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- H-index: **70**
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1. Fang, S., Hemani, G., Richardson, T., Gaunt, T. & Smith, G. Evaluating and implementing block jack-knife resampling mendelian randomization to mitigate bias induced by overlapping samples. Human Molecular Genetics (2023).
2. Tintle, N., Rice, T., Cheng, I., Jenkins, M., Gallinger, S., et al. The association between genetically elevated polyunsaturated fatty acids and risk of cancer. EBioMedicine (2023).
3. Haycock, P., Borges, M., Burrows, K., Lemaitre, R., Harrison, S., Burgess, S., et al. Design and quality control of large-scale two-sample mendelian randomization studies. International Journal of Epidemiology (2023).
4. Darrous, L., Hemani, G., Smith, G. & Kutalik, Z. PheWAS-based clustering of mendelian randomisation instruments reveals distinct mechanism-specific causal effects between obesity and educational attainment. medRxiv (2023).
5. Forde, A., Hemani, G. & Ferguson, J. Review and further developments in statistical corrections for winner's curse in genetic association studies. PLoS Genetics (2023).
6. Cho, Y., Lin, K., Lee, S., Yu, C., Valle, D., et al. Genetic influences on alcohol flushing in east asian populations. BMC genomics (2023).
7. Singh, M., Dolan, C., Lapato, D., Hottenga, J., Pool, R., et al. 75. PUTATIVE CAUSAL EFFECTS BETWEEN CIGARETTE SMOKING AND PERIPHERAL BLOOD DNA METHYLATION: A MENDELIAN RANDOMIZATION DIRECTION-OF-CAUSATION (MR-DOC) STUDY. European Neuropsychopharmacology (2023).
8. Hemani, G., Gkatzionis, A., Tilling, K. & Smith, G. Sensitivity analyses gain relevance by fixing parameters observable during the empirical analyses. Genetic Epidemiology (2023).
9. Haycock, P., Borges, M., Burrows, K., Lemaitre, R., Harrison, S., Burgess, S., et al. IEA. International Journal of Epidemiology (2023).
10. Shapland, C., Gkatzionis, A., Hemani, G. & Tilling, K. Use of genetic correlations to examine selection bias. medRxiv (2023).
11. Howe, L., Nivard, M., Morris, T., Hansen, A., Rasheed, H., Cho, Y., et al. Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature genetics (2022).
12. Battram, T., Yousefi, P., Crawford, G., Prince, C., Babaei, M., Sharp, G., et al. The EWAS catalog: A database of epigenome-wide association studies. Wellcome open research (2022).
13. Borges, M., Haycock, P., Zheng, J., Hemani, G., Holmes, M., et al. Role of circulating polyunsaturated fatty acids on cardiovascular diseases risk: Analysis using mendelian randomization and fatty acid genetic association data from over 114 .... BMC medicine (2022).
14. Zhao, H., Rasheed, H., Nøst, T., Cho, Y., Liu, Y., et al. Proteome-wide mendelian randomization in global biobank meta-analysis reveals multi-ancestry drug targets for common diseases. Cell Genomics (2022).

15. Woolf, B., Cara, N., Moreno-Stokoe, C., Skrivankova, V., Drax, K., et al. Investigating the transparency of reporting in two-sample summary data mendelian randomization studies using the MR-base platform. International journal of epidemiology (2022).
16. Shen, X., Caramaschi, D., Adams, M., Walker, R., Min, J., Kwong, A., et al. DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. Genome Medicine (2022).
17. Corfield, E., Frei, O., Shadrin, A., Rahman, Z., Lin, A., Athanasiu, L., et al. The norwegian mother, father, and child cohort study (MoBa) genotyping data resource: MoBaPsychGen pipeline v. 1. BioRxiv (2022).
18. Lee, M., Huan, T., McCartney, D., Chittoor, G., Vries, M., Lahousse, L., et al. Pulmonary function and blood DNA methylation: A multiancestry epigenome-wide association meta-analysis. American Journal of Respiratory and Critical Care Medicine (2022).
19. Speyer, L., Neaves, S., Hall, H., Hemani, G., Lombardo, M., Murray, A., et al. Polygenic risks for joint developmental trajectories of internalizing and externalizing problems: Findings from the ALSPAC cohort. Journal of Child Psychology and Psychiatry (2022).
20. Battram, T., Gaunt, T., Relton, C., Timpson, N. & Hemani, G. A comparison of the genes and genesets identified by GWAS and EWAS of fifteen complex traits. Nature communications (2022).
21. Howe, L., Evans, D., Hemani, G., Smith, G. & Davies, N. Evaluating indirect genetic effects of siblings using singletons. PLoS Genetics (2022).
22. Wade, K., Yarmolinsky, J., Giovannucci, E., Lewis, S., Millwood, I., et al. Applying mendelian randomization to appraise causality in relationships between nutrition and cancer. Cancer Causes & Control (2022).
23. Mitchell, D., Stone, E., Andrews, O., Bamber, J., Bingham, R., Browse, J., et al. The bristol CMIP6 data hackathon. Weather (2022).
24. Robinson, J., Hemani, G., Babaei, M., Huang, Y., Baird, D., Tsai, E., et al. An efficient and robust tool for colocalisation: Pair-wise conditional and colocalisation (PWCoCo). bioRxiv (2022).
25. Borges, M., Haycock, P., Zheng, J., Hemani, G., Howe, L., Schmidt, A., et al. The impact of fatty acids biosynthesis on the risk of cardiovascular diseases in europeans and east asians: A mendelian randomization study. Human Molecular Genetics (2022).
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34. Vösa, U., Claringbould, A., Westra, H., Bonder, M., Deelen, P., Zeng, B., et al. Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature genetics (2021).
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38. Brooks-Pollock, E., Christensen, H., Trickey, A., Hemani, G., Nixon, E., et al. High COVID-19 transmission potential associated with re-opening universities can be mitigated with layered interventions. Nature communications (2021).
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43. Wang, J., Zhao, Q., Bowden, J., Hemani, G., Smith, G., Small, D., et al. Causal inference for heritable phenotypic risk factors using heterogeneous genetic instruments. PLoS genetics (2021).
44. Liu, Y., Elsworth, B., Erola, P., Haberland, V., Hemani, G., et al. EpiGraphDB: A database and data mining platform for health data science. Bioinformatics (2021).
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