HUGEN 2029: Introduction to Gene Mapping
3 credits / Fall Term 2022 / Mondays 9:30-10:55 am / Wednesdays 8:30-9:55 am; 3121C

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Office Hours: By appointment

Faculty Availability: I welcome your questions and suggestions. Please feel free to set up an appointment. Also, if you are having any problems with the course, please contact me as soon as possible. E-mail is a good way to reach me. Since I get many e-mails, please use an informative subject line starting with "HUGEN 2029".

Course Description: This course presents a literature-based approach to understanding and interpreting results from gene mapping papers in the field of human genetics. Traditional and state-of-the-art genetic mapping methodologies will be discussed.

COVID: If you are required to isolate or quarantine, become sick, or are unable to come to class, contact me as soon as possible to discuss arrangements (see contact info above).

It is important that you abide by the public health regulations (COVID-19 | Health Department | Allegheny County), the University of Pittsburgh's health standards and guidelines (COVID-19 Standards and Guidelines | Office of Policy Development and Management | University of Pittsburgh), and Pitt's Health Rules (Pitt's Health Rules | Power of Pitt | University of Pittsburgh). These rules have been developed to protect the health and safety of all of us. The University's requirements for face coverings will at a minimum be consistent with CDC guidance and masks are required indoors (campus buildings and shuttles) on campuses in which COVID-19 Community Levels are High. This means that when COVID-19 Community Levels are High, you must wear a face covering that properly covers your nose and mouth when you are in the classroom. If you do not comply, you will be asked to leave class. It is your responsibility to have the required face covering when entering a university building or classroom. Masks are optional indoors for campuses in which county levels are Medium or Low. Be aware of your Community Level as it changes each Thursday (COVID-19 by County | CDC). Read answers to frequently asked questions regarding face coverings (Frequently Asked Questions About Face Coverings | Power of Pitt | University of Pittsburgh). For the most up-to-date information and guidance, please visit the Power of Pitt site (Power of Pitt | University of Pittsburgh) and check your Pitt email for updates before each class.

Course Overview and Learning Objectives:

This course covers the (currently) most commonly-used technologies and methodologies for discovering and exploring genotype-phenotype associations. Each methodology will be covered in one or two didactic class sessions, and then participants will read, critique, and present papers that apply the methodology.

At the end of this course, participants should be able to:

- Describe the mathematical and scientific underpinnings of each methodology
- Discuss how the choice of study design influences the choice of methodology (and vice versa)
- Discuss the strengths and limitations of each methodology
- Evaluate gene mapping results in the current literature
- Critique the study design and methodology choices in published gene-mapping studies

Texts/assigned materials:

Participants will need to read and be prepared to discuss assigned materials that will be posted for personal use on Canvas. There is no required textbook for this course.

Exams and Assignments:

- Exams: There will be two (take-home) exams, a mid-term exam and a final exam, to assess students' ability to understand and critique gene mapping methods. The format will be open-ended questions.

- Student presentations: Each student will review, present and discuss a (recently) published paper in class. Presentations should be short, approximately *15 minutes*, and primarily be an introduction to the topic and briefly highlight the paper. The student will subsequently lead a discussion of the paper (*10-15 minutes*). The goal of these presentations is to learn to critically review papers, evaluate the strengths and weaknesses of the papers, and to gain experience in public speaking. Everyone is expected to have read the selected papers in advance and come prepared to discuss.

- Discussions: In addition to the student presentations, the class as a whole will review and discuss several papers. Everyone is expected to have read the selected papers in advance and come prepared to discuss.

Student Performance Evaluation:

All course requirements must be completed to receive credit for the course. Evaluation will be based on the following components:

- Attendance and Quality of Contribution to Discussion (25% of final grade)
Attendance, active participation in class discussions, and evidence of being prepared for class (including having read the assigned readings and completion of assignments) are expected. While cell phones and laptops/tablets may be used to access slides or assigned readings, take notes, etc., please do not use them during class time for non-class purposes. If you will miss a class, please let me know in advance if possible (bbd3@pitt.edu).

- Student Presentations (25% of final grade)

- Mid-term Exam (25% of final grade)
Take-home mid-term exam will be posted on Canvas on Friday October 21. The mid-term exam is due on Wednesday October 26 (by midnight; please submit to: bbd3@pitt.edu).

- Final Exam (25% of final grade)
Take-home final exam will be posted on CANVAS on Friday December 9. The final exam is due on Wednesday December 14 (by midnight; please submit to: bbd3@pitt.edu).

Grade option:	**Grading scale:**		
Letter grade	97 - 100% A+	77 – 79.9% C+	< 60% F
	93 – 96.9% A	73 – 76.9% C	
	90 – 92.9% A-	70 – 72.9% C-	
	87 – 89.9% B+	67 – 69.9% D+	
	83 – 86.9% B	63 – 66.9% D	
	80 – 82.9% B-	60 – 62.9% D-	

Canvas:

The University's Canvas will be used to post announcements, assignments, and readings for personal use.

Course Policies:

The Internet generally should not be accessed during class, except to access course slides or assigned readings, help resolve a disputed point in discussion or otherwise enhance discussion. Students should check their email regularly to ensure that they receive relevant communication regarding the course.

Students should familiarize themselves also with the following policies:

- Academic Integrity Policy:
All individuals (students, faculty, post-doctoral researchers, and staff) at Pitt Public Health abide by the University's policy on academic integrity. In accordance with this policy, the school maintains an outline of the procedural sequence of events to occur when violations of academic integrity are brought to the attention of administrative leaders. The full policy is available in the Academic Handbook.

All students are expected to adhere to the school's standards of academic honesty. Cheating/plagiarism will not be tolerated. The School of Public Health's policy on academic integrity, which is based on the University policy, is available online in the Pitt Public Health Academic Handbook www.publichealth.pitt.edu/home/academics/academic-requirements. The policy includes obligations for faculty and students, procedures for adjudicating violations, and other critical information. Please take the time to read this policy.

Students should be especially mindful of guidelines on academic integrity and take care to avoid plagiarizing the work - including the ideas or words - of their colleagues (fellow course participants) or other authors. Students are encouraged to discuss their ideas and work together; however, a citation to a fellow student should be provided when appropriate.

- Diversity and Academic Civility Statement:
In this course, students, faculty and guests represent a diversity of individual perspectives, backgrounds, and experiences, which enriches our classes. We urge all to be respectful of others.

The University of Pittsburgh School of Public Health considers the diversity of its students, faculty, and staff to be a strength and critical to its educational mission. Pitt Public Health is committed to creating and fostering inclusive learning environments that value human dignity and equity and promote social justice. Every member of our community is expected to be respectful of the individual perspectives, experiences, behaviors, worldviews, and backgrounds of others. While intellectual disagreement may be constructive, no derogatory statements, or demeaning or discriminatory behavior will be permitted.

If you feel uncomfortable or would like to discuss a situation, please contact any of the following:
• the course instructor (bbd3@pitt.edu or see phone number above);
• the Pitt Public Health Associate Dean responsible for diversity and inclusion (Dr. Tiffany Gary-Webb: tgary@pitt.edu // 412-624-3131);
• the University's Office of Diversity and Inclusion at 412-648-7860 or https://www.diversity.pitt.edu/make-report/report-form (anonymous reporting form)

- Accommodation for Students with Disabilities:
If you have any disability for which you may require accommodation, you are encouraged to notify both your instructor (bbd3@pitt.edu) and the Office of Disability Resources and Services (DRS), 140 William Pitt Union (Voice or TTD 412-648-7890), http://www.studentaffairs.pitt.edu/drs/, drsrecep@pitt.edu, as early as possible in the term.

- Copyright Notice:
Course materials may be protected by copyright. United States copyright law, 17 USC section 101, et seq., in addition to University policy and procedures, prohibit unauthorized duplication or retransmission of course materials. See Library of Congress Copyright Office and the University Copyright Policy.

- Classroom Recording:
To ensure the free and open discussion of ideas, students may not record classroom lectures, discussion and/or activities without the advance permission of the instructor, and any such recording properly approved in advance can be used solely for the student's own private use or for all students enrolled in this class only but may not be further copied, distributed, published, or otherwise used for any other purpose without the express written consent of the course instructors. Any student who records a class session must provide a copy of the recording to the instructors if requested to do so.

- Sexual Misconduct, Required Reporting, and Title IX:
The University is committed to combatting sexual misconduct. As a result, you should know that University faculty and staff members are required to report any instances of sexual misconduct, including harassment and

sexual violence, to the University's Title IX office so that the victim may be provided appropriate resources and support options. What this means is that as your professor, I am required to report any incidents of sexual misconduct that are directly reported to me, or of which I am somehow made aware.

There are two important exceptions to this requirement about which you should be aware:

(1) A list of the designated University employees who, as counselors and medical professionals, do not have this reporting responsibility and can maintain confidentiality, can be found here: https://www.diversity.pitt.edu/civil-rights-title-ix/make-report/report-form

(2) An important exception to the reporting requirement exists for academic work. Disclosures about sexual misconduct that are shared as part of an academic project, classroom discussion, or course assignment, are not required to be disclosed to the University's Title IX office

If you are the victim of sexual misconduct, Pitt encourages you to reach out to these resources:

• Title IX Office: 412-648-7860 (https://www.titleix.pitt.edu/)

• SHARE @ the University Counseling Center: 412-648-7930 (8:30 A.M. TO 5 P.M. M-F) and 412-648-7856 (AFTER BUSINESS HOURS)

If you have a safety concern, please contact the University of Pittsburgh Police, 412-624-2121.

HUGEN 2029: Introduction to Gene Mapping
Fall Term 2022 Schedule (version: 9/20/22)
(Mondays 9:30-10:55 am / Wednesdays 8:30-9:55 am; 3121C)

Date	Topics	
Monday September 5	**LABOR DAY HOLIDAY – No class (university closed)**	
Wednesday September 7	Course introduction; Study design, study populations, diversity	
September 9-11	**Human Genetics retreat - Pymatuning**	
Monday September 12	Candidate gene association studies / discussion	
Wednesday September 14	Genome-wide association studies (GWAS)	
Monday September 19	GWAS – imputation and combining datasets	
Wednesday September 21	GWAS follow-up; eQTL analysis, gene set analysis	
Monday September 26	GWAS discussion	
Wednesday September 28	GWAS discussion	
Monday October 3	Polygenic risk scores (and what about the environment?)	
Wednesday October 5	PRS discussion	
Monday October 10	Sequencing - biochemistry, rare variants, and cancer	
Wednesday October 12	Family-based designs, linkage analysis	
Monday October 17	Sequencing/family-based studies discussion	
Wednesday October 19	Sequencing/family-based studies discussion	
Friday October 21	**Mid-term exam posted on Canvas**	
Monday October 24	**No class**	
October 25-29	**ASHG** https://www.ashg.org/meetings/2022-annual-meeting/	
Wednesday October 26	**No class – mid-term exam due (by midnight)**	
Monday October 31	Epigenetics, methylation	
Wednesday November 2	Methylation studies discussion	
Monday November 7	Expression data, transcriptome-wide association studies, RNA-seq, single cell RNA-seq	
Wednesday November 19	Expression discussion	
Monday November 14	Copy number variants (CNVs) / role of CNVs in disease	
Wednesday November 16	CNV discussion	
Monday November 21	**THANKSGIVING HOLIDAY – No class**	
Wednesday November 23	**THANKSGIVING HOLIDAY – No class**	
Monday November 28	Multi-omics approaches, post-transcriptional control - Discussion	
Wednesday December 1	Discussion	
Monday December 5	Other genomes - Discussion	
Wednesday December 7	Discussion	
Friday December 9	**Final exam posted on Canvas**	
Monday December 12	Mendelian randomization	
Wednesday December 14	**No class – final exam due (by midnight)**	

Background/suggested readings - HUGEN 2029: Introduction to Gene Mapping

September 7, 2023 – Intro:

- Buffalo gave us spicy wings and the 'book of life.' Here's why that's undermining personalized medicine (STAT news, March 11, 2019): https://www.statnews.com/2019/03/11/human-reference-genome-shortcomings/

- Hindorff et al. Prioritizing diversity in human genomics research. *Nat Rev Genet*. 2018 Mar;19(3):175-185. https://pubmed.ncbi.nlm.nih.gov/29151588/

- Diversity matters. *Nat Rev Genet*. 2019 August. https://www.nature.com/articles/s41576-019-0162-y

- Gurdasani, D. et al. Genomics of disease risk in globally diverse populations. *Nat Rev Genet*. 2019 August. https://www.nature.com/articles/s41576-019-0144-0

- Ballouz et al. Is it time to change the reference genome? https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1774-4

- The Human Pangenome Project, see https://newsroom.uw.edu/news/scientists-set-out-map-worlds-genomic-diversity and Nature paper outlining the project (The Human Pangenome Project: a global resource to map genomic diversity, April 2022): https://www.nature.com/articles/s41586-022-04601-8

- Too many scientists still say Caucasian. Racist ideas of categories for human identity continue to warp research and medicine. Alice B. Popejoy Too many scientists still say Caucasian (nature.com)

Candidate gene association studies:

- Paul R Burton, Martin D Tobin, John L Hopper. Key concepts in genetic epidemiology. Lancet 2005; 366: 941–51

- Cordell and Clayton. Genetic association studies. Lancet 2005; 366:1121-31

- Hattersley and McCarthy. What makes a good genetic association study? Lancet 2005; 366: 1115-23

- Jorgensen et al. Hypothesis-driven candidate gene association studies: practical design and analytical considerations. Am J Epidemiol 2009;170:986–993

Genome-wide association studies:

- Manolio T.A. Genomewide Association Studies and Assessment of the Risk of Disease. N Engl J Med 2010;363:166-76. https://www.nejm.org/doi/full/10.1056/nejmra0905980

- Manolio T.A. Bringing genome-wide association findings into clinical use. Nat Rev Genet. 2013 Aug;14(8):549-58. doi: 10.1038/nrg3523. https://pubmed.ncbi.nlm.nih.gov/23835440/

-Sud A, Kinnersley B, Houlston RS. Genome-wide association studies of cancer: current insights and future perspectives. Nat Rev Cancer. 2017 Nov;17(11):692-704. https://www.nature.com/articles/nrc.2017.82

- Making the case for more inclusive GWAS. Nat Rev Genetics 20, 500–501 (2019) https://www.nature.com/articles/s41576-019-0160-0

- Wojcik, G. L. et al. Genetic analyses of diverse populations improves discovery for complex traits. Nature 570, 514–518 (2019) https://www.nature.com/articles/s41586-019-1310-4

- Benefits and limitations of genome-wide association studies. Tam V, Patel N, Turcotte M, Bossé Y, Paré G, Meyre D. Nat Rev Genet. 2019 Aug;20(8):467-484. https://www.nature.com/articles/s41576-019-0127-1

- Genome-wide association studies. Emil Uffelmann, Qin Qin Huang, Nchangwi Syntia Munung, Jantina de Vries, Yukinori Okada, Alicia R. Martin, Hilary C. Martin, Tuuli Lappalainen & Danielle Posthuma. Nature

Reviews Methods Primers volume 1, Article number: 59 (2021). https://www.nature.com/articles/s43586-021-00056-9

- Laurie et al. Quality control and quality assurance in genotypic data for genome-wide association studies. Genet Epidemiol. 2010 Sep;34(6):591-602. https://pubmed.ncbi.nlm.nih.gov/20718045/

- Jake Lever, Martin Krzywinski & Naomi Altman. Principal component analysis. Nature Methods volume 14, pages641–642 (2017). https://www.nature.com/articles/nmeth.4346

- Das et al. Genotype Imputation from Large Reference Panels. Annu Rev Genomics Hum Genet. 2018 Aug 31;19:73-96. https://pubmed.ncbi.nlm.nih.gov/29799802/

- Howie et al. Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nature Genetics 2012. https://pubmed.ncbi.nlm.nih.gov/22820512/

- Marchini and Howie. Genotype imputation for genome-wide association studies. Nature Reviews Genetics 2010. https://www.nature.com/articles/nrg2796

- van Leeuwen EM, Kanterakis A, Deelen P, Kattenberg MV; Genome of the Netherlands Consortium, Slagboom PE, de Bakker PI, Wijmenga C, Swertz MA, Boomsma DI, van Duijn CM, Karssen LC, Hottenga JJ. Population-specific genotype imputations using minimac or IMPUTE2. Nat Protoc. 2015 Sep;10(9):1285-96. https://pubmed.ncbi.nlm.nih.gov/26226460/ IMPUTE2: a genotype imputation and haplotype phasing program based on ideas from Howie et al. 2009 https://mathgen.stats.ox.ac.uk/impute/impute_v2.html

GWAS follow-up:

- Genome-wide association studies. Emil Uffelmann, Qin Qin Huang, Nchangwi Syntia Munung, Jantina de Vries, Yukinori Okada, Alicia R. Martin, Hilary C. Martin, Tuuli Lappalainen & Danielle Posthuma. Nature Reviews Methods Primers volume 1, Article number: 59 (2021). https://www.nature.com/articles/s43586-021-00056-9

- Spinning convincing stories for both true and false association signals. Genet Epidemiol, 2019 Jun;43(4):356-364. https://pubmed.ncbi.nlm.nih.gov/30657194/

- Gallagher and Chen-Plotkin The Post-GWAS Era: From Association to Function. Am J Hum Genet. 2018 May 3;102(5):717-730. https://pubmed.ncbi.nlm.nih.gov/29727686/

On eQTL:

- Gilad et al. Revealing the architecture of gene regulation: the promise of eQTL studies. Trends Genet. 2008 Aug;24(8):408-15. https://pubmed.ncbi.nlm.nih.gov/18597885/

- Nica and Dermitzakis. Expression quantitative trait loci: present and future. Philos Trans R Soc Lond B Biol Sci. 2013 May 6;368(1620):20120362. https://pubmed.ncbi.nlm.nih.gov/23650636/

- Westra and Franke. From genome to function by studying eQTLs. Biochim Biophys Acta. 2014 Oct;1842(10):1896-1902. https://pubmed.ncbi.nlm.nih.gov/24798236/

On GTEx:

- GTEx portal: https://gtexportal.org/home/

- The GTEx Consortium. The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. SCIENCE 8 May 2015 Vol 348, Issue 6235 https://www.science.org/doi/10.1126/science.1262110

- The GTEx Consortium. The Genotype-Tissue Expression (GTEx) project. Nature Genetics volume 45, pages580–585 (2013). https://www.nature.com/articles/ng.2653

- The GTEx Consortium. The GTEx Consortium atlas of genetic regulatory effects across human tissues. SCIENCE 11 Sep 2020 Vol 369, Issue 6509 pp. 1318-1330. https://www.science.org/doi/10.1126/science.aaz1776

- Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. Nature Genetics volume 49, pages1664–1670 (2017). https://www.nature.com/articles/ng.3969

Polygenic risk scores:

- What are polygenic risk scores and why are they important? JAMA May 14, 2019 Volume 321, Number 18. https://pubmed.ncbi.nlm.nih.gov/30958510/

- Ali Torkamani, Nathan E. Wineinger & Eric J. Topol. The personal and clinical utility of polygenic risk scores. Nature Reviews Genetics volume 19, pages581–590 (2018). https://www.nature.com/articles/s41576-018-0018-x

- Martin et al. Clinical use of current polygenic risk scores may exacerbate health disparities. Nat Genet. 2019 Apr;51(4):584-591. https://www.nature.com/articles/s41588-019-0379-x

- Duncan et al. Analysis of polygenic risk score usage and performance in diverse human populations. Nature Communications volume 10, Article number: 3328 (2019). https://www.nature.com/articles/s41467-019-11112-0

- Wan Choi et al. Tutorial: a guide to performing polygenic risk score analyses. Nat Protoc. 2020 Sep;15(9):2759-2772. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7612115/

- Lewis and Vassos. Polygenic risk scores: from research tools to clinical instruments. Genome Medicine (2020) https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-020-00742-5

- Wand H, Lambert SA, Tamburro C, et al. Improving reporting standards for polygenic scores in risk prediction studies. Nature. Published online March 10, 2021. https://www.nature.com/articles/s41586-021-03243-6

- Lambert et al. The Polygenic Score Catalog as an open database for reproducibility and systematic evaluation. Nature Genetics 2021. https://www.nature.com/articles/s41588-021-00783-5

- Collister et al. Calculating Polygenic Risk Scores (PRS) in UK Biobank: A Practical Guide for Epidemiologists. Front. Genet., 18 February 2022 Sec. Statistical Genetics and Methodology. https://doi.org/10.3389/fgene.2022.81857

- Kaplan and Fullerton. Polygenic risk, population structure and ongoing difficulties with race in human genetics. Philos Trans R Soc Lond B Biol Sci. 2022 Jun 6;377(1852):20200427. https://pubmed.ncbi.nlm.nih.gov/35430888/

Sequencing:

Jay Shendure et al DNA sequencing at 40: past, present and future. Nature volume 550, pages345–353 (2017)

Daniel C. Koboldt Best practices for variant calling in clinical sequencing. Genome Medicine volume 12, Article number: 91 (2020)

DePristo et al. A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nature Genetics volume 43, pages491–498 (2011)

Paul L Auer and Guillaume Lettre. Rare variant association studies: considerations, challenges and opportunities. Genome Med. 2015 Feb 23;7(1):16. doi: 10.1186/s13073-015-0138-2.

Lee et al. Rare-variant association analysis: study designs and statistical tests. Am J Hum Genet 2014 Jul 3;95(1):5-23. doi: 10.1016/j.ajhg.2014.06.009.

Family-based Approaches:

Ellen Wijsman. Family-based approaches: design, imputation, analysis, and beyond. BMC Genetics 2016, 17(Suppl2):9: https://bmcgenomdata.biomedcentral.com/articles/10.1186/s12863-015-0318-5Links to an external site.

Ott et al. Family-based designs for genome-wide association studies. Nature Reviews, July 2011: https://pubmed.ncbi.nlm.nih.gov/21629274/Links to an external site.

Ott et al. Genetic linkage analysis in the age of whole-genome sequencing. Nature Reviews Genetics volume 16, pages275–284 (2015): https://www.nature.com/articles/nrg3908

Epigenetics, methylation:

- Maria Pia Campagna et al. Epigenome-wide association studies: current knowledge, strategies and recommendations. Clinical Epigenetics volume 13, Article number: 214 (2021). https://clinicalepigeneticsjournal.biomedcentral.com/articles/10.1186/s13148-021-01200-8Links to an external site.

- Vardhman K. Rakyan et al. Epigenome-wide association studies for common human diseases. Nature Reviews Genetics volume 12, pages529–541 (2011). https://www.nature.com/articles/nrg3000Links to an external site.

- Andrew E. Teschendorff & Caroline L. Relton Statistical and integrative system-level analysis of DNA methylation data. Nature Reviews Genetics volume 19, pages129–147 (2018). https://www.nature.com/articles/nrg.2017.86Links to an external site.

- Karin B Michels et al. Recommendations for the design and analysis of epigenome-wide association studies. Nature Methods volume 10, pages949–955 (2013) https://www.nature.com/articles/nmeth.2632Links to an external site.

Chromatin related:

- Chromatin accessibility profiling methods. Nature Reviews Methods Primers volume 1, Article number: 11 (2021) . (Highlights the main chromatin accessibility profiling methods. These methods include DNase-seq, ATAC-seq, MNase-seq, and DNA methylation-based methods to assess open chromatin and regulatory elements.) Chromatinmethodss43586-020-00010-1.pdf Download Chromatinmethodss43586-020-00010-1.pdf

- Liesbeth Minnoye et al. Chromatin accessibility profiling methods. Nature Reviews Methods Primers volume 1, Article number: 10 (2021) chromatinprofilingmethodss43586-020-00008-9.pdf Download chromatinprofilingmethodss43586-020-00008-9.pdf

- Feng Yan et al. From reads to insight: a hitchhiker's guide to ATAC-seq data analysis. Genome Biology volume 21, Article number: 22 (2020). ATACseqs13059-020-1929-3.pdf

Gene expression, TWAS, RNA-seq:

- Wainberg, M., Sinnott-Armstrong, N., Mancuso, N. et al. Opportunities and challenges for transcriptome-wide association studies. Nat Genet 51, 592–599 (2019). https://doi.org/10.1038/s41588-019-0385-z.

- Gusev, A., Ko, A., Shi, H. et al. Integrative approaches for large-scale transcriptome-wide association studies. Nat Genet 48, 245–252 (2016). https://doi.org/10.1038/ng.3506

- Stark, R., Grzelak, M. & Hadfield, J. RNA sequencing: the teenage years. Nat Rev Genet 20, 631–656 (2019). https://doi.org/10.1038/s41576-019-0150-2

- McDermaid et al. Interpretation of differential gene expression results of RNA-seq data: review and integration. Brief Bioinform 2019 Nov 27;20(6):2044-2054. https://doi.org/10.1093/bib/bby067

- Corchete, L.A., Rojas, E.A., Alonso-López, D. et al. Systematic comparison and assessment of RNA-seq procedures for gene expression quantitative analysis. Sci Rep 10, 19737 (2020). https://doi.org/10.1038/s41598-020-76881-x

- Van den Berge et al. RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science. Vol. 2:139-173 (Volume publication date July 2019). https://www.annualreviews.org/doi/full/10.1146/annurev-biodatasci-072018-021255

- Geng Chen, Baitang Ning and Tieliu Shi. Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. Front. Genet., 05 April 2019. https://www.frontiersin.org/articles/10.3389/fgene.2019.00317/full

- Haque, A., Engel, J., Teichmann, S.A. et al. A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. Genome Med 9, 75 (2017). https://doi.org/10.1186/s13073-017-0467-4.

Structural variation, CNV:

- Wang et al. PennCNV: An integrated hidden Markov model designed for high-resolution copy number variation detection in whole-genome SNP genotyping data. https://pubmed.ncbi.nlm.nih.gov/17921354/.

- Tech note from Illumina: Interpreting Infinium® Assay Data for Whole-Genome Structural Variation https://www.illumina.com/Documents/products/technotes/technote_cytoanalysis.pdf

- Lin et al. Analyzing Copy Number Variation using SNP Array Data: Protocols for Calling CNV and Association Tests. Curr Protoc Hum Genet. 2014 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4015338/

- Zarrei et al. A copy number variation map of the human genome. Nature Reviews Genetics 2015 https://www.nature.com/articles/nrg3871

- Feuk, L., Carson, A. & Scherer, S. Structural variation in the human genome. Nat Rev Genet 7, 85–97 (2006). https://doi.org/10.1038/nrg1767

Collins, R.L., Brand, H., Karczewski, K.J. et al. A structural variation reference for medical and population genetics. Nature 581, 444–451 (2020). https://doi.org/10.1038/s41586-020-2287-8.

- Moreno-Cabrera et al. Evaluation of CNV detection tools for NGS panel data in genetic diagnostics Eur J Hum Genet. 2020 Dec;28(12):1645-1655. https://pubmed.ncbi.nlm.nih.gov/32561899/

Multi-omic approaches:

- Hasin et al. Multi-omics approaches to disease. Genome Biology volume 18, Article number: 83 (2017). https://genomebiology.biomedcentral.com/articles/10.1186/s13059-017-1215-1

- Joshi, A., Rienks, M., Theofilatos, K. et al. Systems biology in cardiovascular disease: a multiomics approach. Nat Rev Cardiol 18, 313–330 (2021). https://doi.org/10.1038/s41569-020-00477-1

Other genomes:

On mitochondria:

- Stewart, J.B., Chinnery, P.F. Extreme heterogeneity of human mitochondrial DNA from organelles to populations. Nat Rev Genet 22, 106–118 (2021). https://doi.org/10.1038/s41576-020-00284-x

On microbiome:

- Sanna, S., Kurilshikov, A., van der Graaf, A. et al. Challenges and future directions for studying effects of host genetics on the gut microbiome. Nat Genet 54, 100–106 (2022). https://doi.org/10.1038/s41588-021-00983-z

- Allaband et al. Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. Clinical Gastroenterology and Hepatology 2019;17:218–230.

- Fan, Y., Pedersen, O. Gut microbiota in human metabolic health and disease. Nat Rev Microbiol 19, 55–71 (2021). https://doi.org/10.1038/s41579-020-0433-9

- Martino, C., Dilmore, A.H., Burcham, Z.M. et al. Microbiota succession throughout life from the cradle to the grave. Nat Rev Microbiol 20, 707–720 (2022). https://doi.org/10.1038/s41579-022-00768-z

Mendelian randomization:

- Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians BMJ 2018; 362 doi: https://doi.org/10.1136/bmj.k601

- A two minute primer on mendelian randomisation: https://www.youtube.com/watch?v=LoTgfGotaQ4

- 30TH THOMAS FRANCIS JR MEMORIAL LECTURE ‘Mendelian randomization’: can genetic epidemiology contribute to understanding environmental determinants of disease?* George Davey Smith and Shah Ebrahim 320001_dyg070.pdf Download 320001_dyg070.pdf

- Rebecca C Richmond, George Davey Smith. Mendelian Randomization: Concepts and Scope Review Cold Spring Harb Perspect Med. 2022 Jan 4;12(1):a040501. doi: 10.1101/cshperspect.a040501.

General Outline for Student Presentations – HUGEN 2029

- Paper title, journal, authors (1 slide)

- Introduction: brief description of the central question addressed in the paper and its significance (1-2 slides).
  What is the goal of the described study? What is the hypothesis?

- Previous studies: summarize previous studies relevant to the paper (1-2 slides).

- Study design: give overview of study design used.
  Anything in previous studies or background that made going with this design obvious or that argues against this type of design? What are the strengths and limitations of this design? Would you have used this design? Discuss why or why not?

- Methods: describe what methods are used in the paper.
  What are the strengths and limitations of the methods used? Do the methods employed make sense given the study design? Would you have used these/similar methods? Discuss why or why not?

- Results: show and discuss the results.
  Do the results make sense? Do you agree with the authors' interpretation of the results? Discuss why or why not.

- Summary/Conclusions: briefly reiterate key findings and the strengths and limitations of the study in particular in relation to study design and methods employed.
  Did the authors use appropriate design and methods? Do you agree with the interpretation of the results? Discuss why or why not.

Rubric for Student Presentations – HUGEN 2029

Category	Elements	Weight
Knowledge and explanation of topic, discussion:	• Conveys understanding • Presents the essential information • Accurate description of methodology, study design, goals and hypotheses, etc. • Good discussion of strengths and limitations	**75**
Overall organization of section/talk	• Content introduced in logical, easy-to-follow sequence • Main points emphasized, repeated • Use of transition statements	**10**
Overall effectiveness of slides (text and visuals) and delivery	• Good balance of text & figures/tables • Text/figures/tables large enough to be seen • Not too many or too few slides • Confident, enthusiastic delivery • Eye contact • Get to main points quickly	**15**