carcinoma, and large-cell carcinoma, respectively, were estimated to be 12 center dot 4, 7 center dot 7, 3 center dot 6, and 2 center dot 6 per 100 000 person-years in males and 8 center dot 3, 1 center dot 6, 1 center dot 3, and 0 center dot 9 per 100 000 person-years in females worldwide. The incidence rates of adenocarcinoma exceeded those of squamous cell carcinoma in 150 of 185 countries in males and in all 185 countries in females. The highest age-standardised incidence rates per 100 000 person-years for adenocarcinoma, squamous cell carcinoma, small-cell carcinoma, and large-cell carcinoma, respectively, for males occurred in eastern Asia (23 center dot 5), central and eastern Europe (17 center dot 5), western Asia (7 center dot 2), and south-eastern Asia (11 center dot 0); and for females occurred in eastern Asia (16 center dot 0), northern America (5 center dot 4), northern America (4 center dot 7), and south-eastern Asia (3 center dot 4). The incidence of each subtype showed a clear gradient according to the Human Development Index for male and female individuals, with increased rates in high and very high Human Development Index countries. Interpretation Adenocarcinoma has become the most common subtype of lung cancer globally in 2020, with incidence rates in males exceeding those of squamous cell carcinoma in most countries, and in females in all countries. Our findings provide new insights into the nature of the

Population

global lung cancer burden and facilitates tailored national preventive actions within each world region.
Copyright (c) 2023 World Health Organization. Published by Elsevier Ltd. All rights reserved.

Keywords
Keywords Plus
AIR-POLLUTIONTRENDSADENOCARCINOMAPATTERNSSMOKINGBURDENRATESRISK

دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Population

10-Metabolic Dysfunction-Associated Steatotic Liver Disease Is Associated With Accelerated Brain Ageing: A Population-Based Study

---

By Wang, J (Wang, Jiao) [1] , [2] ; Yang, RR (Yang, Rongrong) [2] , [3] ; Miao, YY (Miao, Yuyang) [4] ; Zhang, XJ (Zhang, Xinjie) [5] ; Paillard-Borg, S (Paillard-Borg, Stephanie) [6] ; Fang, ZZ (Fang, Zhongze) [7] ; Xu, WL (Xu, Weili) [2] , [4] (provided by Clarivate) **Source LIVER INTERNATIONAL**
Volume 45 Issue 6 DOI 10.1111/liv.70109 Article Number e70109 Published JUN 2025 Indexed 2025-06-08 Document Type Article

Abstract

Background Metabolic dysfunction-associated steatotic liver disease (MASLD) is linked to cognitive decline and dementia risk. We aimed to investigate the association between MASLD and brain ageing and explore the role of low-grade inflammation. Methods Within the UK Biobank, 30 386 chronic neurological disorders-free participants who underwent brain magnetic resonance imaging (MRI) scans were included. Individuals were categorised into no MASLD/related SLD and MASLD/related SLD (including subtypes of MASLD, MASLD with increased alcohol intake [MetALD] and MASLD with other combined aetiology). Brain age was estimated using machine learning by 1079 brain MRI phenotypes. Brain age gap (BAG) was calculated as the difference between brain age and chronological age. Low-grade inflammation (INFLA) was calculated based on white blood cell count, platelet, neutrophil granulocyte to lymphocyte ratio and C-reactive protein. Data were analysed using linear regression and structural equation models. Results At baseline, 7360 (24.2%) participants had MASLD/related SLD. Compared to participants with no MASLD/related SLD, those with MASLD/related SLD had significantly larger BAG (beta = 0.86, 95% CI = 0.70, 1.02), as well as those with MASLD (beta = 0.59, 95% CI = 0.41, 0.77) or MetALD (beta = 1.57, 95% CI = 1.31, 1.83). The association between MASLD/related SLD and larger BAG was significant across middle-aged (< 60) and older (>= 60) adults, males and females, and APOE epsilon 4 carriers and non-carriers. INFLA mediated 13.53% of the association between MASLD/related SLD and larger BAG (p < 0.001). Conclusion MASLD/related SLD, as well as MASLD and MetALD, is associated with accelerated brain ageing, even among middle-aged adults and APOE epsilon 4 non-carriers. Low-grade systemic inflammation may partially mediate this association.

Keywords
Author Keywords
brain ageinflammationmagnetic resonance imagingMASLDmediation

Keywords Plus
MIDDLE-AGED ADULTSUK BIOBANKINFLAMMATIONPREVALENCEHEALTH

Population

11-Trends and cross-country inequalities in the global burden of osteoarthritis, 1990-2019: A population-based study

---

By Cao, F (Cao, Fan) [1] ; Xu, ZW (Xu, Zhiwei) [2] ; Li, XX (Li, Xiao-Xiao) [3] ; Fu, ZY (Fu, Zi-Yue) [4] ; Han, RY (Han, Rong-Ying) [5] ; Zhang, JL (Zhang, Jun-Lin) [5] ; Wang, P (Wang, Peng) [6] ; Hou, SP (Hou, Shengping) [1] ; Pan, HF (Pan, Hai-Feng) [3] (provided by Clarivate) Source AGEING RESEARCH REVIEWS Volume 99 DOI 10.1016/j.arr.2024.102382 Article Number 102382 Published AUG 2024 Early Access JUL 2024 Indexed 2024-07-14 Document Type Review

Abstract

Objective: To evaluate the trends and cross-country inequalities of global osteoarthritis (OA) burden over the last 30 years, and further predicted its changes to 2035. Methods: The estimates and 95 % uncertainty intervals (UIs) for incidence, prevalence, and disability -adjusted life -years (DALYs) of OA were extracted from Global Burden of Diseases, Injuries, and Risk Factors Study (GBD) 2019. We described OA epidemiology at global, regional, and national levels, analyzed 1990 -2019 trends in OA burden from overall, local, and multi -dimension scopes, decomposed OA burden according to population size, age structure, and epidemiologic changes, quantified cross-country inequalities in OA burden using standard health equity methods recommended by World Health Organization, and predicted changes of OA burden to 2035. Results: GBD 2019 estimated 527,811,871 (95 % UIs: 478,667,549 to 584,793,491) prevalent cases, 41,467,542 (95 % UIs: 36,875,471 to 46,438,409) incident cases and 18,948,965 (95 % UIs: 9,571,298 to 37,659,660) DALYs cases of OA worldwide in 2019, with the highest cases in East Asia and highest age -standardized rate (ASR) in high -income North America. The global burden of OA increased overall from 1990 to 2019 with the fastest growth observed in the first decade of the 21st century. Decomposition analysis revealed that OA knee (62.78 %), women (60.47 %), and middle sociodemographic index (SDI) quintile (32.35 %) were responsible for the most significant DALYs, whose changes were primarily driven by population growth and aging. A significant increase in SDI -related inequalities was detected, and the gap in DALYs between the highest SDI country and the lowest SDI country increased from 179.5 [95 % confidence interval (CI): 149.3 -209.8] per 100,000 in 1990 to 341.9 (95 % CI: 309.5 - 374.4) per 100,000 in 2019. Notably, although the ASR of incidence, prevalence, and DALYs of OA was predicted to decrease annually from 2020 to 2035, the case number of these metrics was predicted to keeping increasing, with predicted values of 52,870,737 [95 % credible interval (Crl): 39,330,063 to 66,411,411], 727,532,373 (95 % Crl: 542,765,783 to 912,298,962), and 25,986,983 (95 % Crl: 19,216,928 to 32,757,038) in 2035, respectively. Conclusions: As a major public health issue, the global burden of OA showed an overall increasing trend from 1990 to 2019, which was primarily driven by population growth and aging. Countries with high SDI shouldered disproportionately high OA burden, and the SDI -related inequalities across countries exacerbated over time. This study highlighted great challenges in the control and management of OA, including both growing case number and distributive inequalities worldwide, which may be instructive for better making public health policy and reasonably allocating medical source.

Keywords
Author Keywords

دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Population

OsteoarthritisIncidencePrevalenceDisability-adjusted life-yearsTrendsHealth inequalities

Keywords Plus
PERIOD-COHORT ANALYSISKNEE OSTEOARTHRITISINTRINSIC ESTIMATORHIPAGEDISEASEOBESITYIMPACTMORTALITYAMERICA

Population

12-Colorectal cancer incidence trends in younger versus older adults: an analysis of population-based cancer registry data

---

By Sung, HYA (Sung, Hyuna) [1] ; Siegel, RL (Siegel, Rebecca L.) [1] ; Laversanne, M (Laversanne, Mathieu) [2] ; Jiang, CX (Jiang, Chenxi) [1] ; Morgan, E (Morgan, Eileen) [2] ; Zahwe, M (Zahwe, Mariam) [2] ; Cao, Y (Cao, Yin) [3] , [4] , [5] ; Bray, F (Bray, Freddie) [2] ; Jemal, A (Jemal, Ahmedin) [1] (provided by Clarivate) Source LANCET ONCOLOGY Volume 26 Issue 1 Page 51-63 DOI 10.1016/S1470-2045(24)00600-4 Published JAN 2025 Early Access JAN 2025 Indexed 2025-01-25 Document Type Article

Abstract

Background Previous studies have shown that colorectal cancer incidence is increasing among younger adults (aged <50 years) in multiple high-income western countries in contrast with stabilising or decreasing trends in incidence in older adults (aged >= 50 years). This study aimed to investigate contemporary colorectal cancer incidence trends in younger adults versus older adults. Methods Colorectal cancer incidence data, including year of diagnosis, sex, and 5-year age group for 50 countries and territories, were extracted from the WHO-International Agency for Research on Cancer Cancer Incidence in Five Continents Plus database. The Human Development Index 2022 was retrieved from the United Nations Development Programme and grouped into very high (>080), high (070-079), medium (055-069), and low (<055) categories. Age-standardised incidence rates (ASR) per 100 000 person-years of early-onset (diagnosed between ages 25 to 49 years) and late-onset (diagnosed between ages 50 to 74 years) colorectal cancer (ICD 10th revision, C18-20), diagnosed between 1943-2003 and 2015-17, were calculated using the direct method and Segi-Doll world standard population). The primary study objective was to examine contemporary colorectal cancer incidence trends in younger adults versus older adults using data until 2017 from 50 countries and territories. Temporal trends were visualised and quantified with joinpoint regression, stratified by age at diagnosis (25-49 years or 50-74 years). Average annual percentage changes (AAPC) were estimated. Findings In the most recent 5 years (2013-17 for all countries analysed, except for Japan [2011-15], Spain [2012-16], and Costa Rica [2012-16]), the incidence rate of early-onset colorectal cancer was highest in Australia (ASR 165 [95% CI 161-169]), the USA (Puerto Rico; 152 [142-162]), New Zealand (148 [140-156]), the USA (148 [147-149]), and South Korea (143 [140-145]) and lowest in Uganda (44 [36-52]) and India (35 [33-37]). The highest incidence rates among older adults were found in the Netherlands (168 center dot 4 [1669-1700]) and Denmark (158 center dot 3 [1558-1609]) and the lowest were in Uganda (45 center dot 9 [385-514]) and India (23 center dot 5 [228-243]). In terms of AAPC, in the most recent 10 years, incidence rates of early-onset colorectal cancer were stable in 23 countries, but increased in 27 countries with the greatest annual increases in New Zealand (AAPC 397% [95% CI 244-552]), Chile (396% [126-674]), Puerto Rico (381% [268-496]), and England (359% [312-406]). 14 of the 27 countries and territories showed either stable (Argentina, France, Ireland, Norway, and Puerto Rico) or decreasing (Australia, Canada, Germany, Israel, New Zealand, Slovenia, England, Scotland, and the USA) trends in older adults.

For the 13 countries with increasing trends in both age groups, the average annual percentage increase in younger compared to older adults was higher in Chile, Japan, Sweden, the Netherlands, Croatia, and Finland; lower in Thailand, France (Martinique), Denmark, and Costa Rica; and similar in T & uuml;rkiye,

Population

Ecuador, and Belarus. The rise in early-onset colorectal cancer was faster among men than women in Chile, Puerto Rico, Argentina, Ecuador, Thailand, Sweden, Israel, and Croatia, whereas faster increase among women compared to men was in England, Norway, Australia, T & uuml;rkiye, Costa Rica, and Scotland. Interpretation Early-onset colorectal cancer incidence rates are rising in 27 of 50 countries and territories examined, with the rise either exclusive to early-onset disease or faster than the increase in older adults in 20 of the 27 countries. The findings underscore the need for intensified efforts to identify factors driving these trends and increase awareness to help facilitate early detection. Copyright (c) 2024 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY-NC-ND 4.0 license

Keywords
Keywords Plus
RISKCOUNTRIESMORTALITYOBESITY

Population

13-A 100 m gridded population dataset of China's seventh census using ensemble learning and big geospatial data

---

By Chen, YH (Chen, Yuehong) [1] ; Xu, CC (Xu, Congcong) [1] ; Ge, Y (Ge, Yong) [2] ; Zhang, XX (Zhang, Xiaoxiang) [1] ; Zhou, YN (Zhou, Ya'nan) [1] (provided by Clarivate) Source EARTH SYSTEM SCIENCE ATA Volume 16 Issue 8 Page 3705-3718 DOI 10.5194/essd-16-3705-2024 Published AUG 16 2024 Indexed 2024-08-21 Document Type Article

Abstract

China has undergone rapid urbanization and internal migration in the past few years, and its up-to-date gridded population datasets are essential for various applications. Existing datasets for China, however, suffer from either outdatedness or failure to incorporate data from the latest Seventh National Population Census of China, conducted in 2020. In this study, we develop a novel population downscaling approach that leverages stacking ensemble learning and big geospatial data to produce up-to-date population grids at a 100 m resolution for China using seventh census data at both county and town levels. The proposed approach employs stacking ensemble learning to integrate the strengths of random forest, XGBoost, and LightGBM through fusing their predictions in a training mechanism, and it delineates the inhabited areas from big geospatial data to enhance the gridded population estimation. Experimental results demonstrate that the proposed approach exhibits the best-fit performance compared to individual base models. Meanwhile, the out-of-sample town-level test set indicates that the estimated gridded population dataset (R-2=0.8936) is more accurate than existing WorldPop (R-2=0.7427) and LandScan (R-2=0.7165) products for China in 2020. Furthermore, with the inhabited area enhancement, the spatial distribution of population grids is intuitively more reasonable than the two existing products. Hence, the proposed population downscaling approach provides a valuable option for producing gridded population datasets. The estimated 100 m gridded population dataset of China holds great significance for future applications, and it is publicly available at https://doi.org/10.6084/m9.figshare.24916140.v1 (Chen et al., 2024b).

Keywords
Keywords Plus
GLOBAL POPULATIONNIGHTTIME LIGHTDENSITYLEVEL

Population

14-Intelligent rehabilitation in an aging population: empowering human-machine interaction for hand function rehabilitation through 3D deep learning and point cloud

---

By Xing, ZZ (Xing, Zhizhong) [1] , [2] , [3] ; Meng, ZJ (Meng, Zhijun) [2] ; Zheng, GF (Zheng, Gengfeng) [3] ; Ma, GL (Ma, Guolan) [4] , [5] ; Yang, L (Yang, Lin) [6] , [7] ; Guo, XJ (Guo, Xiaojun) [8] ; Tan, L (Tan, Li) [1] ; Jiang, YQ (Jiang, Yuanqiu) [1] ; Wu, HD (Wu, Huidong) [1]

(provided by Clarivate) Source FRONTIERS IN COMPUTATIONAL NEUROSCIENCE Volume 19 DOI 10.3389/fncom.2025.1543643 Article Number 1543643 Published MAY 2 2025
Indexed 2025-05-20 Document Type Article

Abstract

Human-machine interaction and computational neuroscience have brought unprecedented application prospects to the field of medical rehabilitation, especially for the elderly population, where the decline and recovery of hand function have become a significant concern. Responding to the special needs under the context of normalized epidemic prevention and control and the aging trend of the population, this research proposes a method based on a 3D deep learning model to process laser sensor point cloud data, aiming to achieve non-contact gesture surface feature analysis for application in the field of intelligent rehabilitation of human-machine interaction hand functions. By integrating key technologies such as the collection of hand surface point clouds, local feature extraction, and abstraction and enhancement of dimensional information, this research has constructed an accurate gesture surface feature analysis system. In terms of experimental results, this research validated the superior performance of the proposed model in recognizing hand surface point clouds, with an average accuracy of 88.72%. The research findings are of significant importance for promoting the development of non-contact intelligent rehabilitation technology for hand functions and enhancing the safe and comfortable interaction methods for the elderly and rehabilitation patients.

Keywords

Author Keywords

3D perceptionneural networkhuman-machine interactiondeep learningnon-contact rehabilitation

Population

15-Newton-Raphson-based optimizer: A new population-based metaheuristic algorithm for continuous optimization problems

---

By Sowmya, R (Sowmya, Ravichandran) [1] ; Premkumar, M (Premkumar, Manoharan) [2] ; Jangir, P (Jangir, Pradeep) [3] (provided by Clarivate) Source ENGINEERING APPLICATIONS OF ARTIFICIAL INTELLIGENCE Volume 128 DOI 10.1016/j.engappai.2023.107532 Article Number 107532 Published FEB 2024 Early Access DEC 2023 Indexed 2024-01-24 Document Type Article

Abstract

The Newton-Raphson-Based Optimizer (NRBO), a new metaheuristic algorithm, is suggested and developed in this paper. The NRBO is inspired by Newton-Raphson's approach, and it explores the entire search process using two rules: the Newton-Raphson Search Rule (NRSR) and the Trap Avoidance Operator (TAO) and a few groups of matrices to explore the best results further. The NRSR uses a Newton-Raphson method to improve the exploration ability of NRBO and increase the convergence rate to reach improved search space positions. The TAO helps the NRBO to avoid the local optima trap. The performance of NRBO was assessed using 64 benchmark numerical functions, including 23 standard benchmarks, 29 CEC2017 constrained benchmarks, and 12 CEC2022 benchmarks. In addition, the NRBO was employed to optimize 12 CEC2020 real-world constrained engineering optimization problems. The proposed NRBO was compared to seven state-of-the-art optimization algorithms, and the findings showed that the NRBO produced promising results due to its features, such as high exploration and exploitation balance, high convergence rate, and effective avoidance of local optima capabilities. In addition, the NRBO also validated on challenging wireless communication problem called the internet of vehicle problem, and the NRBO was able to find the optimal path for data transmission. Also, the performance of NRBO in training the deep reinforcement learning agents is also studied by considering the mountain car problem. The obtained results also proved the NRBO's excellent performance in handling challenging real-world engineering problems.

Keywords

Author Keywords

Constrained problemsInternet of vehicleMetaheuristicsNewton-Raphson-based optimizerNewton-Raphson search ruleTrap avoidance operator

Keywords Plus

BIO-INSPIRED OPTIMIZERSYSTEM OPTIMIZATIONCOLONYTIMES

Population

16-Newton-Raphson-based optimizer: A new population-based metaheuristic algorithm for continuous optimization problems

---

By Sowmya, R (Sowmya, Ravichandran) [1] ; Premkumar, M (Premkumar, Manoharan) [2] ; Jangir, P (Jangir, Pradeep) [3] (provided by Clarivate) Source ENGINEERING APPLICATIONS OF ARTIFICIAL INTELLIGENCE Volume 128 DOI 10.1016/j.engappai.2023.107532 Article Number 107532
Published FEB 2024 Early Access DEC 2023 Indexed 2024-01-24 Document Type Article

Abstract

The Newton-Raphson-Based Optimizer (NRBO), a new metaheuristic algorithm, is suggested and developed in this paper. The NRBO is inspired by Newton-Raphson's approach, and it explores the entire search process using two rules: the Newton-Raphson Search Rule (NRSR) and the Trap Avoidance Operator (TAO) and a few groups of matrices to explore the best results further. The NRSR uses a Newton-Raphson method to improve the exploration ability of NRBO and increase the convergence rate to reach improved search space positions. The TAO helps the NRBO to avoid the local optima trap. The performance of NRBO was assessed using 64 benchmark numerical functions, including 23 standard benchmarks, 29 CEC2017 constrained benchmarks, and 12 CEC2022 benchmarks. In addition, the NRBO was employed to optimize 12 CEC2020 real-world constrained engineering optimization problems. The proposed NRBO was compared to seven state-of-the-art optimization algorithms, and the findings showed that the NRBO produced promising results due to its features, such as high exploration and exploitation balance, high convergence rate, and effective avoidance of local optima capabilities. In addition, the NRBO also validated on challenging wireless communication problem called the internet of vehicle problem, and the NRBO was able to find the optimal path for data transmission. Also, the performance of NRBO in training the deep reinforcement learning agents is also studied by considering the mountain car problem. The obtained results also proved the NRBO's excellent performance in handling challenging real-world engineering problems.

Keywords
Author Keywords
Constrained problemsInternet of vehicleMetaheuristicsNewton-Raphson-based optimizerNewton-Raphson search ruleTrap avoidance operator

Keywords Plus
BIO-INSPIRED OPTIMIZERSYSTEM OPTIMIZATIONCOLONYTIMES

Population

17-Exploring the relationship between city size and carbon emissions: An integrated population-land framework

---

By Pu, JF (Pu, Jinfang) [1] , [2] ; Xia, FZ (Xia, Fangzhou) [1] (provided by Clarivate) Source APPLIED GEOGRAPHY Volume 177 DOI 10.1016/j.apgeog.2025.103571 Article Number 103571 Published APR 2025 Early Access FEB 2025 Indexed 2025-03-13 Document Type Article

Abstract

As global climate change intensifies and urbanization accelerates, research on urban climate change has become a global concern. Urban decision-makers must determine optimal city sizes to achieve net-zero emissions. However, previous studies have mainly focused on average relationships between city size and carbon emissions, overlooking non-linear dynamics. This study used urban scaling laws to investigate relationships between city size and carbon emissions from population and land perspective across 294 Chinese cities. Results showed a sublinear relationship between urban population size (UPS) and carbon emissions and a super-linear relationship between urban land size (ULS) and carbon emissions. Regionally, cities in central regions demonstrated higher carbon emission performance than those in western and eastern regions. The land perspective indicated lower carbon emission performance compared to the population perspective. Both perspectives revealed non-linear relationships between city size and urban scaling exponent for carbon emissions, characterized by multiple minima. Multiple city sizes can achieve optimal carbon emissions; however, only one ULS is ideal for a specific city size to ensure environmental sustainability. This study provides valuable policy insights for decision-makers in formulating reasonable low-carbon strategies.

Keywords

Author Keywords

City sizeCarbon emissionsPopulationUrban scaling laws

Keywords Plus

CO2 EMISSIONSDIOXIDE EMISSIONSRIVER DELTAURBAN FORMSURBANIZATIONIMPACTINCOMECHINADETERMINANTSFOOTPRINT

Population

18-Population genomics analyses reveal the role of hybridization in the rapid invasion of fall armyworm

---

By Wang, X (Wang, Xuan) [1] , [2] , [3] ; Du, ZY (Du, Zhenyong) [1] , [2] , [3] ; Duan, YE (Duan, Yuange) [1] , [2] , [3] ; Liu, SL (Liu, Shanlin) [1] , [2] , [3] ; Liu, J (Liu, Jie) [2] , [4] ; Li, BY (Li, Bingyan) [1] , [2] , [3] ; Ma, L (Ma, Ling) [1] , [2] , [3] ; Wu, YF (Wu, Yunfei) [5] ; Tian, L (Tian, Li) [1] , [2] , [3] ; Song, F (Song, Fan) [1] , [2] , [3] ; (provided by Clarivate) Source JOURNAL OF ADVANCED RESEARCH Volume 74 Page 43-55 DOI 10.1016/j.jare.2024.09.028 Published
AUG 2025 Indexed 2025-08-26 Document Type Article

Abstract

Introduction: Invasive species pose a major threat to global biodiversity and agricultural productivity, yet the genomic mechanisms driving their rapid expansion into new habitats are not fully understood. The fall armyworm, Spodoptera frugiperda, originally from the Americas, has expanded its reach across the Old World, causing substantial reduction in crop yield. Although the hybridization between two genetically distinct strains has been well-documented, the role of such hybridization in enhancing the species' invasive capabilities remains largely unexplored. Objectives: This study aims to investigate the contributions of hybridization and natural selection to the rapid invasion of the fall armyworm. Methods: We analyzed the whole-genome resequencing data from 432 individuals spanning its global distribution. We identified the genomic signatures of selection associated with invasion and explored their linkage with the Tpi gene indicating strain differentiation. Furthermore, we detected signatures of balancing selection in native populations for candidate genes that underwent selective sweeps during the invasion process. Results: Our analysis revealed pronounced genomic differentiation between native and invasive populations. Invasive populations displayed a uniform genomic structure distinctly different from that of native populations, indicating hybridization between the strains during invasion. This hybridization likely contributes to maintaining high genetic diversity in invasive regions, which is crucial for survival and adaptation. Additionally, polymorphisms on genes under selection during invasion were possibly preserved through balancing selection in their native environments. Conclusion: Our findings reveal the genomic basis of the fall armyworm's successful invasion and rapid adaptation to new environments, highlighting the important role of hybridization in the dynamics of invasive species. (c) 2024 The Authors. Published by Elsevier B.V. on behalf of Cairo University. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

Keywords
Author Keywords
Spodoptera frugiperdaFall armywormInvasionHybridizationBalancing selection

Keywords Plus
SPODOPTERA-FRUGIPERDAHOST STRAINSEVOLUTIONARY GENETICSLEPIDOPTERANOCTUIDAEHISTORYDIFFERENTIATIONIDENTIFICATIONSPECIATIONINFERENCE

Population

19-Little Red Dots: An Abundant Population of Faint Active Galactic Nuclei at $z \sim 5$ Revealed by the EIGER and FRESCO JWST Surveys

---

By Matthee, J (Matthee, Jorryt) [1] , [2] ; Naidu, RP (Naidu, Rohan P.) [3] ; Brammer, G (Brammer, Gabriel) [4] ; Chisholm, J (Chisholm, John) [5] ; Eilers, AC (Eilers, Anna-Christina) [3] ; Goulding, A (Goulding, Andy) [6] ; Greene, J (Greene, Jenny) [6] ; Kashino, D (Kashino, Daichi) [7] , [8] ; Labbe, I (Labbe, Ivo) [9] ; Lilly, SJ (Lilly, Simon J.) [1] ; (provided by Clarivate) **Source** ASTROPHYSICAL JOURNAL Volume 963 Issue 2 DOI 10.3847/1538-4357/ad2345, **Article Number** 129 **Published** MAR 1 2024 **Indexed** 2024-03-20 **Document Type** Article

Abstract

Characterizing the prevalence and properties of faint active galactic nuclei (AGNs) in the early Universe is key for understanding the formation of supermassive black holes (SMBHs) and determining their role in cosmic reionization. We perform a spectroscopic search for broad H alpha emitters at z approximate to 4-6 using deep JWST/NIRCam imaging and wide field slitless spectroscopy from the EIGER and FRESCO surveys. We identify 20 H alpha lines at z = 4.2-5.5 that have broad components with line widths from similar to 1200-3700 km s(-1), contributing similar to 30%-90% of the total line flux. We interpret these broad components as being powered by accretion onto SMBHs with implied masses similar to 10(7-8)M(circle dot). In the UV luminosity range M-UV,M-AGN+host = -21 to -18, we measure number densities of approximate to 10(-5) cMpc(-3). This is an order of magnitude higher than expected from extrapolating quasar UV luminosity functions (LFs). Yet, such AGN are found in only <1% of star-forming galaxies at z similar to 5. The number density discrepancy is much lower when compared to the broad H alpha LF. The SMBH mass function agrees with large cosmological simulations. In two objects, we detect complex H alpha profiles that we tentatively interpret as caused by absorption signatures from dense gas fueling SMBH growth and outflows. We may be witnessing early AGN feedback that will clear dust-free pathways through which more massive blue quasars are seen. We uncover a strong correlation between reddening and the fraction of total galaxy luminosity arising from faint AGN. This implies that early SMBH growth is highly obscured and that faint AGN are only minor contributors to cosmic reionization.

Keywords

Keywords Plus

STAR-FORMING GALAXIESBLACK-HOLE MASSQUASAR LUMINOSITY FUNCTIONLY-ALPHA-EMITTERSDIGITAL SKY SURVEYSTRONG H-BETALYMAN CONTINUUMHIGH-REDSHIFTCOSMIC REIONIZATIONSTELLAR MASS

Population

20-JWST meets *Chandra*: a large population of Compton thick, feedback-free, and intrinsically X-ray weak AGN, with a sprinkle of SNe

---

By Maiolino, R (Maiolino, Roberto) [1] , [2] , [3] ; Risaliti, G (Risaliti, Guido) [4] ; Signorini, M (Signorini, Matilde) [6] ; Trefoloni, B (Trefoloni, Bartolomeo) [1] , [4] , [5] ; Juodzbalis, I (Juodzbalis, Ignas) [1] , [2] ; Scholtz, J (Scholtz, Jan) [1] , [2] ; Übler, H (Ubler, Hannah) [1] , [2] ; D'Eugenio, F (D'Eugenio, Francesco) [2] ; Carniani, S (Carniani, Stefano) [7] , [12] ; Fabian, A (Fabian, Andy) [8] ;

(provided by Clarivate) Source MONTHLY NOTICES OF THE ROYAL ASTRONOMICAL SOCIETY
Volume 538 Issue 3 Page 1921-1943 DOI 10.1093/mnras/staf359 Published MAR 21 2025
Indexed 2025-03-28 Document Type Article

Abstract

We investigate the X-ray properties of a sample of 71 broad- and narrow-line active galactic nucleus (AGN) at 2<z<="" p="" style="font-family: "Source Sans Pro", "Noto Kufi Arabic", Arial, Helvetica, sans-serif; -webkit-font-smoothing: subpixel-antialiased !important;"></z

Keywords
Author Keywords
galaxies: high-redshiftgalaxies: nucleiquasars: supermassive black holesinfrared: galaxiesX-rays: galaxies

Keywords Plus
ACTIVE GALACTIC NUCLEISUPER-EDDINGTON ACCRETIONSIMILAR-TO 5ABSORBING COLUMN DENSITIESSUPERMASSIVE BLACK-HOLESABSORPTION-LINE QUASARSFIELD-NORTH SURVEYRED DOTSLUMINOSITY FUNCTIONCOSMIC EVOLUTION

Population

21-Worldwide trends in diabetes prevalence and treatment from 1990 to 2022: a pooled analysis of 1108 population-representative studies with 141 million participants

---

By Zhou, B (Zhou, Bin) ; Rayner, AW (Rayner, Archie W.) ; Gregg, EW (Gregg, Edward W.) ; Sheffer, KE (Sheffer, Kate E.) ; Carrillo-Larco, RM (Carrillo-Larco, Rodrigo M.) ; Bennett, JE (Bennett, James E.) ; Shaw, JE (Shaw, Jonathan E.) ; Paciorek, CJ (Paciorek, Christopher J.) ; Singleton, RK (Singleton, Rosie K.) ; Pires, AB (Pires, Ana Barradas) ; Group Author NCD Risk Factor Collaboration NCD-RisC (NCD Risk Factor Collaboration NCD-RisC) (provided by Clarivate) Source LANCET Volume 404 Issue 10467 Page 2077-2093 DOI 10.1016/S0140-6736(24)02317-1 Published NOV 23 2024 Early Access NOV 2024 Indexed 2025-01-11 Document Type Article

Abstract

Background Diabetes can be detected at the primary health-care level, and effective treatments lower the risk of complications. There are insufficient data on the coverage of treatment for diabetes and how it has changed. We estimated trends from 1990 to 2022 in diabetes prevalence and treatment for 200 countries and territories.

Methods We used data from 1108 population-representative studies with 141 million participants aged 18 years and older with measurements of fasting glucose and glycated haemoglobin (HbA(1c)), and information on diabetes treatment. We defined diabetes as having a fasting plasma glucose (FPG) of 7.0 mmol/L or higher, having an HbA(1c) of 6.5% or higher, or taking medication for diabetes. We defined diabetes treatment as the proportion of people with diabetes who were taking medication for diabetes. We analysed the data in a Bayesian hierarchical meta-regression model to estimate diabetes prevalence and treatment.

Findings In 2022, an estimated 828 million (95% credible interval [CrI] 757-908) adults (those aged 18 years and older) had diabetes, an increase of 630 million (554-713) from 1990. From 1990 to 2022, the age-standardised prevalence of diabetes increased in 131 countries for women and in 155 countries for men with a posterior probability of more than 0.80. The largest increases were in low-income and middle-income countries in southeast Asia (eg, Malaysia), south Asia (eg, Pakistan), the Middle East and north Africa (eg, Egypt), and Latin America and the Caribbean (eg, Jamaica, Trinidad and Tobago, and Costa Rica). Age-standardised prevalence neither increased nor decreased with a posterior probability of more than 0.80 in some countries in western and central Europe, sub-Saharan Africa, east Asia and the Pacific, Canada, and some Pacific island nations where prevalence was already high in 1990; it decreased with a posterior probability of more than 0.80 in women in Japan, Spain, and France, and in men in Nauru. The lowest prevalence in the world in 2022 was in western Europe and east Africa for both sexes, and in Japan and Canada for women, and the highest prevalence in the world in 2022 was in countries in Polynesia and Micronesia, some countries in the Caribbean and the Middle East and north Africa, as well as Pakistan and Malaysia. In 2022, 445 million (95% CrI 401-496) adults aged 30 years or older with diabetes did not receive treatment (59% of adults aged 30 years or older with diabetes), 3.5 times the number in 1990. From 1990 to 2022, diabetes treatment coverage increased in 118 countries for women and 98 countries for men with a posterior probability of more than 0.80. The largest improvement in treatment coverage was in some countries from central and western Europe and Latin America (Mexico, Colombia, Chile, and

Population

Costa Rica), Canada, South Korea, Russia, Seychelles, and Jordan. There was no increase in treatment coverage in most countries in sub-Saharan Africa; the Caribbean; Pacific island nations; and south, southeast, and central Asia. In 2022, age-standardised treatment coverage was lowest in countries in sub-Saharan Africa and south Asia, and treatment coverage was less than 10% in some African countries. Treatment coverage was 55% or higher in South Korea, many high-income western countries, and some countries in central and eastern Europe (eg, Poland, Czechia, and Russia), Latin America (eg, Costa Rica, Chile, and Mexico), and the Middle East and north Africa (eg, Jordan, Qatar, and Kuwait).

Interpretation In most countries, especially in low-income and middle-income countries, diabetes treatment has not increased at all or has not increased sufficiently in comparison with the rise in prevalence. The burden of diabetes and untreated diabetes is increasingly borne by low-income and middle-income countries. The expansion of health insurance and primary health care should be accompanied with diabetes programmes that realign and resource health services to enhance the early detection and effective treatment of diabetes. Copyright (c) 2024 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY 4.0 license.

Keywords

Keywords Plus

IMPAIRED GLUCOSE-TOLERANCELIFE-STYLE INTERVENTIONCARDIOVASCULAR-DISEASEGLOBAL EPIDEMICPLASMA-GLUCOSEFOLLOW-UPPREVENTIONMANAGEMENTMELLITUSHEALTH

Population

22-Worldwide trends in diabetes prevalence and treatment from 1990 to 2022: a pooled analysis of 1108 population-representative studies with 141 million participants

---

By Zhou, B (Zhou, Bin) ; Rayner, AW (Rayner, Archie W.) ; Gregg, EW (Gregg, Edward W.) ; Sheffer, KE (Sheffer, Kate E.) ; Carrillo-Larco, RM (Carrillo-Larco, Rodrigo M.) ; Bennett, JE (Bennett, James E.) ; Shaw, JE (Shaw, Jonathan E.) ; Paciorek, CJ (Paciorek, Christopher J.) ; Singleton, RK (Singleton, Rosie K.) ; Pires, AB (Pires, Ana Barradas) ; Group Author NCD Risk Factor Collaboration NCD-RisC (NCD Risk Factor Collaboration NCD-RisC) (provided by Clarivate) **Source LANCET Volume 404 Issue 10467 Page 2077-2093 DOI 10.1016/S0140-6736(24)02317-1 Published NOV 23 2024 Early Access NOV 2024 Indexed 2025-01-11 Document Type Article**

Abstract

Background Diabetes can be detected at the primary health-care level, and effective treatments lower the risk of complications. There are insufficient data on the coverage of treatment for diabetes and how it has changed. We estimated trends from 1990 to 2022 in diabetes prevalence and treatment for 200 countries and territories. Methods We used data from 1108 population-representative studies with 141 million participants aged 18 years and older with measurements of fasting glucose and glycated haemoglobin (HbA(1c)), and information on diabetes treatment. We defined diabetes as having a fasting plasma glucose (FPG) of 7.0 mmol/L or higher, having an HbA(1c) of 6.5% or higher, or taking medication for diabetes. We defined diabetes treatment as the proportion of people with diabetes who were taking medication for diabetes. We analysed the data in a Bayesian hierarchical meta-regression model to estimate diabetes prevalence and treatment.Findings In 2022, an estimated 828 million (95% credible interval [CrI] 757-908) adults (those aged 18 years and older) had diabetes, an increase of 630 million (554-713) from 1990. From 1990 to 2022, the age-standardised prevalence of diabetes increased in 131 countries for women and in 155 countries for men with a posterior probability of more than 0.80. The largest increases were in low-income and middle-income countries in southeast Asia (eg, Malaysia), south Asia (eg, Pakistan), the Middle East and north Africa (eg, Egypt), and Latin America and the Caribbean (eg, Jamaica, Trinidad and Tobago, and Costa Rica). Age-standardised prevalence neither increased nor decreased with a posterior probability of more than 0.80 in some countries in western and central Europe, sub-Saharan Africa, east Asia and the Pacific, Canada, and some Pacific island nations where prevalence was already high in 1990; it decreased with a posterior probability of more than 0.80 in women in Japan, Spain, and France, and in men in Nauru. The lowest prevalence in the world in 2022 was in western Europe and east Africa for both sexes, and in Japan and Canada for women, and the highest prevalence in the world in 2022 was in countries in Polynesia and Micronesia, some countries in the Caribbean and the Middle East and north Africa, as well as Pakistan and Malaysia. In 2022, 445 million (95% CrI 401-496) adults aged 30 years or older with diabetes did not receive treatment (59% of adults aged 30 years or older with diabetes), 3.5 times the number in 1990. From 1990 to 2022, diabetes treatment coverage increased in 118 countries for women and 98 countries for men with a posterior probability of more than 0.80. The largest improvement in treatment coverage was in some countries from central and western Europe and Latin America (Mexico, Colombia, Chile, and Costa Rica), Canada, South Korea, Russia, Seychelles, and Jordan.

دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Population

There was no increase in treatment coverage in most countries in sub-Saharan Africa; the Caribbean; Pacific island nations; and south, southeast, and central Asia. In 2022, age-standardised treatment coverage was lowest in countries in sub-Saharan Africa and south Asia, and treatment coverage was less than 10% in some African countries. Treatment coverage was 55% or higher in South Korea, many high-income western countries, and some countries in central and eastern Europe (eg, Poland, Czechia, and Russia), Latin America (eg, Costa Rica, Chile, and Mexico), and the Middle East and north Africa (eg, Jordan, Qatar, and Kuwait). Interpretation In most countries, especially in low-income and middle-income countries, diabetes treatment has not increased at all or has not increased sufficiently in comparison with the rise in prevalence. The burden of diabetes and untreated diabetes is increasingly borne by low-income and middle-income countries. The expansion of health insurance and primary health care should be accompanied with diabetes programmes that realign and resource health services to enhance the early detection and effective treatment of diabetes. Copyright (c) 2024 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY 4.0 license.

Keywords

Keywords Plus

IMPAIRED GLUCOSE-TOLERANCELIFE-STYLE INTERVENTIONCARDIOVASCULAR-DISEASEGLOBAL EPIDEMICPLASMA-GLUCOSEFOLLOW-UPPREVENTIONMANAGEMENTMELLITUSHEALTH

Population

23-Global, regional, and national lifetime risks of developing and dying from gastrointestinal cancers in 185 countries: a population-based systematic analysis of GLOBOCAN

By Wang, SM (Wang, Shaoming) [1] ; Zheng, RS (Zheng, Rongshou) [1] ; Li, JY (Li, Jiayue) [1] ; Zeng, HM (Zeng, Hongmei) [1] ; Li, L (Li, Li) [1] ; Chen, R (Chen, Ru) [1] ; Sun, KX (Sun, Kexin) [1] ; Han, BF (Han, Bingfeng) [1] ; Bray, F (Bray, Freddie) [2] ; Wei, WQ (Wei, Wenqiang) [1] ;

(provided by Clarivate) Source LANCET GASTROENTEROLOGY & HEPATOLOGY Volume 9 Issue 3 Page 229-237 DOI 10.1016/S2468-1253(23)00366-7 Published MAR 2024 Early Access FEB 2024 Indexed 2024-03-18 Document Type Article

Abstract

Background Gastrointestinal cancers account for a quarter of the global cancer incidence and a third of cancer-related deaths. We sought to estimate the lifetime risks of developing and dying from gastrointestinal cancers at the country, world region, and global levels in 2020. Methods For this population-based systematic analysis, we obtained estimates of gastrointestinal cancer incidence and mortality rates from GLOBOCAN for 185 countries, alongside all-cause mortality and population data from the UN. Countries were categorised into quartiles of the Human Development Index (HDI). The lifetime risk of gastrointestinal cancers was estimated with a standard method that adjusts for multiple primaries, taking into account competing risks of death from causes other than cancer and life expectancy. Findings The global lifetime risks of developing and dying from gastrointestinal cancers from birth to death was 8 center dot 20% (95% CI 8 center dot 18-8 center dot 21) and 6 center dot 17% (6 center dot 16-6 center dot 18) in 2020. For men, the risk of developing gastrointestinal cancers was 9 center dot 53% (95% CI 9 center dot 51-9 center dot 55) and of dying from them 7 center dot 23% (7 center dot 22-7 center dot 25); for women, the risk of developing gastrointestinal cancers was 6 center dot 84% (6 center dot 82-6 center dot 85) and of dying from them 5 center dot 09% (5 center dot 08-5 center dot 10). Colorectal cancer presented the highest risk, accounting for 38 center dot 5% of the total lifetime risk of developing, and 28 center dot 2% of dying from, gastrointestinal cancers, followed by cancers of the stomach, liver, oesophagus, pancreas, and gallbladder. Eastern Asia has the highest lifetime risks for cancers of the stomach, liver, oesophagus, and gallbladder, Australia and New Zealand for colorectal cancer, and Western Europe for pancreatic cancer. The lifetime risk of gastrointestinal cancers increased consistently with increasing level of HDI; however, high HDI countries (the third HDI quartile) had the highest death risk. Interpretation The global lifetime risk of gastrointestinal cancers translates to one in 12 people developing, and one in 16 people dying from, gastrointestinal cancers. The identified high risk and observed disparities across countries warrants context-specific targeted gastrointestinal cancer control and health systems planning.

Keywords
Keywords Plus
MORTALITYTRENDSSURVEILLANCEMULTICENTERREGISTRIESDISEASEBURDEN

Author Information

Corresponding Address

دانشگاه علوم پزشکی و خدمات بهداشتی درمانی ایران
کتابخانه دانشکده بهداشت

Population

Wei, Wenqiang (corresponding author)

Population

24- Insulin resistance assessed by estimated glucose disposal rate and risk of incident cardiovascular diseases among individuals without diabetes: findings from a nationwide, population based, prospective cohort study

---

By Zhang, ZL (Zhang, Zenglei) [1] ; Zhao, L (Zhao, Lin) [1] ; Lu, YT (Lu, Yiting) [1] ; Xiao, Y (Xiao, Yan) [1] ; Zhou, XL (Zhou, Xianliang) [1] (provided by Clarivate) Source CARDIOVASCULAR DIABETOLOGY Volume 23 Issue 1 DOI 10.1186/s12933-024-02256-5 Article Number 194 Published JUN 6 2024 Indexed 2024-06-21 Document Type Article

Abstract

Background Recent studies have suggested that insulin resistance (IR) contributes to the development of cardiovascular diseases (CVD), and the estimated glucose disposal rate (eGDR) is considered to be a reliable surrogate marker of IR. However, most existing evidence stems from studies involving diabetic patients, potentially overstating the effects of eGDR on CVD. Therefore, the primary objective of this study is to examine the relationship of eGDR with incidence of CVD in non-diabetic participants. Method The current analysis included individuals from the China Health and Retirement Longitudinal Study (CHARLS) who were free of CVD and diabetes mellitus but had complete data on eGDR at baseline. The formula for calculating eGDR was as follows: eGDR (mg/kg/min) = 21.158 - (0.09 x WC) - (3.407 x hypertension) - (0.551 x HbA1c) [WC (cm), hypertension (yes = 1/no = 0), and HbA1c (%)]. The individuals were categorized into four subgroups according to the quartiles (Q) of eGDR. Crude incidence rate and hazard ratios (HRs) with 95% confidence intervals (CIs) were computed to investigate the association between eGDR and incident CVD, with the lowest quartile of eGDR (indicating the highest grade of insulin resistance) serving as the reference. Additionally, the multivariate adjusted restricted cubic spine (RCS) was employed to examine the dose-response relationship. Results We included 5512 participants in this study, with a mean age of 58.2 +/- 8.8 years, and 54.1% were female. Over a median follow-up duration of 79.4 months, 1213 incident CVD cases, including 927 heart disease and 391 stroke, were recorded. The RCS curves demonstrated a significant and linear relationship between eGDR and all outcomes (all P for non-linearity > 0.05). After multivariate adjustment, the lower eGDR levels were founded to be significantly associated with a higher risk of CVD. Compared with participants with Q1 of eGDR, the HRs (95% CIs) for those with Q2 - 4 were 0.88 (0.76 - 1.02), 0.69 (0.58 - 0.82), and 0.66 (0.56 - 0.79). When assessed as a continuous variable, per 1.0-SD increase in eGDR was associated a 17% (HR: 0.83, 95% CI: 0.78 - 0.89) lower risk of CVD, with the subgroup analyses indicating that smoking status modified the association (P for interaction = 0.012). Moreover, the mediation analysis revealed that obesity partly mediated the association. Additionally, incorporating eGDR into the basic model considerably improve the predictive ability for CVD. Conclusion A lower level of eGDR was found to be associated with increased risk of incident CVD among non-diabetic participants. This suggests that eGDR may serve as a promising and preferable predictor and intervention target for CVD.

Keywords

Author Keywords

دانشگاه علوم پزشکی و خدمات بهداشتی، درمانی ایران
کتابخانه دانشکده بهداشت

Population

Insulin resistanceCardiovascular diseasesEstimated glucose disposal rateNon-diabetesPredictive performance

Keywords Plus

ALL-CAUSE MORTALITYGLOBAL BURDENHYPERGLYCEMIAASSOCIATIONTOLERANCE

Population

25-Effectiveness and impact of universal prophylaxis with nirsevimab in infants against hospitalisation for respiratory syncytial virus in Galicia, Spain: initial results of a population-based longitudinal study

---

By Ares-Gómez, S (Ares-Gomez, Sonia) [1] , [2] , [3] ; Mallah, N (Mallah, Narmeen) [1] , [2] , [4] , [5] ; Santiago-Pérez, MI (Santiago-Perez, Maria-Isolina) [6] ; Pardo-Seco, J (Pardo-Seco, Jacobo) [1] , [2] , [3] , [8] ; Pérez-Martínez, O (Perez-Martinez, Olaia) [6] ; Otero-Barrós, MT (Otero-Barros, Maria-Teresa) [6] ; Suárez-Gaiche, N (Suarez-Gaiche, Nuria) [6] ; Kramer, R (Kramer, Rolf) [9] ; Jin, J (Jin, Jing) [9] ; Platero-Alonso, L (Platero-Alonso, Leticia) [9] ; Group Author NIRSE-GAL Study Grp (NIRSE-GAL Study Grp) (provided by Clarivate) Source LANCET INFECTIOUS DISEASES Volume 24 Issue 8 Page 817-828 DOI 10.1016/S1473-3099(24)00215-9 Published AUG 2024 Indexed 2024-08-01 Document Type Article

Abstract

Background Galicia (Spain) was one of the first regions worldwide to incorporate nirsevimab for universal respiratory syncytial virus (RSV) prophylaxis in infants into its immunisation programme. The NIRSE-GAL longitudinal population-based study aimed to assess nirsevimab effectiveness in preventing hospitalisations (ie, admittance to hospital).

Methods The 2023-24 immunisation campaign with nirsevimab in Galicia began on Sept 25, 2023, and concluded on March 31, 2024. The campaign targeted three groups: infants born during the campaign (seasonal group), infants younger than 6 months at the start of the campaign (catch-up group), and infants aged 6-24 months with high-risk factors at the start of the campaign (high-risk group). Infants in the seasonal group were offered immunisation on the first day of life before discharge from hospital. Infants in the catch-up and high-risk groups received electronic appointments to attend a public hospital or health-care centre for nirsevimab administration. For this interim analysis, we used data collected from Sept 25 to Dec 31, 2023, from children born up to Dec 15, 2023. Data were retrieved from public health registries. Nirsevimab effectiveness in preventing RSV-associated lower respiratory tract infection (LRTI) hospitalisations; severe RSV-related LRTI requiring intensive care unit admission, mechanical ventilation, or oxygen support; all-cause LRTI hospitalisations; and all-cause hospitalisations was estimated using adjusted Poisson regression models. Data from five past RSV seasons (2016-17, 2017-18, 2018-19, 2019-20, and 2022-23), excluding the COVID-19 pandemic period, were used to estimate the number of RSV-related LRTI hospitalisations averted along with its IQR. The number needed to immunise to avoid one case in the 2023-24 season was then estimated from the averted cases. Nirsevimab safety was routinely monitored. The NIRSE-GAL study protocol was registered on ClinicalTrials.gov (NCT06180993), and follow-up of participants is ongoing.

Findings 9408 (91.7%) of 10 259 eligible infants in the seasonal and catch-up groups received nirsevimab, including 6220 (89.9%) of 6919 in the catch-up group and 3188 (95.4%) of 3340 in the seasonal group. 360 in the high-risk group were offered nirsevimab, 348 (97%) of whom received it. Only infants in the seasonal and catch-up groups were included in analyses to estimate nirsevimab effectiveness and impact because there were too few events in the high-risk group. In the catch-up and seasonal groups combined, 30 (0.3%) of 9408 infants who received nirsevimab and 16 (1.9%) of 851 who did not receive nirsevimab were hospitalised for RSV-related LRTI, corresponding to an effectiveness of 82.0% (95% CI 65.6-90.2).

Population

Effectiveness was 86.9% (69.1-94.2) against severe RSV-related LRTI requiring oxygen support, 69.2% (55.9-78.0) against all-cause LRTI hospitalisations, and 66.2% (56.0-73.7) against all-cause hospitalisations. Nirsevimab effectiveness against other endpoints of severe RSV-related LRTI could not be estimated because of too few events. RSV-related LRTI hospitalisations were reduced by 89.8% (IQR 87.5-90.3), and the number needed to immunise to avoid one RSV-related LRTI hospitalisation was 25 (IQR 24-32). No severe adverse events related to nirsevimab were registered.

Interpretation Nirsevimab substantially reduced infant hospitalisations for RSV-associated LRTI, severe RSV-associated LRTI requiring oxygen, and all-cause LRTI when given in real-world conditions. These findings offer policy makers and health authorities robust, real-world, population-based evidence to guide the development of strategies for RSV prevention. Copyright (c) 2024 Elsevier Ltd. All rights reserved, including those for text and data mining, AI training, and similar technologies.

Population

26-National, regional, and global trends in insufficient physical activity among adults from 2000 to 2022: a pooled analysis of 507 population-based surveys with 5.7 million participants

---

By Strain, T (Strain, Tessa) [1] ; Flaxman, S (Flaxman, Seth) [2] ; Guthold, R (Guthold, Regina) [3] ; Semenova, E (Semenova, Elizaveta) [2] , [4] ; Cowan, M (Cowan, Melanie) [5] ; Riley, LM (Riley, Leanne M.) [5] ; Bull, FC (Bull, Fiona C.) [6] , [7] ; Stevens, GA (Stevens, Gretchen A.) [5]
Group Author Country Data Author Grp (Country Data Author Grp) (provided by Clarivate)
Source LANCET GLOBAL HEALTH Volume 12 Issue 8 Page E1232-E1243 DOI 10.1016/S2214-109X(24)00150-5 Published AUG 2024 Early Access JUL 2024 Indexed 2025-02-20 Document Type Article

Abstract

Background Insufficient physical activity increases the risk of non-communicable diseases, poor physical and cognitive function, weight gain, and mental ill-health. Global prevalence of adult insufficient physical activity was last published for 2016, with limited trend data. We aimed to estimate the prevalence of insufficient physical activity for 197 countries and territories, from 2000 to 2022. Methods We collated physical activity reported by adults (aged >= 18 years) in population-based surveys. Insufficient physical activity was defined as not doing 150 minutes of moderate-intensity activity, 75 minutes of vigorous-intensity activity, or an equivalent combination per week. We used a Bayesian hierarchical model to compute estimates of insufficient physical activity by country or territory, year, age, and sex. We assessed whether countries or territories, regions, and the world would meet the global target of a 15% relative reduction of the prevalence of insufficient physical activity by 2030 if 2010-22 trends continue. Findings We included 507 surveys across 163 countries and territories. The global age-standardised prevalence of insufficient physical activity was 31.3% (95% uncertainty interval 28.6-34.0) in 2022, an increase from 23.4% (21.1-26.0) in 2000 and 26.4% (24.8-27.9) in 2010. Prevalence was increasing in 103 (52%) of 197 countries and territories and six (67%) of nine regions, and was declining in the remainder. Prevalence was 5 percentage points higher among female (33.8% [29.9-37.7]) than male (28.7% [25.0-32.6]) individuals. Insufficient physical activity increased in people aged 60 years and older in all regions and both sexes, but age patterns differed for those younger than 60 years. If 2010-22 trends continue, the global target of a 15% relative reduction between 2010 and 2030 will not be met (posterior probability <0.01); however, two regions, Oceania and sub-Saharan Africa, were on track with considerable uncertainty (posterior probabilities 0.70-0.74). Interpretation Concerted multi-sectoral efforts to reduce insufficient physical activity levels are needed to meet the 2030 target. Physical activity promotion should not exacerbate sex, age, or geographical inequalities. Copyright (c) 2024. World Health Organization. Published by Elsevier Ltd. All rights reserved. This is an Open Access article published under the CC BY 3.0 IGO license which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. In any use of this Article, there should be no suggestion that WHO endorses any specific organisation, products or services. The use of the WHO logo is not permitted. This notice should be preserved along with the Article's original URL.

Population

27- Association between the triglyceride glucose-body mass index and future cardiovascular disease risk in a population with Cardiovascular-Kidney-Metabolic syndrome stage 0-3: a nationwide prospective cohort study

---

By Li, WP (Li, Weipeng) [1] , [2] , [3] ; Shen, CN (Shen, Chaonan) [1] , [2] , [3] ; Kong, WY (Kong, Weiya) [4] ; Zhou, XH (Zhou, Xiaohui) [1] ; Fan, HM (Fan, Huimin) [2] , [5] ; Zhang, YZ (Zhang, Yuzhen) [1] , [2] ; Liu, ZM (Liu, Zhongmin) [1] , [2] ; Zheng, L (Zheng, Liang) [1] , [2] (provided by Clarivate) Source CARDIOVASCULAR DIABETOLOGY Volume 23 Issue 1 DOI 10.1186/s12933-024-02352-6 Article Number 292 Published AUG 7 2024 Indexed 2024-08-13 Document Type Article

Abstract

Background The American Heart Association (AHA) has recently introduced the concept of Cardiovascular-Kidney-Metabolic (CKM) syndrome, which is the result of an increasing emphasis on the interplay of metabolic, renal and cardiovascular diseases (CVD). Furthermore, there is substantial evidence of a correlation between the triglyceride glucose-body mass index (TyG-BMI) and CVD as an assessment of insulin resistance (IR). However, it remains unknown whether this correlation exists in population with CKM syndrome. Methods All data for this study were obtained from the China Health and Retirement Longitudinal Study (CHARLS). The exposure was the participants' TyG-BMI at baseline, which was calculated using a combination of triglycerides (TG), fasting blood glucose (FBG) and body mass index (BMI). The primary outcome was CVD, which were determined by the use of a standardised questionnaire during follow-up. To examine the relationship between TyG-BMI and CVD incidence in population with CKM syndrome, both Cox regression analyses and restricted cubic spline (RCS) regression analyses were performed. Results A total of 7376 participants were included in the final analysis. Of these, 1139, 1515, 1839, and 2883 were in CKM syndrome stages 0, 1, 2, and 3, respectively, at baseline. The gender distribution was 52.62% female, and the mean age was 59.17 +/- 9.28 (years). The results of the fully adjusted COX regression analyses indicated that there was a 6.5% increase in the risk of developing CVD for each 10-unit increase in TyG-BMI,95% confidence interval (CI):1.041-1.090. The RCS regression analyses demonstrated a positive linear association between TyG-BMI and the incidence of CVD in the CKM syndrome population (P for overall < 0.001, P for nonlinear = 0.355). Conclusions This cohort study demonstrated a positive linear association between TyG-BMI index and increased CVD incidence in a population with CKM syndrome stage 0-3. This finding suggests that enhanced assessment of TyG-BMI index may provide a more convenient and effective tool for individuals at risk for CVD in CKM syndrome stage 0-3.

Keywords
Author Keywords
Cardiovascular kidney metabolic syndromeCVDIRTyG-BMI
Keywords Plus
INSULIN-RESISTANCEPROFILEIMPACT

Population

28-Full spectrum fitting with photometry in ppxf: stellar population versus dynamical masses, non-parametric star formation history and metallicity for 3200 LEGA-C galaxies at redshift z ≈ 0.8

By Cappellari, M (Cappellari, Michele) [1] (provided by Clarivate) Source MONTHLY NOTICES OF THE ROYAL ASTRONOMICAL SOCIETY Volume 526 Issue 3 Page 3273-3300 DOI 10.1093/mnras/stad2597 Published OCT 10 2023 Early Access OCT 2023 Indexed 2023-11-30 Document Type Article

Abstract

I introduce some improvements to the ppxf method, which measures the stellar and gas kinematics, star formation history (SFH) and chemical composition of galaxies. I describe the new optimization algorithm that ppxf uses and the changes I made to fit both spectra and photometry simultaneously. I apply the updated ppxf method to a sample of 3200 galaxies at redshift 0.6 < z < 1 (median z = 0.76, stellar mass M-circle dot), using spectroscopy from the LEGA-C survey (DR3) and 28-bands photometry from two different sources. I compare the masses from new JAM dynamical models with the ppxf stellar population M-* and show the latter are more reliable than previous estimates. I use three different stellar population synthesis (SPS) models in ppxf and both photometric sources. I confirm the main trend of the galaxies' global ages and metallicity [M/H] with stellar velocity dispersion sigma (*) (or central density), but I also find that [M/H] depends on age at fixed sigma (*). The SFHs reveal a sharp transition from star formation to quenching for galaxies with (), or average mass density within 1 kpc (), or with , or with Sersic index (). However, the transition is smoother as a function of M-*. These results are consistent for two SPS models and both photometric sources, but they differ significantly from the third SPS model, which demonstrates the importance of comparing model assumptions.

Keywords

Author Keywords

techniques: photometrictechniques: spectroscopicsoftware: data analysisgalaxies: evolutiongalaxies: formationgalaxies: high-redshift

Keywords Plus

INTEGRAL-FIELD SPECTROSCOPYMASSIVE QUIESCENT GALAXIESDATA-ANALYSIS PIPELINEDIGITAL SKY SURVEYENERGY-DISTRIBUTIONSATLAS(3D) PROJECTDARK-MATTERLIGHT RATIOVELOCITY DISPERSIONSFUNDAMENTAL PLANE