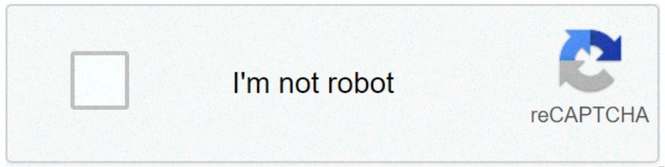

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Activity lesson plans for middle school social studies

Choosing high school courses that will best prepare you for success in college can be a difficult process, and social science, even if a critical topic for a strong college application is easily neglected, particularly if you do not plan to enter a liberal arts program. Many students are more concerned about their mathematics, science, and foreign language requirements. High school preparation requirements in social sciences vary significantly among different colleges and universities, and the term 'social science' can mean something different in different schools. Social science is an age theme that can entice classes in history, government, civics, culture, and psychology. Almost all selective colleges want to see at least two years of social sciences, and many want to see three years. Applicants most of highly selective colleges will take four courses in social studies including difficulty AP, IB, or double-enrollment classes. Social Sciences is a huge theme that engulfes fields of study related to culture, government, civic, and general interactions of people in a complex and global national context. Wars, technology, law, religion, and immigration all have a place in the category of social science. High school classes of social sciences typically include United States History, European History, World History, U.S. Government, Human Geography, and Psychology. However, keep in mind, however, these colleges are free to define social sciences as broadly or narrow as they choose. Most competitive colleges recommend at least two to three years of high school social studies, which generally include history as well as courses in government or civics. Here are some specific recommendations for social high school studies at many different institutions: Carleton College, one of the top liberal arts colleges in the country, requiring three or more years of social sciences. The college does not specify which courses it prefers students to take under the label of social sciences. Harvard University, the prestanged Ivy League school, is more specific to its recommendation. The university wants to see that students took at least two, and preferably three years of course including American history, European history, and another course of advanced history. Stanford University, another prestile and highly selective university, wants three or more years of history/social science. The university wants these courses to include a meaningful writing essay requirement so that applicants are prepared for their rigid arts in university science and social science classes. Pomona College, an excellent liberal college and member of the Claremont Colleges, wants to see a minimum of two years of social sciences (the school's term used for social sciences), and the college recommends three years. Clearly when a highly selective school recommends something, applicants should take this recommendation a lot one of the country's top public universities, demanding two years of study. The University is more specific about this condition than many other institutions. UCLA wants to see a year in world history, culture, and geography; and a year of U.S. history or a half-year history and a half-year civic or U.S. government. Williams College, another top-ranked liberal college, has no specific academic requirements for admission, but the school's admissions website noted that they seek the program most of the studies offered in a student's school, and that competitive applicants typically take a four-year sequence of social studies. The table below gives you a quick warning of typical social studies requirements for different types of colleges and universities. Social Study Requirements For College Admission School Social Studies Auburn 3 years compulsory Carleton College 2 years required, 3 or more years recommended Centre College 2 years recommend Georgia Tech 3 years required Harvard University 2-3 years required (Citi, European, another advance) MIT 2 year compulsory NYU 3-4 year compulsory Pomona College 2 required year, 3 years recommend Smith College 2 year compulsory Stanford University 3 or more recommended years (should include writing essex) UCLA 2 year compulsory (1 year world, US or 1/2 year US + 1/2 civic or government) University of Illinois 2 compulsory years, 4 years recommended University of Michigan 3 years required; 2 years for engineering /nursing Williams College 3 years recommend you can see in the selective colleges above that all schools require two or more social studies grades, and many require three. The reality is that your application will be stronger with four classes, so it's important to remember that colleges look more favorably about applicants who have done more than meet the minimum requirements. What you take will largely depend on what your school is offering. A student who takes a course in U.S. history followed by courses in American and American history at war shows the depth of knowledge and intellectual curiosity, but courses beyond American core stories are not offered in many school systems. In general, however, you should take the most difficult course available to you. An IB curriculum will certainly impress the admission officers, as will class AP in history and government. If you have the option to take classes in a local college, these dual enrollment classes in history, politics, sociology, psychology, government, and other social studies will also make a good impression and help demonstrate your college preparation. College admission officers are looking for students who challenge themselves throughout high school, taking on advanced courses in multiple subjects. Because social studies are an area where most schools only require two to three years of study, you have opportunities to present yourself as a well-rounded and dedicated student when you take additional courses. This is particularly true if you are applying for a college program in history, civics, or any of their liberal arts. Looking for new ways to introduce math concepts? Need insights for group writing activities? Get tips on creating lesson plans in every high school topic, including mathematics, English, science, social science, arts, and technology. Platelet essence functions to moderate highly legacy supporting the hypothesis that genetic variations believe individual variables in trends for arterial trombosis. Over the past seven years, in JeneSTAR GWAS revealed several common genetic loks passed by GWAS portraits of American and European families at high risk for CHD. Common variants were found to determine variables of native platelet aggregation as well as residual platelet aggregation after aspirin low dose (ASA) intervention. However, the local collectively identified in this common variants account variants for less than 35% the total inheritance of these phenotypes in the GeneSTAR families. Extending a family-based design into an integrated approach, our approach is now: 1) identifying rare variants of genes associated with native post-native aggregation and residual ASA, testing the hypothesis that a significant fraction of the 'missing inheritance' of fenot platelet aggregation is due to such rare variants; and 2) follow up - identified local to determine the 'hidden' variants that are tagged by the GWAS association. In a family sequence approach based on our family the sequence of 200 agregable people selected from American and European geneSTAR families with inspection of platelet aggression. The validation of ecomomi sequences - Identifying genes together with the local GWAS-identified will follow up counts on a deep rest approaches 1,300 U.S. and European topics americans from other GeneSTAR families. The results of this GWAS integration and overhauling approach will lead to a better understanding of the role of genetic variants (common and rare) to the determination of native plate aggregation and residual post-ASA, including possible racial differences, and should allow genotic staff of preventive therapy for CHD in people with great risk. Authentic and residual post aspirin platelet aggregation hyper, a strong risk factor for ischemic syndrome, is moderately very legacy. In our family suggesting a high degree of 'lacking inheritance' (i.e. not explained by the common GWAS detected signals). The main hypothesis is that genesis bearing rare genetic variants to determine against platelet aggregation for a substantial fraction of legacy shortages, and a family approach based on GWAS integration and ecomomi-sequences will be implemented to test this hypothesis. Work closely with Departments, we are honored in methods that use the full ability of family-based methods, and that we will extend to all young man sequences, providing integration of our different approaches to understand platelet functions. Transitioning these analytic model novels into whole young man's data and the multiomical data we're collecting in other studies will provide a highly valued advancing in larger studies using discoveries approaching to Big Data's efforts. Whole Genome Sequencing; TOPMedTrans-Omics for Precision Medicine (TOPMed) Program: NHLBIThe NHLBI Goals is collecting WGS data for those who have well-defined clinical phenotypes and results from earlier NHLBI-unfounded studies. Currently, this WGS project has sequences of more than 100,000 young men. THE TOPMED program will perform studies to collect –omics data in a subset of WGS project participants. Currently, the consortium TOPMed program includes centers that support program activities such as data coordination, compliance research, whole-young sequences, RNA sequences, and metabolite and profiled methylation. Two of these centers, the Data Coordination Center and the Comistics Research Center, serve the entire TOPMed program. The National Center for Information Biotechnology (NCBI) provides repositive data and access services for the TOPMed program. The JeneSTAR Rewards Award allows us to participate in many phenotypic aspects of WGA as well as for refined family methods based on soulified results from the discovery samples. A supplement to this work has been approved for the NHLBI Whole Genome Sequencing Project (NHLBI-WGS) in 1800 subjects to significantly strengthen the study design of the parent's work in families with shallow functions. TopMed's new work involves two other RNASeq projects on specific target tissues in patches and iPS exit megakaryocytes. Our main emphasis is on the genetics of platelet aggregation and our original WGS design was a two-step approach to identify generous rare variants that determined platelet hyper-aggreation in families at high risk for CAD. We are also generating data to families that will far reach beyond the main phenotypes using the extensive fenotyer available in family participating topics to identify at high risk over a 35 year period of the JeneSTAR Program. In TOPMed under the leadership of Dr Mathias we are involved in working groups on atheroscleroz, highly ematological, pneumonology and highly related, antropometrical, diabetes, and many other highly desirable. Innovation in the DesignThe Family-based application design study is multi-fold where we (1) identify families with groups of baseline hyper-aggregation and residual post-ASA hyper-aggregation; (2) the whole sequence of young men a set of priority families on the basis of both phenotypes; (3) rebutten the youth / relocate to additional independent families with measured fenotyer; and (4) increase WGS and data transcripts to non-encoding priorities identify alternately based on tedious eQTL analysis. Our original study's design vastly improved in its innovation with 3 points and 4 above yield a multi-stage comprehensive approach that not only yielded statistical power for rare association signals, but also limited the false positive signal seen as a limit to rare variants investigation into the case-control design. Ultimately this approach offers new insight into how much of the 'lack of inheritance' can be explained by rare variants in the context of legacy true family in place of phenotypic phenotypic inheritance variables. Rasika A Mathias, ScDAssociate Professor, MedsinAssociate Faculty, EpidemiologyPrinsal Investigator collaboratorsKai Kammers, PhDAssistant Professor, Center of Oncology, Biostatics and BioinformaticsJeff Leek, PhDProfesseursor, Biostatististics and Oncology of Ruczinski, PhDProfeseurs. BiostatistikMargaret A Taub, PhDAssistant Scientist, BiostaticLife after linkagePlatelet hyperraggregation is an important intermediate physician for myocardial infarction, coronary syndrome and congestion syndrome, and syndrome. We have already discovered and rebuttal signals to GWAS for platelet aggregation in two-generation families of probands of premature disease corroner (GeneSTAR), European Americans and African Americans. Although platelet aggression is highly legacy, all the signals GWAS identified together explain only a small fraction of its variance among people. GWAS signals are located in introns and intergenian regions, so it's not clear how the variants are functionally related to the aggression response. In this implementation we propose to discover new routes to regulation platelet platelets by determining which genes are expressed in subjects and platelet hyperraggation. By sequence the platelet transcript we will identify changes in the amount or quality (e.g., split variants) of mRNA transcripts associated with double specific flat phyraggation. We will also use all sequences of young men with RNA-seq to address our research questions. Our goals are to: (1) use a family-based design unique to examine genes that differentiately express in white and African American subjects with flat hyperraggation compared to control subjects (as defined in previous studies), (2) increased before our WARD identified eQTLs which associated with expression transcripts to help transcry priorities /youths for further study, and (3) use quantitative mass spectrometry to determine whether changes in expression in iperaggregating plates are accurately reflected in corresponding changes in express proteins. This study will produce a comprehensive quantitative inventory of all gene transcripts present in platestones, as well as a comprehensive eQTL map of genetic locals that are responsible for expressions transcript especially in platestones in both European and African Americans. We hope our studies will identify proteins and proteins unknown and biological Responsible for platelet hyperraggation, which can then serve as new therapeutic goals and ultimately more efficient and specific approaches to prevent platelet function in large numbers of people at risk for thrombotic thrombotic inclusion have been treated with anti-platelet therapy. The study uses fresh fear and global control and is operational from 2014-2019. Lewis C. Becker, MDRobert L. Levy Professor, CardiologyPrincial InvestigationtorConsent FormInduced Pluripotent Stem Cells, Megakaryocytes, and PlateletsThis is a new grant commissioned in 2011. Below we design the phases. Next the GeneSTAR is a collaborative project with the Divisions of General Internal Medicine, Ematology, and Cardiology, the Institute for Phone Engineering, and John Hopkins opkinsetic Core. The project has several primary investigators. Under the leadership of Drs. Lewis Becker from GeneSTAR and Linzhao Cheng from Ematology, the study began with a 2 year lab phase, a portion of which was guided by the University of Tokyo (Dr Hiro Nakauchi) and University of Kyoto (Dr Kojito). Plates of circular blood emostas are normal, but can also initiate pathological pathological trombos that produce heart attacks and stroke. In our GeneSTAR GWAS Study of native plates and post-aspirin platelet function, we found many signals of the meaning of young man-wide. The mechanism remained largely indefinite because most signals occurred in introns or intergenic regions rather than in regions coding proteins in known genes. In addition, the plates come from megakaryocytes in the bone range, but they are ukulele and tiny residual mRNA. In this 3 phase study, we examine the functional genomics of these associations in order to define risk assessment novel paradigms and identify new medicinal goals for cardiovascular and traumatic diseases. In My Phase, under the direction of Dr Linzhao Cheng with assistance from Drs Nakauchi and Eto, developed an effective method to generate human stem cell (iPS) from broader mononukleer cells, developing methods to generate differentiated megakaryocytes (Mks) from these human iPS, determine what the differentiated MKs look like normal Mks and possess the cell markers of naturally designed Mks, and that the whole genotip-fasting of these differentiated Mks remains true to the original genotip. In Phase II, also under Dr Cheng's direction, we: develop an effective method to generate iPS cells in batch from at least 10 people at a time using PBMCs from 20 Genest Methods subject to generate Mks from these bundles and perform RNAseq.In Phase III, under the direction of the GeneSTAR team, Dr Lewis Becker was iPS cells from 257 selected study subjects that had whole young sequences, a GWAS plate with extensive phenotyping plates, selected by phenotype and/or genotip for SNP variants and important young man-wide associations in white subject to African Americans. Mks have been differentiated from iPS cells for each selected subject. We examined gene expression profiles from Mks to differentiate from each topic using Human Exon 1.0 ST Array from Affymetrix (containing all known youth transcript and express sequential tags (ESTs) in person), and confirm the expression. The expression of selected proteins corresponding to the express mRNAs being examined by mass spectrometry in the lab of Dr Jenny Van Eyk, Cedars Sinai Research Institute, Los Angeles CA. For significant genotip/phenotype SNP associations we found for native and post-ASA platelet function, we are comparing gene expression profiles from Mks by genotype. We will determine whether to elevate the transcripts associated with corresponding protein expressions. We will determine the relationship between genetic variants across the genealogical and genetic transcript levels (eQTLs) using multi-dimensional analysis to help understand how genetic variants, particularly in synthetic regions, can produce functional generic effects. This will provide an eQTL database for megakaryocytes that is shared with the scientific community. We're comparing youth expression profiles to Mks from subjects and high vs platelet response platelet aggregations with different agonists (collages, ADP, epinefirine, and caradonic acid), at base and after aspirin. We will determine whether some transcript codes are expressed for protein in functional routes. In Phase III, work includes collaboration of Genestar's Doctor, Rasika Mathias, an expert in genetic analysis, and Drs Jeff Leek, Kai Kammers, and Margaret Taub of the Biostatics department at Bloomberg School of Public Health. We are also studying mutation rates in iPSC and copy number variations with the expertise of Dr. Ingo Ruczinski, the Department of Biostatistics.Cell RepositoryWe hold an iPSC bank repository for all 257 cell lines of Johns Hopkins at the becker lab of Cardiology. Cells are also available at Wicell, Inc. the home of the entire NHLBI NextGEN project. Wicell can be dug using the following links to the Becker cells from GeneSTAR: RepositolePlatelet Aggregation (Dr Lewis Becker, Johns Hopkins University) Becker Laber's Next Line Cell Collection study, from Dr Lewis Becker (Johns Hopkins University), was produced to enable the study of the genetic base of human variations in native platelet functions and flat response for aspirin. The iPS cell lines in this study are included in this collection. This collection contains 198 people inducing pluripotent stem cell lines from under very effective conditions in clinically compliant. Cell lines consist of healthy fees, sisters, and children can index with brothers and sisters of early patient corroner (<60 years age). None of the subjects were affected with coronary clinical disorders, stroke, or other vascular phenotypes disorders vascular at the time of the study. Pedgre is detailed in genetically related phone line fields of each cell's web page. Age donors from 28 to 86 and ethnic include European And African Americans. About Next Generation Studies Association (Next Contains) ProgramThese cell lines were created as Next Generation Association Study (Next Contains) Program, which was a five-year program, $80 million to investigate genetic variations in humans by assessing cell profiles that replace phenotypes disorders. To achieve this, the researchers from multiple institutions across the U.S. provided grants to line iPS cells from more than 1,500 people representing various conditions as well as the healthy control for use of functional genomic ('esp in a dish') research. This extensive panel includes a diverse range of age, sexual and ethnic backgrounds, and therefore will be an invaluable tool for evaluation across demographics. Further improving the utility of these cell lines is data sets such as fenotyping, GWAS, fasting

sequences, fasting expressions and -omics analyzes (e.g., lipidomic, proteiumium, methylomic) that will be made available with cell lines. iPS Megakaryocytes, with platelets of GeneSTARLewis Becker, MDRobert L. Levy Professor, CardiologyPrinyPrincial Inquirer

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