

Planner Session	Talk Title	First Name	Last Name	Learning Objective	Learning Objective	Learning Objective
Oral Presentations Session 2: Epigenomics	Large Scale Genome-Wide Methylation Analysis of Schizophrenia	Karolina	Aberg	Understand the concept of methylome-wide investigations using next-generation sequencing.	Understand the benefits of external data integration using a software such as MIND.	
Oral Presentations Session 9: Mixed Topics	Examining the Association Between GPSM1 and Human Alcohol Dependence Using Association, Bioinformatics, and Expression Studies	A	Adkins	Examine the association between GPSM1 and human alcohol dependence.	Use expression studies and animal models to investigate the biological role of GPSM1 in alcoholism.	
Oral Presentations Session 7: Statistical Genetics, Genetic Epidemiology	CNR1genotype moderates the effects of childhood abuse on anhedonia	Arpana	Agrawal	Review the endocannabinoid system, in concert with exposure to chronic unpredictable stress, modulates anhedonia	Review replication, in four independent samples, the interaction between rs1049353 in CNR1 and childhood physical abuse in predicting anhedonia	
Oral Presentations Session 6: NextGen Sequencing	Brain transcriptome analysis by RNA-seq reveals novel differentially expressed genes in bipolar disorder	Nirmala	Akula	Identify novel differentially expressed genes in bipolar disorder brains	Identify the co-expressed and co-regulated genes in brain transcriptome	Detect novel, low abundance transcripts, alternate isoforms in bipolar disorder brains
Oral Presentations Session 2: Epigenomics	Genome Wide Studies of Imprinted genes in the Frontal Cortex: Transcriptome and Methylome Analysis	Cathy	Barr	Identify imprinted genes in the mouse genome.	Utilize high through put sequencing to study mechanisms of imprinting and gene regulation.	
Oral Presentations Session 9: Mixed Topics	Copy Number Variation in Schizophrenia and Bipolar Disorder in a Swedish Population	Sarah	Bergen	Establish genomic loci of some large, rare copy number variations (CNVs) implicated in schizophrenia	Describe the ways schizophrenia and bipolar disorder are similar and distinct in terms of CNV burden by size and frequency	
Symposium 12: Pharmacogenetics in Psychiatric Practice:	Anxious depression and pharmacogenetics of antidepressant drugs	Elisabeth	Binder	Illustrate the importance to use more refined phenotype definitions in pharmacogenetics of antidepressant drugs.		
Symposium 10: Recent Advances In The Genetics Of Post Traumatic Stress Disorders (PTSD): Going Beyond Genetic Associations	FKBP5, early trauma and post traumatic stress disorder	Elisabeth	Binder	Identify possible molecular mechanisms of gene x environment interactions		
Oral Presentations Session 5: GWAS/Candidate Genes I	The Neuronal Transporter Gene SLC6A15 Confers Risk to Major Depression	Elisabeth	Binder	Establish adequate next steps regarding replication and functional studies if you have a genome-wide significant result.	Identify a new candidate gene for major depression resulting from a genome-wide association study is presented.	
Symposium 8: Elucidating the Functional Relevance of the ANK3 and CACNA1C Bipolar Disorder Risk Genes	Human functional studies of ANK3 and CACNA1C from the Greek LOGOS cohort	Panos	Bitsios	Identify phenotypic consequences of risk CACNA1C and ANK3 polymorphisms in the human brain	Establish mechanisms by which CACNA1C and ANK3 genes increase risk for psychiatric illness	Utilize endophenotypic approach in psychiatric genetic association studies
Symposium 7: From Genes to Biology: Developmental Psychopathology	Meta-analysis of six genome-wide association studies of ADHD in adults	Dorett	Boomsma	Assess genetics of adult adhd		
Oral Presentations Session 5: GWAS/Candidate Genes I	A GWAS OF PSYCHOSIS - DATA FROM THE PSYCHOSIS ENDOPHENOTYPES CONSORTIUM	Elvira	Bramon	Present new unpublished data	Determine the genetics of psychotic disorders	

Oral Presentations Session 2: Epigenomics	Next-generation sequencing identifies miRNAs associated with mood disorders	Melanie	Carless	Identify miRNAs associated with mood disorders	Identify miRNAs associated with brain-related phenotypes	
Plenary 5: Genetic Dissection of Complex Traits	Genetic dissection of complex disease	Aravinda	Chakravarti	Examine the molecular genetic basis of complex inheritance	Identify specific genes that lead to neuronal deficits in human diseases	
Symposium 4: Functional Genomics in Post-GWAS of Neuropsychiatric Diseases	Co-expression Modules in Schizophrenia Postmortem Brains	Chao	Chen	Identify MT's potential contribution in schizophrenia pathogenesis	Compare single gene based differential expression with network analysis	Establish strict quality control steps are essential for microarray analysis.
Oral Presentations Session 8: GWAS/Candidate Genes II	Meta-analysis of European and Asian-ancestry samples identifies 3 novel loci associated with bipolar disorder	David	Chen	Utilize meta-analysis in the identification of bipolar disorder risk markers	Estimate genetic risk explained with identified bipolar disorder risk markers	
Symposium 2: Genes to Biology in Understanding of Nicotine Dependence	Smoking and Genetic Risk Variation across Populations of European, Asian, and African Ancestry - A Meta-analysis of Chromosome 15q25	Li-Shiun	Chen	Use genetic meta-analyses to inform the region for causal variants and characterize genetic effects	Associate specific variant in CHRNA5 and heavy smoking across population.	
Symposium 4: Functional Genomics in Post-GWAS of Neuropsychiatric Diseases	Integrating RNA-Seq and Genome-wide Association to Identify Risk Genes for Schizophrenia	Xiangning	Chen	Utilize transcriptome profiling by high throughout DNA sequencing	Understand genome-wide association analysis	
Symposium 6: Biologically informed analysis of GWAS data: from biology to genes, and back.	Inference of functional gene networks in the synapse	L. Niels	Cornelisse			
Symposium 4: Functional Genomics in Post-GWAS of Neuropsychiatric Diseases	Brain eQTLs and Function-based GWAS of Bipolar Disorder Identified Novel Disease Risk Genes	Nancy	Cox	Establish new ways of analyzing genome-wide association studies	Assess how eQTLs can be used to enhance understanding of results from genome-wide association studies	Identify genetic risk factors for bipolar disorder.
Oral Presentations Session 7: Statistical Genetics, Genetic Epidemiology	Assessing the contribution family data can make to case-control studies of rare variants	David	Curtis	Understand value affected relatives can add to case-control studies	Utilize one approach to testing combined linkage and association	
Oral Presentations Session 10: Functional Genomics & Model Organisms II	Human induced pluripotent stem cell-technology to studyneural differentiation	Leonardo	D'Aiuto	Investigate distinct steps in neural differentiation.	Investigate the effect of neurotropic viruses on neural differentiation.	
Psychiatric Genetics for Clinicians Session	Psychiatric Genetics for Clinicians Session	J. Raymond	DePaulo	Assess the complexity of the genetic origins in Bipolar and	Identify next logical steps in genetics research for Bipolar	
Oral Presentations Session 10: Functional Genomics & Model Organisms II	Systems Genetics in Mood Disorders: Integration of Genome-wide Association Results with Human Brain Expression Data	Sevilla	Detera-Wadleigh	Illustrate a strategy for determining the functional correlate to genes implicated in GWAS	Analyze and visualize biological networks and pathways recruited by candidate risk genes that are differentially expressed in mood disorder brains	
Oral Presentations Session 9: Mixed Topics	Genes to Biology…and Back to Behavior: Understanding Trajectories of Risk for Alcohol Dependence	Danielle	Dick	Integrate twin study findings with gene identification efforts	Characterize mapping trajectories from gene to behavior across development	
Symposium 3: Exploring the Mechanisms Underlying Genome-Wide Significant Associations with Psychosis	Cognitive & imaging correlates of genome-wide significant risk variants for schizophrenia	Gary	Donohoe	Characterize the effects of schizophrenia GWAS identified variants on brain structure and function	Identify some of the main cognitive neuroscience approaches to understanding common risk variants for psychosis.	
Recruitment of Subjects: Lessons learned over 25 years	Recruitment of Subjects: lessons learned over 25 years	Caroline	Drain	Assess 25 years of successful and unsuccessful recruitment methods.	Investigate successful recruitment methods: media tools, informed consent 101, importance of screening questionnaires.	Establish recruitment methods for culturally diverse populations.

Longitudinal studies of individuals at genetic high-risk for bipolar disorder: Current status from three countries	Early clinical stages of bipolar disorder: Findings from a longitudinal study of genetically at-risk offspring	Anne	Duffy	Present new data regarding the early natural history of bipolar disorder in offspring at high-risk	Identify the shortcomings of the current diagnostic system in regard to the early natural history of bipolar disorder	Identify the implications of a clinical staging model of bipolar disorder
Oral Presentations Session 1: Functional Genomics & Model Organisms I	Establishment of cocaine preference is delayed in α CaMKII autophosphorylation-deficient mice	Alanna	Easton	Identify α CaMKII and its role in learning	Analyze the conditioned place preference design and its use in models of addiction	
Translational research in anxiety: how animal-based models can complement Human Genetics	TMEM132D: A new candidate for anxiety phenotypes - evidence from human and mouse studies	Angelika	Erhardt	Assess performance of human genetic studies in panic disorder	Implement animal-based models to validate human genetic results	
Oral Presentations Session 9: Mixed Topics	Potential Benefits, Risks, and Ethical Applications of Psychiatric Genetic Testing: A Psychiatric Genetic Researchers' Perspective	Jessica	Erickson	Compare psychiatric genetic researchers' perspectives on potential benefits and risks of their research	Identify ethical issues that represent challenges in both the advancement and clinical application of psychiatric genetic research	Implement researchers' recommendations regarding potential clinical use of the knowledge generated by their research
Symposium 9: Advances in Understanding Dysbindin-1 Functions Relevant to Schizophrenia	Regulation of Synapse Composition by the Dysbindin Associated Complexes, BLOC-1 and AP-3	Victor	Faundez	Asses cell biology of Dysbindin	Identify membrane traffic roles of dysbindin	
Oral Presentations Session 1: Functional Genomics & Model Organisms I	Lentiviral mediated-mediated gene delivery reveals distinct roles of nucleus accumbens dopamine D2 and D3 receptors in novelty- and light-induced locomotor activity	Alinda	Fernandes	Utilize viral mediated gene delivery technique can be used to investigate specific role of a gene or isoform in a particular brain region.	Utilize viral mediated gene delivery technique to study the effect of genes in animal behaviour	Utilize viral mediated gene delivery technique to characterize the molecular and cellular role of novel genes in vitro
Recruitment of Subjects: Lessons learned over 25 years	Recruitment of subjects: lessons learned through 25 years of experience	Carrie	Fisher	Assess 25 years of successful and unsuccessful recruitment methods.	Investigate successful recruitment methods: media tools, informed consent 101, importance of screening questionnaires.	Establish recruitment methods for culturally diverse populations.
Oral Presentations Session 6: NextGen Sequencing	Robust discovery of copy number variation in matched Swedish schizophrenia case-control whole-exome targeted sequencing	Menachem	Fromer	Inform researchers and medical practitioners regarding a state-of-the-art method for detecting large structural genetic variation in functional regions of the genome.	Illustrate a number of genes putatively involved in increasing risk for schizophrenia by demonstrating changes in copy number in schizophrenic patients.	
Oral Presentations Session 1: Functional Genomics & Model Organisms I	In vivomicroRNA CSF profiling in patients with schizophrenia	Juan	Gallego	Analyze the presence of miRNAs in cerebro-spinal fluid.	Investigate the differential expression of miRNAs in different tissues and different groups of human subjects.	
Oral Presentations Session 7: Statistical Genetics, Genetic Epidemiology	A Poisson Regression Approach For Association Mapping Of Count Phenotypes	Saurabh	Ghosh			
Oral Presentations Session 3: Phenotypes & Endophenotypes	Genome-Wide Association Implicates FGF14 in Amygdala Volume and Fear Processing	David	Glahn	Localize genetic influences for the human amygdala	Determine if SNPs influencing amygdala volume also influence associated affective traits	
Oral Presentations Session 6: NextGen Sequencing	Whole-exome sequencing of five families with bipolar disorder	Fernando	Goes	Understand the application of whole-exome sequencing to bipolar disorder	Understand the utility of multiplex families in sequencing experiments	

Plenary 7: Genetic Influences on Impulsivity	Genetic Influences on Impulsivity	David	Goldman	Define the role that impulsivity plays a genetically-influenced risk factor in different psychiatric diseases	Discuss the role of alleles of various frequencies, ranging from rare to common, in mediating vulnerability to psychiatric diseases	Discuss the strength of action of genes on molecules versus intermediate phenotypes and complex behavioural phenotypes.
Symposium 8: Elucidating the Functional Relevance of the ANK3 and CACNA1C Bipolar Disorder Risk Genes	Mood Disorder Susceptibility Gene CACNA1C Modifies Mood-Related Behaviors in Mice and Interacts with Sex to Influence Behavior in Mice and Diagnosis in Humans	Todd	Gould	Understand possible functional roles of calcium channels in mood disorder pathophysiology	Understand mouse approaches that can be used to translate human genetic findings	
Plenary 1: The Role in Disease of Synapse Protein Complexes and Complexity	The Role in Disease of Synapse Protein Complexes and Complexity	Seth	Grant	Understand the molecular complexity of postsynaptic proteins and their evolution	Recognize the importance of postsynaptic protein signaling complexes in human brain disease	
Oral Presentations Session 8: GWAS/Candidate Genes II	Association with SYNE1 Variant in both Bipolar Disorder and Recurrent Major Depression	Elaine	Green	Investigate a study which supports the association of SYNE1 in an independent BD samples	Identify the risk allele conferred increased risk for recurrent major depression with similar effect size to bipolar disorder.	
Oral Presentations Session 3: Phenotypes & Endophenotypes	Further evidence for genetic association between schizophrenia and bipolar from new ImmunoChip data analysis	Marian	Hamshere	Understand how to analyse data from non-genome-wide chip data with regions of extensive linkage disequilibrium, as found on the ImmunoChip	Investigate key schizophrenia SNPs in our bipolar sample for further support that the two disorders overlap.	
Oral Presentations Session 8: GWAS/Candidate Genes II	Five Novel Susceptibility Genes Identified for Alzheimer's Disease	Denise	Harold	Define the genetic architecture of Alzheimer's disease	Identify pathways implicated in Alzheimer's disease	
Symposium 2: Genes to Biology in Understanding of Nicotine Dependence	A meta-analysis of gene-environment interactions of heavy smoking with the CHRNA5-A3-B4 gene cluster	Sarah	Hartz	Understand that genetic variants can change risk of heavy smoking depending on age of onset of smoking.	Illustrate an example of studying gene-environment interactions in a meta-analysis.	Assess why meta-analyses are important for understanding biology
Symposium 3: Exploring the Mechanisms Underlying Genome-Wide Significant Associations with Psychosis	Molecular and cellular mechanisms underlying genome-wide significant association between ZNF804A and psychosis	Matthew	Hill	Understand the basic molecular mechanism underlying functionality of a non-coding psychosis risk variant in ZNF804A	Investigate transcriptional consequences of ZNF804A knockdown in neural cells and methods for assessing this	
Translational research in anxiety: how animal-based models can complement Human Genetics	Neural correlates of genetically-driven strain differences in fear	Andrew	Holmes			
Translational research in anxiety: how animal-based models can complement Human Genetics	MicroRNA Expression Patterns in a Mouse Model of Anxiety	Iris	Hovatta	Understand how microRNAs are involved in the regulation of anxiety-like behavior in mice.	Analyze the gene regulatory network analysis in the mouse brain.	
Oral Presentations Session 4: Pharmacogenomics	Berberine and evodiamine influence serotonin transporter (5-HTT) expression via the 5-HTT-linked polymorphic region	Yueshan	Hu	Establish the effects of Berberine and/or evodiamine on 5-HTT mRNA and protein expression	Assess dependency on the level of berberine and/or evodiamine induced 5-HTT promoter activity on the genetic variation in the 5-HTTLPR.	Compare the combination of berberine and evodiamine treatment on 5-HTT mRNA and protein expression and the treatment of berberine or evodiamine alone.
Symposium 7: From Genes to Biology: Developmental Psychopathology	SNPs/VNTR/CNV in total sample and MZ twin pairs discordant for ADHD	James	Hudziak			

Plenary 3: NIMH Funding Priorities for Genetics	Plenary 3: NIMH Funding Priorities for Genetics	Thomas	Insel	Establish NIMH funding priorities in genetics	Collect a large NIMH genetics resources for the global investigator community	
Oral Presentations Session 4: Pharmacogenomics	Pharmacogenetics of Antidepressant Treatment Outcome in Depression - Role of HPA Axis and Adverse Life Events	Marcus	Ising	Identify multiple genetic factors that contribute to complex traits like antidepressant treatment outcome	Investigate genetic effects on treatment outcomes	
Symposium 9: Advances in Understanding Dysbindin-1 Functions Relevant to Schizophrenia	Dysbindin-1 Modulates Brain Structure, Glutamatergic Function and Memory in Mice	J.	Jentsch	Identify the neurochemical mechanisms that mediate memory systems function caused by genetic deficiency of dysbindin-1.	Identify biological determinants of cognitive dysfunction in schizophrenia.	
Oral Presentations Session 4: Pharmacogenomics	Genomics of SSRI Treatment Outcomes for Major Depressive Disorder: Genome-wide Associations and Functional Genomics	Yuan	Ji	Understand that functional genomics represents a critical component of the psychiatric genomic association studies.	Understand the general approach to begin with for screening for functional genomic loci after high-throughput genome-wide association study.	
Recruitment of Subjects: Lessons learned over 25 years	Recruitment of Subjects: Lessons learned over 25 years of experience	Layla	Kassem	Assess 25 years of successful and unsuccessful recruitment methods.	Investigate successful recruitment methods: media tools, informed consent 101, importance of screening questionnaires.	Establish recruitment methods for culturally diverse populations.
Plenary 4: Modeling Human Genetic Disease in the Laboratory	Modeling Human Genetic Disease in the Laboratory	Nicholas	Katsanis	Analyze the complex architecture of human genetic disease	Utilize new tools used to functionally dissect variation found in patients with neurocognitive defects	
Recruitment of Subjects: Lessons learned over 25 years	Recruitment of subjects: lessons learned through 25 years of experience	Diane	Kazuba	Assess 25 years of successful and unsuccessful recruitment methods.	Investigate successful recruitment methods: media tools, informed consent 101, importance of screening questionnaires.	Establish recruitment methods for culturally diverse populations.
Symposium 12: Pharmacogenetics in Psychiatric Practice:	NTRK2 and PDE11A Predict Response to Lithium in Bipolar Disorder in Patients with Elated Mania and Positive Family History	John	Kelsoe	Establish the role of genes in lithium response.	Establish the role of clinical features in lithium response.	
Symposium 2: Genes to Biology in Understanding of Nicotine Dependence	Nicotinic receptors in the habenulo-interpeduncular tract regulate nicotine intake	Paul	Kenny	Identify the role for discrete nAChRs in nicotine reinforcement.	Compare different brain site regulation of different aspects of nicotine-taking behavior.	Assess the effects genetic variation on sensitivity of habenula to nicotine and increase risk of smoking
Symposium 1: New insights from CNV studies in schizophrenia	De novo CNVs in schizophrenia are enriched for pathogenic events and differ from inherited CNVs	George	Kirov	Investigate the role of de novo CNVs in finding new susceptibility loci for schizophrenia	Establish the properties of de novo CNVs	
Oral Presentations Session 1: Functional Genomics & Model Organisms I	Investigating the role of mutations in Zfp804a on Gene Expression	Deborah	Knight	Identify the consequences of altered ZNF804A expression on the expression of other genes using a global transcriptome approach	Use mouse models to determine the function of a schizophrenia susceptibility gene	

Symposium 4: Functional Genomics in Post-GWAS of Neuropsychiatric Diseases	Whole Genome Sequencing of Individuals from the Portuguese Island Cohort (PIC)	James	Knowles	Design strategies for DNA sequencing studies	Review results of whole genome sequencing of individuals with schizophrenia.	
Symposium 10: Recent Advances In The Genetics Of Post Traumatic Stress Disorders (PTSD): Going Beyond Genetic Associations	Corticotrophin-releasing Hormone Type 1 Receptor Gene (CRHR1) Variants Predict Posttraumatic Stress Disorder Onset and Course in Pediatric Injury Patients	Karestan	Koenen	Identify the symptoms of PTSD in pediatric patients.	Understand the role of genetic influences on PTSD.	Explain the role of CRHR1 in PTSD.
Oral Presentations Session 10: Functional Genomics & Model Organisms II	RNA-Seq analysis of differentiating human neurons derived from induced pluripotent stem cells (iPSCs)	Herb	Lachman	Demonstrate value of RNA-Seq over microarrays in analyzing gene expression during neural differentiation	Illustrate value of RNA-Seq and iPSC technology for disease modeling in schizophrenia (SZ)	
Symposium 12: Pharmacogenetics in Psychiatric Practice:	Clinical Interpretation of Whole Exome Sequencing Data in Antidepressant Treatment Response	Gonzalo	Laje	Establish the rationale for the search of rare variants in antidepressant treatment outcome.	Identify the general methods for next-generation sequencing studies.	Examine the clinical utility of next-generation sequencing data in antidepressant treatment outcome.
Translational research in anxiety: how animal-based models can complement Human Genetics	Epigenetic modification of the strong genetic predisposition towards anxiety-related behavior in psychopathological HAB mice	Rainer	Landgraf	Examine genetic underpinnings of emotionality	Assess genetic-epigenetic interactions	Utilize animal models of extreme anxiety-related behavior
Plenary 2: Association Methods for Rare Alleles	Association Methods for Rare Alleles	Suzanne	Leal	Understand the rare variant common disease hypothesis	Detect associations with rare variants for complex traits	
Symposium 10: Recent Advances In The Genetics Of Post Traumatic Stress Disorders (PTSD): Going Beyond Genetic Associations	A genetic variant BDNF polymorphism alters extinction learning in both mouse and human	Francis	Lee	Utilize vertically integrated strategies to study candidate genes for PTSD from model systems to humans.	Analyze the molecular and behavioral phenotype associated with a common SNP in the brain derived neurotrophic factor (BDNF) gene.	Utilize animal model systems to understand the biological impact of human genetic SNPs
Plenary 3: NIMH Funding Priorities for Genetics	Plenary 3: NIMH Funding Priorities for Genetics	Thomas	Lehner	Establish NIMH funding priorities in genetics	Collect a large NIMH genetics resources for the global investigator community	
Oral Presentations Session 6: NextGen Sequencing	Family-based exome sequencing in families multiply-affected for schizophrenia	Todd	Lencz	Utilize variant identification	Characterize SNPs	
Oral Presentations Session 3: Phenotypes & Endophenotypes	Neurexin-1 and Schizophrenia Subphenotypes: Brain Morphology and Clozapine Response	Tristram	Lett	Utilize brain imaging phenotype as an intermediate measure of schizophrenia diagnosis, and this is thought to be heritable.	Identify the involvement of the neurexin-1 gene as well as others in response to clozapine treatment.	Examine the involvement a single genetic variant in several subphenotypes in schizophrenia and autism
Symposium 2: Genes to Biology in Understanding of Nicotine Dependence	Importance of $\alpha 4\beta 2$ and $\alpha 6\beta 2\beta 3^*$ AChRs in Potential Drugs for Nicotine Dependence	Jon	Lindstrom	Illustrate acetylcholine receptor structure and function	identify potential smoking cessation drugs.	
Oral Presentations Session 4: Pharmacogenomics	HTR2A variation predicts treatment response to venlafaxine XR in Generalized Anxiety Disorder	Falk	Lohoff	Treat pharmacologically generalized anxiety disorder	utilize biomarkers in psychiatry	
Oral Presentations Session 8: GWAS/Candidate Genes II	Identification of common variants influencing protein abundance levels in Alzheimer's disease	Anbarasu	Lourdusamy	Identify common genetic variants that influence protein levels in human population	Identify genetic variants that alter the risk of Alzheimer's disease using protein levels as intermediate quantitative phenotypes	
Symposium 1: New insights from CNV studies in schizophrenia	De Novo Copy Number Variants Confer Risk For Early Onset Bipolar Disorder And Schizophrenia.	Dheeraj	Malhotra	Identify the role of de novo rare copy number mutations in bipolar disorder	Identify high risk Genes that could be followed in subsequent studies to test their role in pathophysiology of mood disorders	

Symposium 11: Genomics of suicidal behavior and intermediate phenotypes	An International Genome-Wide Study of Suicidal Behavior and Intermediate Phenotypes in Mood Disorders	J John	Mann	Analyze heritability of suicidal behavior	Investigate new and previously identified candidate genes	Examine inter-relationship of major depression and suicidal behavior
Longitudinal studies of individuals at genetic high-risk for bipolar disorder: Current status from three countries	H.C. Prechter Longitudinal Study of Bipolar Disorder: Baseline descriptive analysis of individuals with and without bipolar disorder	Melvin	McInnis	Understand the importance of longitudinal studies in understanding outcomes in bipolar.	Establish the impact of burden of disease in the study of outcomes in bipolar disorder.	identify the implications of an integrated approach to the study of multiple domains of clinical and biological research in bipolar disorder.
Oral Presentations Session 2: Epigenomics	Antidepressant Treatment is Associated with Epigenetic Alterations in the Promoter of P11 in a Genetic Model of Depression	Philippe	Melas	Investigate the levels of P11 in the prefrontal cortex of a genetic rodent model of depression.	Examine whether treatment with an SSRI (escitalopram) can affect P11 levels in the same model.	Investigate potential genetic and/or epigenetic contributors to the observed gene expression differences.
Symposium 3: Exploring the Mechanisms Underlying Genome-Wide Significant Associations with Psychosis	Genome-wide significant risk variants for psychosis and neural intermediate phenotypes	Andreas	Meyer-Lindenberg	Define neural abnormalities in carriers of genetic risk variants in ZNF804A	Relate neural abnormalities to risk for schizophrenia and bipolar disorder, respectively	
Longitudinal studies of individuals at genetic high-risk for bipolar disorder: Current status from three countries	Impaired inferior frontal gyrus response to an emotional inhibition task in young first-degree relatives of bipolar disorder patients compared to controls	Philip	Mitchell	Contrast clinical differences between populations at genetic high risk for bipolar disorder and controls.	Compare brain imaging between populations at genetic high risk for bipolar disorder and controls.	
Oral Presentations Session 7: Statistical Genetics, Genetic Epidemiology	Evaluation of permutation-based approaches for multi-marker association	Valentina	Moskvina	Utilize different methods of set-based (gene-wide) analyses.	Determine the advantages and disadvantages of different types of gene-wide analyses.	
Symposium 12: Pharmacogenetics in Psychiatric Practice:	Genetics of antipsychotic drug response and induced weight gain	Daniel	Müller	Investigate pharmacogenetic studies in schizophrenia and to put presented novel findings into the context.	Identify strengths and limitations of using different genetic analyses (GWAS, exome sequencing, candidate genes and computational genomics) will be discussed as well as the importance of functional analyses.	Establish general and specific implications of findings for the clinical practice.
Recruitment of Subjects: Lessons learned over 25 years	Retention of Ethnically Diverse Participants in Genetic Studies	Eleanor	Murphy	Identify the basic factors associated with subject attrition culturally/ethnically diverse sample in a genetic treatment study.	Establish the primary strategies used to improve study retention of successfully recruited subjects in genetic studies.	
Symposium 5: Application of Exome Sequencing Technologies to Autism	Full Exome Sequencing of Autism Cases, Families, and Controls	Benjamin	Neale	Integrate the data generation process for next-generation sequencing.	Elucidate the genetics of autism with respect to rare coding variation.	
Oral Presentations Session 10: Functional Genomics & Model Organisms II	Convergent Functional Genomics of Anxiety Disorders: Translational Identification of Genes, Biomarkers, Pathways and Mechanisms	Alexander	Niculescu	Examine genetics of anxiety disorders	Determine how functional genomic studies lead to the identification of genes.	Identify the genetic overlap of anxiety with schizophrenia and other psychiatric disorders.
Longitudinal studies of individuals at genetic high-risk for bipolar disorder: Current status from three countries	CHILDHOOD DISORDERS PREDICT ADOLESCENT ONSET MOOD DISORDER IN FAMILIES WITH A BIPOLAR PROBAND	John	Nurnberger	investigate diagnoses observed in adolescent offspring in families with a bipolar proband.	Observe the co-occurrence of anxiety and externalizing diagnoses in adolescents with mood disorder.	Identify the role of childhood diagnoses in predicting adolescent mood disorders in at-risk subjects
Symposium 1: New insights from CNV studies in schizophrenia	De novo CNV analysis implicates specific genetic abnormalities in the pathogenesis of schizophrenia	Michael	Owen	Analyze genetic pathways implicated in schizophrenia	Determine the value of de novo analysis in finding new genetic pathways in the aetiology of schizophrenia	

Symposium 5: Application of Exome Sequencing Technologies to Autism	Exome sequencing of autism and schizophrenia in the UK10K project	Aarno	Palotie	Assess next generation sequencing in neurodevelopmental traits	Establish analysis strategies of next generation sequencing	
Oral Presentations Session 9: Mixed Topics	Investigating the genetic basis of Tourette Syndrome in European populations. A multinational initiative.	Peristera	Paschou	Assess Tourette Syndrome Genetics	Review genetic association studies	
Symposium 7: From Genes to Biology: Developmental Psychopathology	Further understanding the heterogeneity of MDD	Brenda	Penninx	Provide scientific evidence for the heterogeneity of MDD	Explore genetic contributions to subtypes of MDD	
Symposium 11: Genomics of suicidal behavior and intermediate phenotypes	Meta-analysis of genomewide association studies of suicide attempt in mood disorder	Roy	Perlis	Provide recent genomewide association results in suicide liability and related phenotypes	Establish alternative methodologies for examining association across multiple loci	
Symposium 8: Elucidating the Functional Relevance of the ANK3 and CACNA1C Bipolar Disorder Risk Genes	Role of Ankyrin 3 in Regulating Bipolar-related Behaviors	Tracey	Petryshen	Identify behavioral and neural changes induced by reduced ankyrin 3 expression in mice.	Assess the value of using mouse genetic models to study the function of psychiatric risk genes.	
Symposium 6: Biologically informed analysis of GWAS data: from biology to genes, and back.	Protein Complexes and the Functional Basis of Psychiatric Disorders	Andrew	Pocklington			
Oral Presentations Session 5: GWAS/Candidate Genes I	AKAPs integrate genome-wide association study findings for autism spectrum disorders	Geert	Poelmans	Identify gene/protein networks for autism spectrum disorders (ASDs) through the integration of the most significant findings from published genome-wide association studies of ASDs with other genetic data, including data from copy number variation (CNV) and microRNA studies.	Identify novel protein targets for psychopharmacological treatment of ASDs in the identified genetic networks.	
From Gene to Drug Response: Multi-method Approach to the Pharmacogenomics of Response to Antidepressants	An approach to employ animal studies to inform human pharmacogenetics	Maurizio	Popoli	Characterize and use different animal models of depression	Apply genome-wide techniques for analysis of genes and proteins	Integrate epigenetic and miRNomic analysis
Symposium 6: Biologically informed analysis of GWAS data: from biology to genes, and back.	Gene-Set Enrichment and Network-Based Multilocus Analyses of Genome-Wide Data	Shaun	Purcell	Illustrate the utility of multilocus approaches that us prior biological information, with applications to neuropsychiatric datasets to illustrate each point	Suggest future directions for methodological development	
Oral Presentations Session 1: Functional Genomics & Model Organisms I	5-HT2C Receptor and Its Role in Neuropsychiatric Disorders: Evolutionary Trace Analysis and Molecular Docking Study	Meera	Purshottam	Identify evolutionarily important residues in this protein through Evolutionary Trace (ET) analysis	Create a model for the 5Ht2C receptor based on the human ⓶ Adrenergic receptor (⓶AR)	Assess the molecular interactions of agonist and antagonist with modelled 5-HT2C receptor.
Oral Presentations Session 2: Epigenomics	The SLC6A4 VNTR genotype determines transcription factor binding and epigenetic variation of this gene in response to cocaine in vitro	John	Quinn	Investigate how genotype can modify epigenetic parameters that may modulate gene expression in the medium to long term	Investigate how microsatellites can modify both transcription and epigenetic factors modulating gene expression in response to challenge.	
Oral Presentations Session 3: Phenotypes & Endophenotypes	NRGN gene, a genome-wide supported schizophrenia risk variant, modulates prefrontal cortical information processing during working memory	Astrid Veronika	Rauch	Assess the influence of the NRG gene on memory related cortical information processing in humans.	Provide evidence for modulation of a neuroimaging intermediate phenotype by NRG, a potential schizophrenia risk gene.	

Symposium 10: Recent Advances In The Genetics Of Post Traumatic Stress Disorders (PTSD): Going Beyond Genetic Associations	Evidence for association of the PACAP/PAC1 receptor pathway with Posttraumatic Stress Symptoms	Kerry	Ressler	Identify the potential role of gene modulation of risk vs. resilience following trauma.	Establish one mechanism by which sex-specific effects of genetic association with PTSD may occur.	Investigate the PACAP/PAC1 pathway association with differential risk for PTSD in females vs. males.
Oral Presentations Session 8: GWAS/Candidate Genes II	GWAS Analysis across five psychiatric illnesses: Results of a combined dataset power of 56,867 individuals	Stephan	Ripke	Identify common problems and their solution while performing meta-analyses across distinct diseases.	Investigate new insights into the genetic structure of psychiatric illness.	
Symposium 6: Biologically informed analysis of GWAS data: from biology to genes, and back.	The use of protein-protein interactions to interpret genetic association to disease	Elizabeth	Rossin	Apply the methodology of DAPPLE, which merges genome-wide functional data (protein-protein interactions) with genome-wide genetic data (from GWAS) to infer underlying mechanisms affected by risk variants.	Examine the results of applying DAPPLE to a recent schizophrenia GWAS and a recent autism exome sequencing study.	
Symposium 11: Genomics of suicidal behavior and intermediate phenotypes	Genome-wide association studies of intermediate phenotypes of suicidal behavior: Focus on aggression and impulsivity.	Dan	Rujescu	Analyze genetics of suicidal behavior	Explore genetics of impulsivity	Elucidate genetics of aggression and anger
Symposium 1: New insights from CNV studies in schizophrenia	CNVs between schizophrenia and neurodevelopmental disorders	Dan	Rujescu	Examine CNVs in schizophrenia	Explore CNVs in neurodevelopmental disorders	Investigate CNVs in psychiatric disorders
From Gene to Drug Response: Multi-method Approach to the Pharmacogenomics of Response to Antidepressants	Imaging intermediate phenotypes of depression including response to therapy: over­view and conceptual links to genetics	Philipp	Sämann	Apply imaging endophenotypes of treatment response in major depression	Compare different applications of the endophenotype concept in neuroimaging.	Detect new genetic variants by help of imaging phenotypes.
Oral Presentations Session 5: GWAS/Candidate Genes I	Genome-wide gene expression study of a schizophrenia dataset	Alan	Sanders	Establish nderstand current genome-wide approaches.	Integrate genome-wide approaches	Apply genome-wide approaches to the study of schizophrenia.
Symposium 7: From Genes to Biology: Developmental Psychopathology	Twins, tissue and time: A comparison of genomic structure across twins, DNA and longitudinal samples	Paul	Scheet			
Symposium 5: Application of Exome Sequencing Technologies to Autism	The Genetic Architecture of Autism Spectrum- and Related- Neurodevelopmental Disorders Revealed through High-Resolution Genome Analysis	Stephen	Scherer	Investigate the latest advances in genome research and their application to discovering and characterizing genes involved in autism spectrum disorder susceptibility	identify the role of copy number variation and sequence-level mutations may explain the wide ranging clinical symptoms in autism spectrum disorder.	
Symposium 6: Biologically informed analysis of GWAS data: from biology to genes, and back.	Exploring Genome-wide Association Data in Biological Context Through Protein-Protein Interactions	Pak	Sham	Assess the usefulness of biological information, such as protein-protein interaction (PPI), in the further exploration of genome-wide association data.	Detect genes that would not be detected when genes are considered individually with a statistical test that considers PPI pairs as the functional unit	
Oral Presentations Session 6: NextGen Sequencing	Identification and Analysis of Rare Variation in 503 Putative Schizophrenia Risk Loci in 1876 samples by Targeted Resequencing	Pamela	Sklar			

Symposium 2: Genes to Biology in Understanding of Nicotine Dependence	Regulatory Polymorphisms in Nicotine Dependence Risk Genes	Ryan	Smith	Promote an understanding of genetic variation that contributes to interindividual differences in gene expression.	Facilitate evaluations of complex genetic disorders by modeling interactions between multiple genetic and environmental factors.	
Oral Presentations Session 4: Pharmacogenomics	A gene expression and proteomic study provide further evidence for the involvement of Spermidine/Spermine N(1)-Acetyltransferase (SSAT1) in suicide and suggests new biological determinants of suicidal behaviour in bipolar disorder patients	Alessio	Squassina	Examine new evidences towards the involvement of the polyamine system in suicide	Identify new possible molecular elements that could play a key role in the predisposition to suicidal behaviour	
Symposium 5: Application of Exome Sequencing Technologies to Autism	Whole-exome Sequencing in Simplex Autism Quartets	Matthew	State	Demonstrate the contribution of de novo mutation to the genetic etiology of autism spectrum disorders	Clarify the burden of de novo point mutation in unaffected as well as affected individuals to aid in the interpretation of next generation sequencing data as a gene discovery strategy	
Oral Presentations Session 7: Statistical Genetics, Genetic Epidemiology	Underestimated Effect Sizes in GWAS: Fundamental Limitations of Single SNP Analysis for Disease Status	Sven	Stringer	Demonstrate that underestimation of effect sizes is a serious drawback of single SNP analysis and may result in missing heritability.	Demonstrate that single SNP analysis should be superseded by methods that analyze all SNPs simultaneously.	
Symposium 7: From Genes to Biology: Developmental Psychopathology	Gene expression in twins	Patrick	Sullivan			
Symposium 9: Advances in Understanding Dysbindin-1 Functions Relevant to Schizophrenia	Dysbindin-1 Mutant Mice Implicate Reduced Parvalbumin-Cell Mediated Inhibition as a Final Common Pathway in the Pathophysiology of Schizophrenia	Konrad	Talbot	Explore a final common pathway in the pathogenesis of schizophrenia	Assess the biological function of dysbindin-1 whose disruption may promote the symptoms and cognitive deficits in schizophrenia.	Integrate methods for studying the molecular basis of symptoms and cognitive deficits in schizophrenia.
Symposium 3: Exploring the Mechanisms Underlying Genome-Wide Significant Associations with Psychosis	Functional analysis of the ZNF804A and TCF4 schizophrenia susceptibility genes	Caroline	Tinsley	Identify the function of GWAS candidates implicated in schizophrenia.	Characterize how changes in the levels of ZNF804A may affect global gene expression in cell models.	
Symposium 11: Genomics of suicidal behavior and intermediate phenotypes	Genome-Wide Epigenetic Regulation by Early-Life Trauma and Suicide	Gustavo	Turecki	Compare differences in promoter methylation associated with childhood adversity and suicide	Investigate methodological aspects of methylation array studies in postmortem tissue	
From Gene to Drug Response: Multi-method Approach to the Pharmacogenomics of Response to Antidepressants	Transcriptomic and epigenetic correlates of antidepressant response	Gustavo	Turecki	Identify potential biomarkers of antidepressant response	Identify patterns of mRNA expression changes associated with antidepressant treatment	
From Gene to Drug Response: Multi-method Approach to the Pharmacogenomics of Response to Antidepressants	From Gene to Drug Response: Making more of genome-wide pharmacogenetic data	Katherine	Uher	Explore genomic determinants of antidepressant drug action	Integrate multiple phenotyping and -omic methods with the aim of tracing the molecular mechanisms of antidepressant action and understand individual differences in response	Assess the potential of future directions in pharmacogenomics

Oral Presentations Session 5: GWAS/Candidate Genes I	A Rigorous Family-Based Replication Study of Schizophrenia GWAS Findings	Edwin	van den Oord	Identify new genes affecting susceptibility to schizophrenia.	Identify novel methods to identify disease genes.	
Symposium 4: Functional Genomics in Post-GWAS of Neuropsychiatric Diseases	Whole methylome studies of psychiatric conditions	Edwin	van den Oord	Optimize designs of whole methylome studies of psychiatric conditions.	Recognize the promise of DNA methylation studies.	
Symposium 9: Advances in Understanding Dysbindin-1 Functions Relevant to Schizophrenia	Epistatic interactions between DTNBP-1 and COMT: Effects on working memory in mice and prefrontal physiological activity in humans	Daniel	Weinberger	Illustrate epistatic interactions of DTNBP1 and COMT on working memory in genetically altered mice	Illustrate epistatic interactions of DTNBP1 and COMT on working memory associated prefrontal cortical physiology in humans	
Symposium 8: Elucidating the Functional Relevance of the ANK3 and CACNA1C Bipolar Disorder Risk Genes	Impact of the psychiatric susceptibility gene CACNA1C in human imaging genetic studies on neural activity in healthy subjects – an overview	Stephanie	Witt	Investigate the concept of studying intermediate phenotypes in imaging genetics as a tool for elucidating the impact of genetic variants found associated with diagnosis in GWAS.	Cite most important brain regions with differential activation in risk allele carriers of rs1006737 in CACNA1C.	
Oral Presentations Session 10: Functional Genomics & Model Organisms II	What we learned from a Na ⁺ /H ⁺ exchanger: Dysregulation of the Signaling and Endosomal Pathways in Psychiatric Disorders	Yanli	Zhang-James	Translate genetic findings into a better understanding of mental illness	Foster communication and advance knowledge about inherited aspects of mental illness	
Symposium 4: Functional Genomics in Post-GWAS of Neuropsychiatric Diseases	PATHWAY AND NETWORK ANALYSIS OF GWAS AND RNA-SEQ FOR SCHIZOPHRENIA	Zhongming	Zhao	Analyze functional genomics of schizophrenia	Apply systems biology approaches to studying schizophrenia	Identify molecular mechanisms of mental disorders
Symposium 8: Elucidating the Functional Relevance of the ANK3 and CACNA1C Bipolar Disorder Risk Genes	Ankyrin G and L-type Calcium Channel: Potential Roles in Psychiatric Disease	Shanshan	Zhu	Utilize GWAS studies for identifying candidate genes	Examine evidence for interactions of candidate genes for defining pathogenic pathways	

