Notice of Award

RESEARCH
Department of Health and Human Services
National Institutes of Health

Federal Award Date: 07/19/2017

NATIONAL INSTITUTE OF BIOMEDICAL IMAGING AND BIOENGINEERING

Grant Number: 5R01EB015611-05
FAIN: R01EB015611

Principal Investigator(s):
PETER V KOCHUNOV, PHD

Project Title: Solar-Eclipse Computational Tools for Imaging Genetics

Paffrath, Dennis Joseph
AVP, Sponsored Programs Administration
University of Maryland, Baltimore
620 West Lexington Street, 4129
Baltimore, MD 212011508

Award e-mailed to: nga@ordmail.umaryland.edu

Period Of Performance:
Budget Period: 08/01/2017 – 07/31/2018
Project Period: 08/01/2012 – 07/31/2020

Dear Business Official:

The National Institutes of Health hereby awards a grant in the amount of $400,000 (see "Award Calculation" in Section I and "Terms and Conditions" in Section III) to UNIVERSITY OF MARYLAND BALTIMORE in support of the above referenced project. This award is pursuant to the authority of 42 USC 241 42 CFR 52 and is subject to the requirements of this statute and regulation and of other referenced, incorporated or attached terms and conditions.

Acceptance of this award including the "Terms and Conditions" is acknowledged by the grantee when funds are drawn down or otherwise obtained from the grant payment system.

Each publication, press release, or other document about research supported by an NIH award must include an acknowledgment of NIH award support and a disclaimer such as "Research reported in this publication was supported by the National Institute Of Biomedical Imaging And Bioengineering of the National Institutes of Health under Award Number R01EB015611. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health." Prior to issuing a press release concerning the outcome of this research, please notify the NIH awarding IC in advance to allow for coordination.

Award recipients must promote objectivity in research by establishing standards that provide a reasonable expectation that the design, conduct and reporting of research funded under NIH awards will be free from bias resulting from an Investigator's Financial Conflict of Interest (FCOI), in accordance with the 2011 revised regulation at 42 CFR Part 50 Subpart F. The Institution shall submit all FCOI reports to the NIH through the eRA Commons FCOI Module. The regulation does not apply to Phase I Small Business Innovative Research (SBIR) and Small Business Technology Transfer (STTR) awards. Consult the NIH website http://grants.nih.gov/grants/policy/coi/ for a link to the regulation and additional important information.

If you have any questions about this award, please contact the individual(s) referenced in Section IV.

Sincerely yours,

Florence Turska
Grants Management Officer
NATIONAL INSTITUTE OF BIOMEDICAL IMAGING AND BIOENGINEERING

Additional information follows

SECTION I – AWARD DATA – 5R01EB015611-05

Award Calculation (U.S. Dollars)

Salaries and Wages	$120,044
Fringe Benefits	$34,647
Personnel Costs (Subtotal)	$154,691
Consultant Services	$7,000
Materials & Supplies	$3,500
Travel	$3,500
Other	$6,817
Subawards/Consortium/Contractual Costs	$128,840
Federal Direct Costs	$304,348
Federal F&A Costs	$95,652
Approved Budget	$400,000
Total Amount of Federal Funds Obligated (Federal Share)	$400,000
TOTAL FEDERAL AWARD AMOUNT	$400,000
AMOUNT OF THIS ACTION (FEDERAL SHARE)	$400,000

SUMMARY TOTALS FOR ALL YEARS		
YR	**THIS AWARD**	**CUMULATIVE TOTALS**
5	$400,000	$400,000
6	$400,001	$400,001
7	$400,001	$400,001

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

Fiscal Information:

CFDA Name:	Discovery and Applied Research for Technological Innovations to Improve Human Health
CFDA Number:	93.286
EIN:	1526002036A1
Document Number:	REB015611B
PMS Account Type:	P (Subaccount)
Fiscal Year:	2017

IC	CAN	2017	2018	2019
EB	8015183	$400,000	$400,001	$400,001

Recommended future year total cost support, subject to the availability of funds and satisfactory progress of the project

NIH Administrative Data:
PCC: HBIR / **OC**: 414E / **Released**: eRA Commons User Name 07/18/2017
Award Processed: 07/19/2017 12:11:18 AM

SECTION II – PAYMENT/HOTLINE INFORMATION – 5R01EB015611-05

For payment and HHS Office of Inspector General Hotline information, see the NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm

SECTION III – TERMS AND CONDITIONS – 5R01EB015611-05

This award is based on the application submitted to, and as approved by, NIH on the above-titled project and is subject to the terms and conditions incorporated either directly or by reference in the following:

a. The grant program legislation and program regulation cited in this Notice of Award.
b. Conditions on activities and expenditure of funds in other statutory requirements, such as those included in appropriations acts.

c. 45 CFR Part 75.
d. National Policy Requirements and all other requirements described in the NIH Grants Policy Statement, including addenda in effect as of the beginning date of the budget period.
e. Federal Award Performance Goals: As required by the periodic report in the RPPR or in the final progress report when applicable.
f. This award notice, INCLUDING THE TERMS AND CONDITIONS CITED BELOW.

(See NIH Home Page at http://grants.nih.gov/grants/policy/awardconditions.htm for certain references cited above.)

Research and Development (R&D): All awards issued by the National Institutes of Health (NIH) meet the definition of "Research and Development" at 45 CFR Part§ 75.2**.** As such, auditees should identify NIH awards as part of the R&D cluster on the Schedule of Expenditures of Federal Awards (SEFA). The auditor should test NIH awards for compliance as instructed in Part V, Clusters of Programs. NIH recognizes that some awards may have another classification for purposes of indirect costs. The auditor is not required to report the disconnect (i.e., the award is classified as R&D for Federal Audit Requirement purposes but non-research for indirect cost rate purposes), unless the auditee is charging indirect costs at a rate other than the rate(s) specified in the award document(s).

An unobligated balance may be carried over into the next budget period without Grants Management Officer prior approval.

This grant is subject to Streamlined Noncompeting Award Procedures (SNAP).

This award is subject to the requirements of 2 CFR Part 25 for institutions to receive a Dun & Bradstreet Universal Numbering System (DUNS) number and maintain an active registration in the System for Award Management (SAM). Should a consortium/subaward be issued under this award, a DUNS requirement must be included. See http://grants.nih.gov/grants/policy/awardconditions.htm for the full NIH award term implementing this requirement and other additional information.

This award has been assigned the Federal Award Identification Number (FAIN) R01EB015611. Recipients must document the assigned FAIN on each consortium/subaward issued under this award.

Based on the project period start date of this project, this award is likely subject to the Transparency Act subaward and executive compensation reporting requirement of 2 CFR Part 170. There are conditions that may exclude this award; see http://grants.nih.gov/grants/policy/awardconditions.htm for additional award applicability information.

In accordance with P.L. 110-161, compliance with the NIH Public Access Policy is now mandatory. For more information, see NOT-OD-08-033 and the Public Access website: http://publicaccess.nih.gov/.

In accordance with the regulatory requirements provided at 45 CFR 75.113 and Appendix XII to 45 CFR Part 75, recipients that have currently active Federal grants, cooperative agreements, and procurement contracts with cumulative total value greater than $10,000,000 must report and maintain information in the System for Award Management (SAM) about civil, criminal, and administrative proceedings in connection with the award or performance of a Federal award that reached final disposition within the most recent five-year period. The recipient must also make semiannual disclosures regarding such proceedings. Proceedings information will be made publicly available in the designated integrity and performance system (currently the Federal Awardee Performance and Integrity Information System (FAPIIS)). Full reporting requirements and procedures are found in Appendix XII to 45 CFR Part 75. This term does not apply to NIH fellowships.

Treatment of Program Income:

SECTION IV – EB Special Terms and Conditions – 5R01EB015611-05

SALARY CAP
None of the funds in this award shall be used to pay the salary of an individual at a rate in excess of the current salary cap per year. Therefore, this award and/or future years are adjusted accordingly, if applicable. Current salary cap levels can be found at the following URL's:
https://grants.nih.gov/grants/guide/notice-files/NOT-OD-17-049.html
http://grants.nih.gov/grants/policy/salcap_summary.htm

GRADUATE STUDENT COMPENSATION
The maximum amount NIH will award for compensation of a graduate student (salary, fringe benefits and tuition remission) receiving support from a research grant is the zero-level Kirschstein-NRSA stipend in effect when NIH issues the grant award (see current levels posted at https://grants.nih.gov/grants/guide/notice-files/NOT-OD-17-003.html

CONSORTIUM/CONTRACTUAL COSTS
This award includes funds for consortium activity with:
- University of Texas Health Science Center at San Antonio
- University of Oxford, United Kingdom

Consortia are to be established and administered as described in the NIHGPS section 15 Consortium Agreements.
http://grants.nih.gov/grants/policy/nihgps/HTML5/section_15/15_consortium_agreements.htm

The NIBIB home page is http://www.nibib.nih.gov/

STAFF CONTACTS

The Grants Management Specialist is responsible for the negotiation, award and administration of this project and for interpretation of Grants Administration policies and provisions. The Program Official is responsible for the scientific, programmatic and technical aspects of this project. These individuals work together in overall project administration. Prior approval requests (signed by an Authorized Organizational Representative) should be submitted in writing to the Grants Management Specialist. Requests may be made via e-mail.

Grants Management Specialist: Angelos Bacas
Email: ab329b@nih.gov **Phone**: (301) 451-4785 **Fax**: (301) 451-5735

Program Official: Edward Ramos
Email: ed.ramos@nih.gov **Phone**: 301-594-3715

SPREADSHEET SUMMARY
GRANT NUMBER: 5R01EB015611-05

INSTITUTION: UNIVERSITY OF MARYLAND BALTIMORE

Budget	Year 5	Year 6	Year 7
Salaries and Wages	$120,044	$116,623	$116,623
Fringe Benefits	$34,647	$33,407	$33,407
Personnel Costs (Subtotal)	$154,691	$150,030	$150,030
Consultant Services	$7,000	$7,000	$7,000
Materials & Supplies	$3,500	$3,500	$3,500
Travel	$3,500	$3,500	$3,500
Other	$6,817	$5,336	$5,336
Subawards/Consortium/Contractual Costs	$128,840	$138,330	$138,330
TOTAL FEDERAL DC	$304,348	$307,696	$307,696
TOTAL FEDERAL F&A	$95,652	$92,305	$92,305

TOTAL COST	$400,000	$400,001	$400,001

Facilities and Administrative Costs	Year 5	Year 6	Year 7
F&A Cost Rate 1	54.5%	54.5%	54.5%
F&A Cost Base 1	$175,508	$169,367	$169,367
F&A Costs 1	$95,652	$92,305	$92,305

A. COVER PAGE

Project Title: Solar-Eclipse Computational Tools for Imaging Genetics	
Grant Number: 5R01EB015611-05	**Project/Grant Period:** 08/01/2012 - 07/31/2020
Reporting Period: 09/15/2016 - 07/31/2017	**Requested Budget Period:** 08/01/2017 - 07/31/2018
Report Term Frequency: Annual	**Date Submitted:** 05/15/2017
Program Director/Principal Investigator Information: PETER V KOCHUNOV , MS MS PHD **Phone number:** (410) 402-6110 **Email:** Personal Info	**Recipient Organization:** UNIVERSITY OF MARYLAND BALTIMORE UNIVERSITY OF MARYLAND BALTIMORE 620 W LEXINGTON ST, 4TH FL BALTIMORE, MD 212011508 **DUNS:** 188435911 **EIN:** 1526002036A1 **RECIPIENT ID:**
Change of Contact PD/PI: N/A	
Administrative Official: MARIE COOLAHAN 620 W. Lexington Street 4th. Floor Baltimore, MD 21201 **Phone number:** 410-706-0011 **Email:** m_coolahan@umaryland.edu	**Signing Official:** MARIE COOLAHAN 620 W. Lexington Street 4th. Floor Baltimore, MD 21201 **Phone number:** 410-706-0011 **Email:** m_coolahan@umaryland.edu
Human Subjects: No	**Vertebrate Animals:** No
hESC: No	**Inventions/Patents:** No

B. ACCOMPLISHMENTS

B.1 WHAT ARE THE MAJOR GOALS OF THE PROJECT?

Aim 1. To shift imaging genetics toward richer, higher resolution imaging analyses and denser genome examination through high performance computing. The shift in imaging genetics toward WGS genotyping and high-resolution multimodal imaging data necessitates improvement of computational efficiency of likelihood calculations. To speed calculations up by 105-6-fold we will implement high-performance computing: novel data decompositions and single-step algorithmic techniques and integration of Massive Universal Linear Model (MULM) GPU library of genetic tools for massively parallel genetic analyses. These developments will enable interactive WGS and GWAS analyses for Big Data project by implementing SOLAR-Eclipse in web-analyses portals such as HCP Dashboard and ENIGMAVis.
Aim 2. To accelerate data sharing and replication in imaging genetics. Demands for high-performance computing and greater reproducibility and transparency in scientific research require a new data format optimized for imaging genetics applications and easy sharing of provenance. Expanding on the work of the International Neuroinformatics Coordinating Facility's Neuroimaging Data Sharing Task Force, we have assembled a panel of community experts to develop a draft of imaging genetic format based on existing neuroimaging formats along with extending on-going provenance efforts to imaging genetic research. We will submit this format and API for formal registration with NIF.
Aim 3. To implement and exploit empirical kinship methods. Empirical kinship algorithms that directly measure the degree of shared genetic variance (such as those used in GCTA/ REACTA and MEGHA) will be integrated for performing polygenic and Quantitative Trait Loci Linkage (QTL-L) analyses in the related, unrelated and mega-genetic samples. We propose to re-invent the Quantitative Trait Loci Linkage (QTL-L) methods for localizing QTLs based on simple empirical similarity in larger (1cM) regions of DNA instead of per-locus GWA-SNP analysis. This will answer questions such as localization of chromosomal segments that are responsible for normal and disorder-related variability in neuroimaging traits. Empirical QTL-L analyses will power chromosomal localization studies with no sharing of raw genotypes for our Big Data partners.
Aim 4. Interactive improvement of developed tools in collaboration with 'big data' partners. Methods developed in Aims 1-3 will 'push' the scientific aims of our Big Data partners, who committed a large (N=10K) sample and effort for three collaborative studies. The high-performance imaging genetics computing and empirical QTL-L techniques (Aims 1 and 3) will be honed by performing the largest genetic localization analyses with ENIGMA, ACP and GOBS projects, and by integrating voxel-wise GWAS analyses in web-analysis portals. Likewise, the utility of new format for data and workflow sharing (Aim 2) will be honed for multi-site Big Data research. Finally, we will develop and rank pioneering resting-state FMRI endophenotypes for Big Data research by demonstrating consistent heritability across samples and pleiotropy with mental disorders. The feedback gathered from our partners will sharpen SOLAR-Eclipse tools for imaging genetics community. We will continue to develop annual workshop at Imaging Genetics Conference to educate our users and disseminate new methods.

B.1.a Have the major goals changed since the initial competing award or previous report?

No

B.2 WHAT WAS ACCOMPLISHED UNDER THESE GOALS?

File uploaded: progress_report_2017_1.pdf

B.3 COMPETITIVE REVISIONS/ADMINISTRATIVE SUPPLEMENTS

For this reporting period, is there one or more Revision/Supplement associated with this award for which reporting is required?

No

B.4 WHAT OPPORTUNITIES FOR TRAINING AND PROFESSIONAL DEVELOPMENT HAS THE PROJECT PROVIDED?

NOTHING TO REPORT

B.5 HOW HAVE THE RESULTS BEEN DISSEMINATED TO COMMUNITIES OF INTEREST?

NOTHING TO REPORT

B.6 WHAT DO YOU PLAN TO DO DURING THE NEXT REPORTING PERIOD TO ACCOMPLISH THE GOALS?

We plan to continue development to support the large NIH-funded imaging genetic initiatives. Specifically, the empirical genetic analyses that are being tested in the moment will be used in pin-pointing chromosomal regions that harbor genetic risk factors for complex polygenic disorder. We will be concentrating on updating our website with videos on the use and how-to documentations on starting genetic imaging analyses. We will restart the SOLAR-Eclipse workshop at Imaging Genetics Conference. It was canceled this year due to the logistical problems of organizing it due to late decision of grant funding.

List the major goals below.

Aim 1. To shift imaging genetics toward richer, higher resolution imaging analyses and denser genome examination through high performance computing. The shift in imaging genetics toward WGS genotyping and high-resolution multimodal imaging data necessitates improvement of computational efficiency of likelihood calculations. To speed calculations up by 10^{5-6}-fold we will implement high-performance computing: novel data decompositions and single-step algorithmic techniques and integration of Massive Universal Linear Model (MULM) GPU library of genetic tools for massively parallel genetic analyses. These developments will enable interactive WGS and GWAS analyses for Big Data project by implementing SOLAR-Eclipse in web-analyses portals such as HCP Dashboard and ENIGMAVis.

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1) major activities and specific objectives

We actively pursued activates along all four specific aims Aims. Activity on Aim 1 included in continues released development version of SOLAR-Eclipse (SE). In total, nine releases were made, each constituting a major change. All distribution was made through the NITRIC website http://www.mdbrain.org/personalpages/solareclipse/, which registered 11000 downloads and became top 23rd most downloaded resource on NITRC. The current production version of SE is used for performing imaging genetic research at several centers, including UCLA, University of South California, Yale University and Human Connectom Project at Washington University. Several novel and important developments were accomplished. Overall, the research performed during this productive year was described in 25 peer-reviewed publications.

Our chief accomplishment was development of accelerated genetic analyses for high-throughput imaging genetics applications. The experimental versions of the additive and association genetic analyses are already available for both CPU and GPU application. We additive genetic acceleration algorithm with permutation based statistical inference was published by our group [1-3]. The algorithm uses eigen value decomposition of the data for related subjects and a single step approximation for measurements of additive genetic variance. The software acceleration achieves about 1,000 fold computational improvement over the full maximum likelihood calculation (Figure 1). Implementation of this algorithm on GPU provided an additional 1,000 fold improvement when used on a dual K-80 GPU computer at the Human Connectome Project/ Washington University. This provided for ability to calculate full scale genomic connectivity matrix (10^10) genetic correlations about 1,000,000 faster than using a full model approach

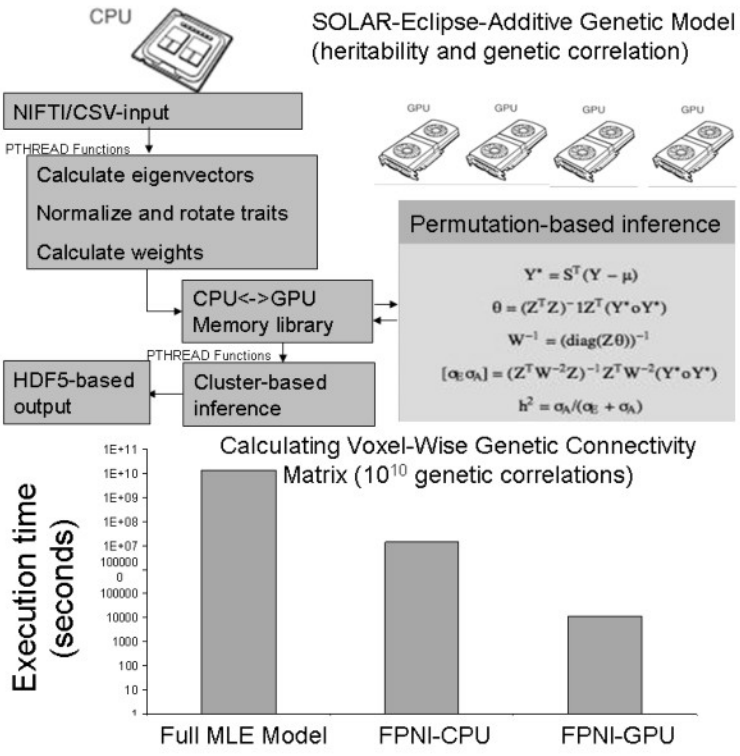

Figure 1. GPU-accelerated voxel-wise genomic connectivity matrix calculated by performing genetic correlation analyses across all voxels in full resolution (1mm isotropic) in 560 related individual achieves 10^6 improvement versus full maximum likelihood analysis. GPU analysis was performed on server with dual NVIDIA K80 GPU (four K-20 accelerators)

We have worked on incorporating similar approach in acceleration of the genetic association analyses in related individuals. The manuscript describing the new algorithm is under internal revisions. Both the CPU and GPU versions of the algorithm was released in the 8.20 version of the software and has already been used in one application [4]. We demonstrate that the use GPU acceleration (Figure 2) provides for practical application of voxel-wise GWA analyses in large (n>1,000) applications. Together, the algorithmic and hardware acceleration approaches will provide the basis for high-performance science portals. Along this direction, we have developed www.enigma-viewer.org website where results of genetic studies can be

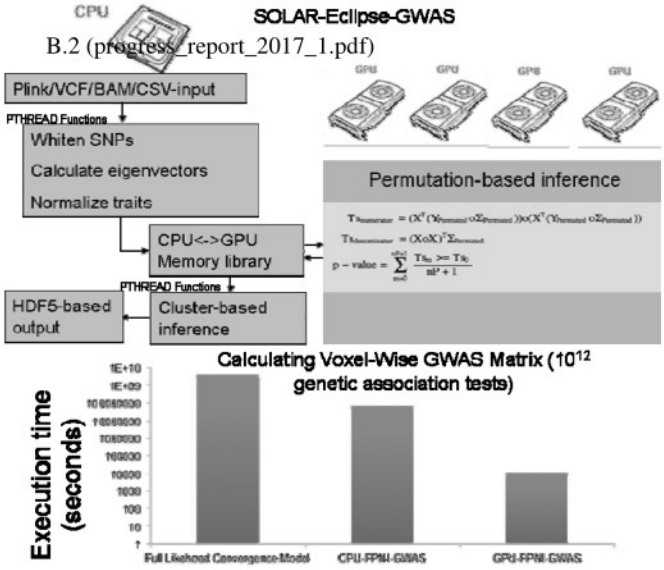

Figure 2. GPU-accelerated voxel-wise genomic association analysis in full spatial (1mm isotropic) and genetic ($2*10^6$ exome snps) resolution in 560 related individual achieves 10^7 improvement versus full maximum likelihood analysis. GPU analysis was performed on server with dual NVIDIA K80 GPU cards (four K-20 accelerators)

viewed as interactive 3D atlas (Figure 3). The interactive viewer software is now made available on NITRC (www.nitrc.org/projects/enigmaviewer_20) Our aim is to increase the usefulness of Big Data studies by first providing visualization of the results and second providing real-time recalculations of the association and heritability studies using high-performance algorithm and GPU acceleration.

The work in Aim 2 included collaborative discussion with the International Neuroinformatics Coordinating Facility's Neuroimaging Data Sharing Task Force on the standardizing the imaging genetic format. At present our team is evaluating several of the proposed data format solution. We have tested the HDF5 based format in the parallel computing environment and found it to perform well for both reading and writing large volumes of data and parallel access from multiple servers.

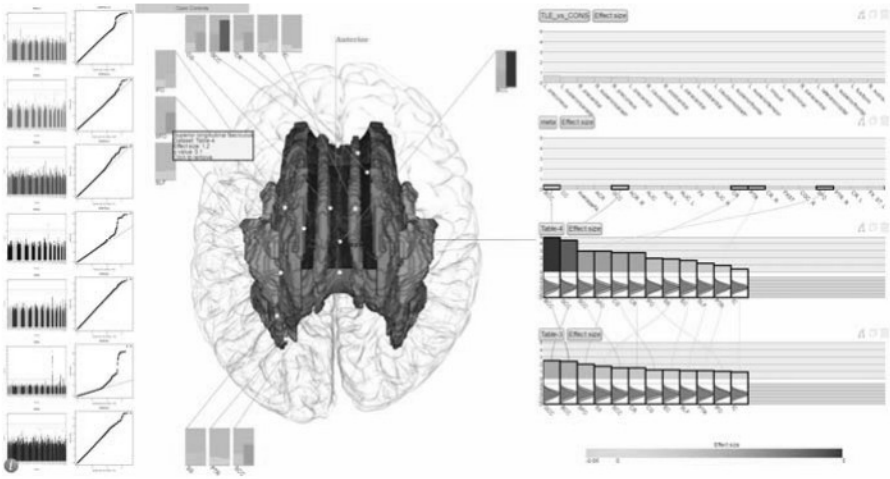

Figure 3. Interactive visualization of Big Data imaging genomic studies, including re-calculation of association and heritability measurements

The work on Aim 3 is on-going. The empirical kinship pedigree calculation functionality is being tested and will be included in the next release of the software. We are working with both University of Texas Rio Grand Valley and Wash U to get access to raw genomic data for large pedigree where the empirical kinship approaches can be tested for chromosomal linkage analyses.

Progress on Aim 4 has led to acknowledgement of SOLAR-Eclipse in publications in high impact journals, including PNAS, Nature, Neuroimage, Human Brain Mapping and others[5-17]. A continued development during this funding period on the multi-site mega-analytical statistical homogenization led to ability to combine large and diverse dataset to analyze the overall effect of the illness on the imaging phenotype. For example, our group used the developed mega-analytical homogenization approach to demonstrate the effects of heterochronicity of white matter development in the largest dataset to date. Briefly. Specifically we tested two hypotheses using the newly-developed mega and then

using the classical meta-statistical approaches. The first hypothesis tested patient-control differences in FA values across different WM areas. The hypotheses tested age-related decline in FA values. In both analyses, the patient-control differences and the age-related declines were compared to the normal rate of FA changes in different WM areas. The mega-analysis implemented in SOLAR-Eclipse was used to normalize data from each cohort to remove scanner-and-cohort related biases in FA values (Figure 3).

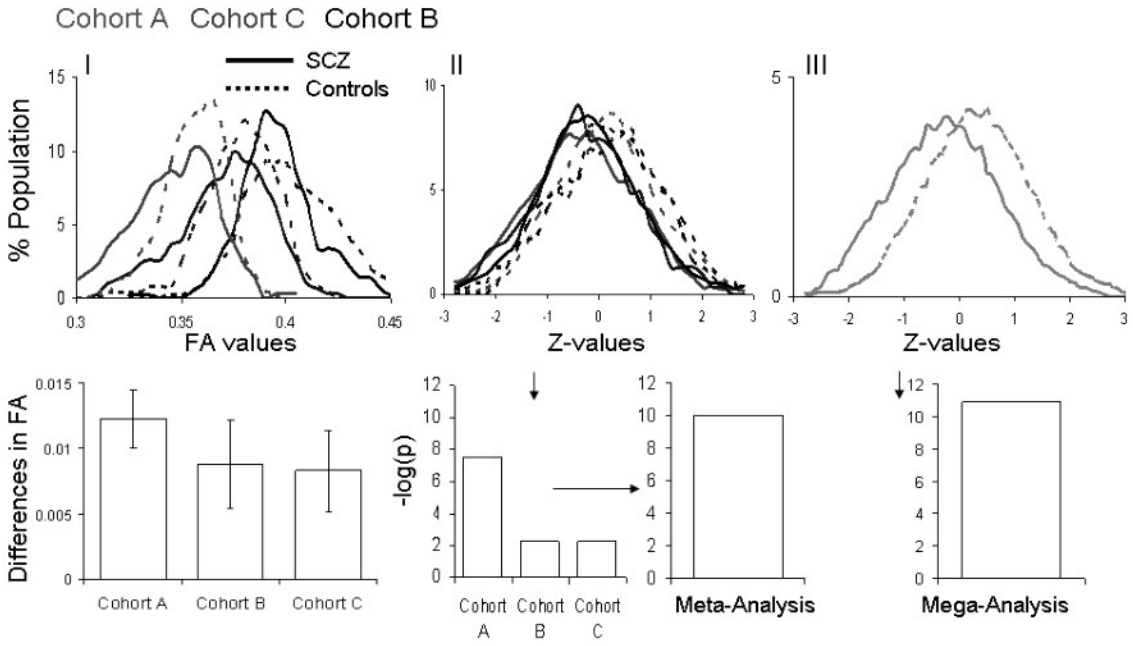

Figure 3. The mega- and meta-analytic analysis workflow developed by ENIGMA-DTI [18] was adapted to analyzed patient-control differences in FA values and aging trends. The ENIGMA-DTI mega-and-meta workflow was developed to harmonize DTI-FA values collected from different sites and scanners. This example demonstrates its use for mega- and meta-analysis of patient-control differences. The patient and controls are treated as the same population by the workflow. Patients and controls are presented as separate histogram (dotted vs. solid lines) to show the impact of the analysis on the main contrast of interest. The raw FA values (*panel I, top*) shows significant site-specific biases, but similar patient-control differences (*panel I, bottom*). In the first step, regression of nuisance covariates (age, sex, age^2, age×sex and age^2×sex) is performed per site (*panel II, top*). The residual patient-control difference is used for N-weighted meta-analysis (*panel II, bottom*). The inverse normal transformation was applied to the residual values to remove any remaining site biases, and to demonstrate the mega-analytic patient control contrast (*panel III, top*). The mega-analysis of patient-control differences in then performed in the combined mega-sample (*panel III, bottom*).

Figure S2. Mega-analytic estimates in three cohorts (A, B and C) are plotted versus mega-analytic estimates in cohorts A and B. Both mega-analytic estimate for patient-control difference (*left*) and accelerated-aging (*right*) showed significant correlation (r=0.96 and 0.91, p<0.01, respectively)

A classical meta-analysis was performed as a validation to demonstrate agreement between mega- and meta-analytical approaches of pooling data. We also repeated analyses in the three cohorts separately to examine if large biases arose from any particular cohort.

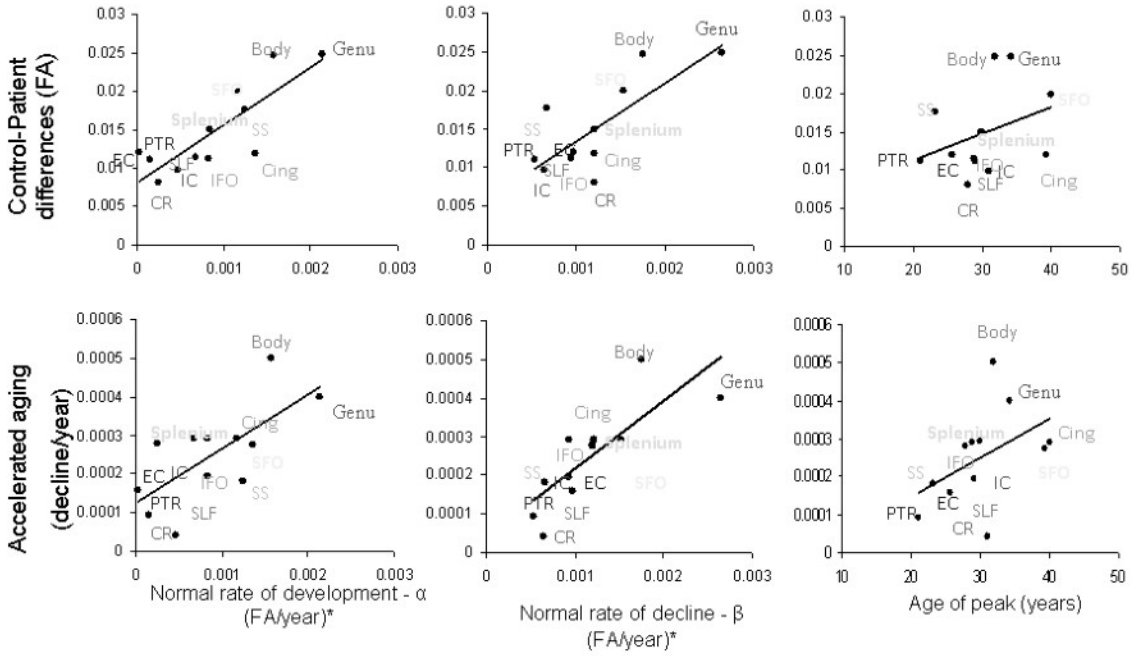

Figure 4. Mega-analysis was used to demonstrate a pattern of heterochronicity in the regional impact of schizophrenia on white matter integrity.

This SOLAR-Eclipse developments enabled the largest schizophrenia DTI analysis to date where the tract-specific heterochronicity of normal WM development was shown to modulate the presentation of patient-control differences in WM FA values in schizophrenia. WM tracts that carry higher cognitive information and continue to mature past the average age-of-onset of schizophrenia are more sensitive to the pathophysiology of this disorder. The finding suggests the importance of implementing better white matter protection and treatment in supporting neurocognitive function and rehabilitation in individuals with this disorder. This study also posits regional WM measurements as promising endophenotypes for future studies of the genetic risks for schizophrenia.

Presently, these developments were disseminated to ENIGMA, SPINS and other groups where they will lay the foundation for several largest imaging genetics analyses to date.

What opportunities for training and professional development has the project provided?

"Nothing to Report."

4) **What do you plan to do during the next reporting period to accomplish the goals?**

We plan to continue development to support the large NIH-funded imaging genetic initiatives. Specifically, the empirical genetic analyses that are being tested in the moment will be used in pin-pointing chromosomal regions that harbor genetic risk factors for complex polygenic disorder. We will be concentrating on updating our website with videos on the use and how-to documentations on starting genetic imaging analyses. We will restart the SOLAR-Eclipse workshop at Imaging Genetics Conference. It was canceled this year due to the logistical problems of organizing it due to late decision of grant funding.

Enter response below (NIH recommended length is up to 1 page. Limit is 8000 characters or approximately 3 pages.)

5) C.1 Publications
Are there publications or manuscripts accepted for publication in a journal or other publication (e.g., book, one-time publication, monograph) during the reporting period resulting directly from this award?

There were 25 peer-reviewed manuscript published for the reporting period. All manuscripts are being timely uploaded and are available through the NIH reporter system

https://projectreporter.nih.gov/project_info_results.cfm?sp=1&aid=9038122&icde=33941288

6) List the URL for any Internet site(s) that disseminates the results of the research activities. A short description of each site should be provided. It is not necessary to include the publications already specified above.
http://solar-eclipse-genetics.org/ is the main site for solar eclipse including manual page.

http://www.nitrc.org/projects/se_linux/ Is the main distribution point for the solar-eclipse software. It also provides the github link for source code and version references

http://enigma-viewer.org/ is the site for reporting results from large mega-analytical cohorts analyzed using solar-eclipse

For awards not designed to create or maintain one or more websites select "Nothing to Report". A description is only required for awards designed to create or maintain one or more websites. Limit the response to this reporting period.

7) **Technologies or techniques**

Identify technologies or techniques that have resulted from the research activities. Describe the technologies or techniques and how they are being shared.

Solar eclipse team is developing novel algorithms for imaging genetics analyses. We distribute our tools as software, analytical pipelines and manuscripts detailing methods and research findings.

References

1. Ganjgahi, H., et al., *Fast and powerful heritability inference for family-based neuroimaging studies.* Neuroimage, 2015.
2. Winkler, A.M., et al., *Faster permutation inference in brain imaging.* Neuroimage, 2016. **141**: p. 502-516.
3. Winkler, A.M., et al., *Multi-level block permutation.* Neuroimage, 2016. **123**: p. 253-268.
4. Bruce, H.A., et al., *Potassium channel gene associations with joint processing speed and white matter impairments in schizophrenia.* Genes, Brain and Behavior, 2016: p. n/a-n/a.
5. Kochunov, P., et al., *Diffusion-weighted imaging uncovers likely sources of processing-speed deficits in schizophrenia.* Proc Natl Acad Sci U S A, 2016. **113**(47): p. 13504-13509.
6. Kochunov, P., et al., *Heritability of complex white matter diffusion traits assessed in a population isolate.* Hum Brain Mapp, 2015.
7. Kochunov, P., et al., *Heterochronicity of white matter development and aging explains regional patient control differences in schizophrenia.* Hum Brain Mapp, 2016.
8. Kochunov, P., et al., *Heritability of fractional anisotropy in human white matter: A comparison of Human Connectome Project and ENIGMA-DTI data.* Neuroimage, 2015. **111**: p. 300-311.

9. Kochunov, P., et al., *The common genetic influence over processing speed and white matter microstructure: Evidence from the Old Order Amish and Human Connectome Projects.* Neuroimage, 2015. **125**: p. 189-197.
10. Adams, H.H.H., et al., *Novel genetic loci underlying human intracranial volume identified through genome-wide association.* Nat Neurosci, 2016. **19**(12): p. 1569-1582.
11. Guadalupe, T., et al., *Human subcortical brain asymmetries in 15,847 people worldwide reveal effects of age and sex.* Brain Imaging and Behavior, 2016: p. 1-18.
12. Sprooten, E., et al., *A comprehensive tractography study of patients with bipolar disorder and their unaffected siblings.* Human Brain Mapping, 2016. **37**(10): p. 3474-3485.
13. Hodgson, K., et al., *Genome-wide significant loci for addiction and anxiety.* European Psychiatry, 2016. **36**: p. 47-54.
14. Rowland, L.M., et al., *Medial Frontal GABA is Lower in Older Schizophrenia: A MEGA-PRESS with Macromolecule Suppression Study.* Molecular psychiatry, 2016. **21**(2): p. 198-204.
15. Thompson, P.M., et al., *ENIGMA and the individual: Predicting factors that affect the brain in 35 countries worldwide.* Neuroimage, 2017. **145, Part B**: p. 389-408.
16. Kuehner, R.M., et al., *Cognitive profiles and heritability estimates in the Old Order Amish.* Psychiatric Genetics, 2016. **26**(4): p. 178-183.
17. Hibar, D.P., et al., *Common genetic variants influence human subcortical brain structures.* Nature, 2015.
18. Jahanshad, N., et al., *Multi-site genetic analysis of diffusion images and voxelwise heritability analysis: A pilot project of the ENIGMA-DTI working group.* Neuroimage, 2013. **doi:pii: S1053-8119(13)00408-4. 10.1016/j.neuroimage.2013.04.061.**

C. PRODUCTS

C.1 PUBLICATIONS

Are there publications or manuscripts accepted for publication in a journal or other publication (e.g., book, one-time publication, monograph) during the reporting period resulting directly from this award?

Yes

Publications Reported for this Reporting Period

Public Access Compliance	Citation
Complete	Kochunov P, Du X, Moran LV, Sampath H, Wijtenburg SA, Yang Y, Rowland LM, Stein EA, Hong LE. Acute nicotine administration effects on fractional anisotropy of cerebral white matter and associated attention performance. Frontiers in pharmacology. 2013;4:117. PubMed PMID: 24065920; PubMed Central PMCID: PMC3776159.
Complete	Ballesteros A, Summerfelt A, Du X, Jiang P, Chiappelli J, Tagamets M, O'Donnell P, Kochunov P, Hong LE. Electrophysiological intermediate biomarkers for oxidative stress in schizophrenia. Clinical neurophysiology : official journal of the International Federation of Clinical Neurophysiology. 2013 November;124(11):2209-15. PubMed PMID: 23823132; PubMed Central PMCID: PMC4030436.
Complete	Wright SN, Kochunov P, Mut F, Bergamino M, Brown KM, Mazziotta JC, Toga AW, Cebral JR, Ascoli GA. Digital reconstruction and morphometric analysis of human brain arterial vasculature from magnetic resonance angiography. NeuroImage. 2013 November 15;82:170-81. PubMed PMID: 23727319; PubMed Central PMCID: PMC3971907.
Complete	Kulkarni T, Slaughter G, Ego-Osuala C, Kochunov P, Bastarrachea RA, Mattern V, Andrade M, Higgins PB, Comuzzie AG, Voruganti VS. Hyperglycemic Challenge and Distribution of Adipose Tissue in Obese Baboons. International journal of diabetology & vascular disease research. 2014 February 17;2(1). PubMed PMID: 25429366; PubMed Central PMCID: PMC4241571.
Complete	Koran ME, Thornton-Wells TA, Jahanshad N, Glahn DC, Thompson PM, Blangero J, Nichols TE, Kochunov P, Landman BA. Impact of family structure and common environment on heritability estimation for neuroimaging genetics studies using Sequential Oligogenic Linkage Analysis Routines. Journal of medical imaging (Bellingham, Wash.). 2014 June 27;1(1):014005. PubMed PMID: 25558465; PubMed Central PMCID: PMC4281883.
Complete	Chiappelli J, Pocivavsek A, Nugent KL, Notarangelo FM, Kochunov P, Rowland LM, Schwarcz R, Hong LE. Stress-induced increase in kynurenic acid as a potential biomarker for patients with schizophrenia and distress intolerance. JAMA psychiatry. 2014 July 1;71(7):761-8. PubMed PMID: 24806441; PubMed Central PMCID: PMC4219570.
Complete	Kochunov P, Jahanshad N, Sprooten E, Nichols TE, Mandl RC, Almasy L, Booth T, Brouwer RM, Curran JE, de Zubicaray GI, Dimitrova R, Duggirala R, Fox PT, Hong LE, Landman BA, Lemaitre H, Lopez LM, Martin NG, McMahon KL, Mitchell BD, Olvera RL, Peterson CP, Starr JM, Sussmann JE, Toga AW, Wardlaw JM, Wright MJ, Wright SN, Bastin ME, McIntosh AM, Boomsma DI, Kahn RS, den Braber A, de Geus EJ, Deary IJ, Hulshoff Pol HE, Williamson DE, Blangero J, van 't Ent D, Thompson PM, Glahn DC. Multi-site study of additive genetic effects on fractional anisotropy of cerebral white matter: Comparing meta and megaanalytical approaches for data pooling. NeuroImage. 2014 July 15;95:136-50. PubMed PMID: 24657781; PubMed Central PMCID: PMC4043878.
Complete	Kochunov P, Chiappelli J, Wright SN, Rowland LM, Patel B, Wijtenburg SA, Nugent K, McMahon RP, Carpenter WT, Muellerklein F, Sampath H, Hong LE. Multimodal white matter imaging to investigate reduced fractional anisotropy and its age-related decline in schizophrenia. Psychiatry research. 2014 August 30;223(2):148-56. PubMed PMID: 24909602; PubMed Central PMCID: PMC4100065.
Complete	Banalagay R, Covington KJ, Wilkes DM, Landman BA. Resource estimation in high performance medical image computing. Neuroinformatics. 2014 October;12(4):563-73. PubMed PMID: 24906466; PubMed Central PMCID: PMC4381797.

Complete	Wright SN, Kochunov P, Chiappelli J, McMahon RP, Muellerklein F, Wijtenburg SA, White MG, Rowland LM, Hong LE. Accelerated white matter aging in schizophrenia: role of white matter blood perfusion. Neurobiology of aging. 2014 October;35(10):2411-8. PubMed PMID: 24680326; PubMed Central PMCID: PMC4087059.
Complete	Acheson A, Wijtenburg SA, Rowland LM, Winkler AM, Gaston F, Mathias CW, Fox PT, Lovallo WR, Wright SN, Hong LE, Dougherty DM, Kochunov P. Assessment of whole brain white matter integrity in youths and young adults with a family history of substance-use disorders. Human brain mapping. 2014 November;35(11):5401-13. PubMed PMID: 24867528; PubMed Central PMCID: PMC4206569.
Complete	McGuire SA, Sherman PM, Wijtenburg SA, Rowland LM, Grogan PM, Sladky JH, Robinson AY, Kochunov PV. White matter hyperintensities and hypobaric exposure. Annals of neurology. 2014 November;76(5):719-26. PubMed PMID: 25164539; PubMed Central PMCID: PMC4219408.
Complete	Wey HY, Phillips KA, McKay DR, Laird AR, Kochunov P, Davis MD, Glahn DC, Blangero J, Duong TQ, Fox PT. Multi-region hemispheric specialization differentiates human from nonhuman primate brain function. Brain structure & function. 2014 November;219(6):2187-94. PubMed PMID: 23928747; PubMed Central PMCID: PMC4219928.
Complete	Acheson A, Wijtenburg SA, Rowland LM, Bray BC, Gaston F, Mathias CW, Fox PT, Lovallo WR, Wright SN, Hong LE, McGuire S, Kochunov P, Dougherty DM. Combining diffusion tensor imaging and magnetic resonance spectroscopy to study reduced frontal white matter integrity in youths with family histories of substance use disorders. Human brain mapping. 2014 December;35(12):5877-87. PubMed PMID: 25044331; PubMed Central PMCID: PMC4219410.
Complete	Jones RM, Cadby G, Blangero J, Abraham LJ, Whitehouse AJ, Moses EK. MACROD2 gene associated with autistic-like traits in a general population sample. Psychiatric genetics. 2014 December;24(6):241-8. PubMed PMID: 25360606; PubMed Central PMCID: PMC4320645.
Complete	Ge T, Nichols TE, Ghosh D, Mormino EC, Smoller JW, Sabuncu MR. A kernel machine method for detecting effects of interaction between multidimensional variable sets: an imaging genetics application. NeuroImage. 2015 April 1;109:505-14. PubMed PMID: 25600633; PubMed Central PMCID: PMC4339421.
Complete	Kochunov P, Jahanshad N, Marcus D, Winkler A, Sprooten E, Nichols TE, Wright SN, Hong LE, Patel B, Behrens T, Jbabdi S, Andersson J, Lenglet C, Yacoub E, Moeller S, Auerbach E, Ugurbil K, Sotiropoulos SN, Brouwer RM, Landman B, Lemaitre H, den Braber A, Zwiers MP, Ritchie S, van Hulzen K, Almasy L, Curran J, deZubicaray GI, Duggirala R, Fox P, Martin NG, McMahon KL, Mitchell B, Olvera RL, Peterson C, Starr J, Sussmann J, Wardlaw J, Wright M, Boomsma DI, Kahn R, de Geus EJ, Williamson DE, Hariri A, van 't Ent D, Bastin ME, McIntosh A, Deary IJ, Hulshoff Pol HE, Blangero J, Thompson PM, Glahn DC, Van Essen DC. Heritability of fractional anisotropy in human white matter: a comparison of Human Connectome Project and ENIGMA-DTI data. NeuroImage. 2015 May 1;111:300-11. PubMed PMID: 25747917; PubMed Central PMCID: PMC4387079.
Complete	Nugent KL, Chiappelli J, Sampath H, Rowland LM, Thangavelu K, Davis B, Du X, Muellerklein F, Daughters S, Kochunov P, Hong LE. Cortisol Reactivity to Stress and Its Association With White Matter Integrity in Adults With Schizophrenia. Psychosomatic medicine. 2015 September;77(7):733-42. PubMed PMID: 26186431; PubMed Central PMCID: PMC4565747.
Complete	Herskovits EH, Hong LE, Kochunov P, Sampath H, Chen R. Edge-Centered DTI Connectivity Analysis: Application to Schizophrenia. Neuroinformatics. 2015 October;13(4):501-9. PubMed PMID: 26078102; PubMed Central PMCID: PMC4704993.
Complete	Wright SN, Hong LE, Winkler AM, Chiappelli J, Nugent K, Muellerklein F, Du X, Rowland LM, Wang DJ, Kochunov P. Perfusion shift from white to gray matter may account for processing speed deficits in schizophrenia. Human brain mapping. 2015 October;36(10):3793-804. PubMed PMID: 26108347; PubMed Central PMCID: PMC4714540.
Complete	Kochunov P, Thompson PM, Winkler A, Morrissey M, Fu M, Coyle TR, Du X, Muellerklein F, Savransky A, Gaudiot C, Sampath H, Eskandar G, Jahanshad N, Patel

	B, Rowland L, Nichols TE, O'Connell JR, Shuldiner AR, Mitchell BD, Hong LE. The common genetic influence over processing speed and white matter microstructure: Evidence from the Old Order Amish and Human Connectome Projects. NeuroImage. 2016 January 15;125:189-97. PubMed PMID: 26499807; PubMed Central PMCID: PMC4691385.
Complete	Kochunov P, Fu M, Nugent K, Wright SN, Du X, Muellerklein F, Morrissey M, Eskandar G, Shukla DK, Jahanshad N, Thompson PM, Patel B, Postolache TT, Strauss KA, Shuldiner AR, Mitchell BD, Hong LE. Heritability of complex white matter diffusion traits assessed in a population isolate. Human brain mapping. 2016 February;37(2):525-35. PubMed PMID: 26538488; PubMed Central PMCID: PMC4718876.
Complete	Rowland LM, Summerfelt A, Wijtenburg SA, Du X, Chiappelli JJ, Krishna N, West J, Muellerklein F, Kochunov P, Hong LE. Frontal Glutamate and γ-Aminobutyric Acid Levels and Their Associations With Mismatch Negativity and Digit Sequencing Task Performance in Schizophrenia. JAMA psychiatry. 2016 February;73(2):166-74. PubMed PMID: 26720179; PubMed Central PMCID: PMC4740214.
Complete	Bao S, Damon SM, Landman BA, Gokhale A. Performance Management of High Performance Computing for Medical Image Processing in Amazon Web Services. Proceedings of SPIE--the International Society for Optical Engineering. 2016 February 27;9789. PubMed PMID: 27127335; PubMed Central PMCID: PMC4845970.
Complete	Winkler AM, Webster MA, Brooks JC, Tracey I, Smith SM, Nichols TE. Non-parametric combination and related permutation tests for neuroimaging. Human brain mapping. 2016 April;37(4):1486-511. PubMed PMID: 26848101; PubMed Central PMCID: PMC4783210.
Unpublished	
Complete	Kuehner RM, Kochunov P, Nugent KL, Jurius DE, Savransky A, Gaudiot C, Bruce HA, Gold J, Shuldiner AR, Mitchell BD, Hong LE. Cognitive profiles and heritability estimates in the Old Order Amish. Psychiatric genetics. 2016 August;26(4):178-83. PubMed PMID: 27105171; PubMed Central PMCID: PMC5241270.
In Process at NIHMS	Unpublished
Complete	Adams HH, Hibar DP, Chouraki V, Stein JL, Nyquist PA, Rentería ME, Trompet S, Arias-Vasquez A, Seshadri S, Desrivières S, Beecham AH, Jahanshad N, Wittfeld K, Van der Lee SJ, Abramovic L, Alhusaini S, Amin N, Andersson M, Arfanakis K, Aribisala BS, Armstrong NJ, Athanasiu L, Axelsson T, Beiser A, Bernard M, Bis JC, Blanken LM,

	Blanton SH, Bohlken MM, Boks MP, Bralten J, Brickman AM, Carmichael O, Chakravarty MM, Chauhan G, Chen Q, Ching CR, Cuellar-Partida G, Braber AD, Doan NT, Ehrlich S, Filippi I, Ge T, Giddaluru S, Goldman AL, Gottesman RF, Greven CU, Grimm O, Griswold ME, Guadalupe T, Hass J, Haukvik UK, Hilal S, Hofer E, Hoehn D, Holmes AJ, Hoogman M, Janowitz D, Jia T, Kasperaviciute D, Kim S, Klein M, Kraemer B, Lee PH, Liao J, Liewald DC, Lopez LM, Luciano M, Macare C, Marquand A, Matarin M, Mather KA, Mattheisen M, Mazoyer B, McKay DR, McWhirter R, Milaneschi Y, Mirza-Schreiber N, Muetzel RL, Maniega SM, Nho K, Nugent AC, Loohuis LM, Oosterlaan J, Papmeyer M, Pappa I, Pirpamer L, Pudas S, Pütz B, Rajan KB, Ramasamy A, Richards JS, Risacher SL, Roiz-Santiañez R, Rommelse N, Rose EJ, Royle NA, Rundek T, Sämann PG, Satizabal CL, Schmaal L, Schork AJ, Shen L, Shin J, Shumskaya E, Smith AV, Sprooten E, Strike LT, Teumer A, Thomson R, Tordesillas-Gutierrez D, Toro R, Trabzuni D, Vaidya D, Van der Grond J, Van der Meer D, Van Donkelaar MM, Van Eijk KR, Van Erp TG, Van Rooij D, Walton E, Westlye LT, Whelan CD, Windham BG, Winkler AM, Woldehawariat G, Wolf C, Wolfers T, Xu B, Yanek LR, Yang J, Zijdenbos A, Zwiers MP, Agartz I, Aggarwal NT, Almasy L, Ames D, Amouyel P, Andreassen OA, Arepalli S, Assareh AA, Barral S, Bastin ME, Becker DM, Becker JT, Bennett DA, Blangero J, van Bokhoven H, Boomsma DI, Brodaty H, Brouwer RM, Brunner HG, Buckner RL, Buitelaar JK, Bulayeva KB, Cahn W, Calhoun VD, Cannon DM, Cavalleri GL, Chen C, Cheng CY, Cichon S, Cookson MR, Corvin A, Crespo-Facorro B, Curran JE, Czisch M, Dale AM, Davies GE, De Geus EJ, De Jager PL, de Zubicaray GI, Delanty N, Depondt C, DeStefano AL, Dillman A, Djurovic S, Donohoe G, Drevets WC, Duggirala R, Dyer TD, Erk S, Espeseth T, Evans DA, Fedko IO, Fernández G, Ferrucci L, Fisher SE, Fleischman DA, Ford I, Foroud TM, Fox PT, Francks C, Fukunaga M, Gibbs JR, Glahn DC, Gollub RL, Göring HH, Grabe HJ, Green RC, Gruber O, Gudnason V, Guelfi S, Hansell NK, Hardy J, Hartman CA, Hashimoto R, Hegenscheid K, Heinz A, Le Hellard S, Hernandez DG, Heslenfeld DJ, Ho BC, Hoekstra PJ, Hoffmann W, Hofman A, Holsboer F, Homuth G, Hosten N, Hottenga JJ, Pol HE, Ikeda M, Ikram MK, Jack CR Jr, Jenkinson M, Johnson R, Jönsson EG, Jukema JW, Kahn RS, Kanai R, Kloszewska I, Knopman DS, Kochunov P, Kwok JB, Lawrie SM, Lemaître H, Liu X, Longo DL, Longstreth WT Jr, Lopez OL, Lovestone S, Martinez O, Martinot JL, Mattay VS, McDonald C, McIntosh AM, McMahon KL, McMahon FJ, Mecocci P, Melle I, Meyer-Lindenberg A, Mohnke S, Montgomery GW, Morris DW, Mosley TH, Mühleisen TW, Müller-Myhsok B, Nalls MA, Nauck M, Nichols TE, Niessen WJ, Nöthen MM, Nyberg L, Ohi K, Olvera RL, Ophoff RA, Pandolfo M, Paus T, Pausova Z, Penninx BW, Pike GB, Potkin SG, Psaty BM, Reppermund S, Rietschel M, Roffman JL, Romanczuk-Seiferth N, Rotter JI, Ryten M, Sacco RL, Sachdev PS, Saykin AJ, Schmidt R, Schofield PR, Sigurdsson S, Simmons A, Singleton A, Sisodiya SM, Smith C, Smoller JW, Soininen H, Srikanth V, Steen VM, Stott DJ, Sussmann JE, Thalamuthu A, Tiemeier H, Toga AW, Traynor BJ, Troncoso J, Turner JA, Tzourio C, Uitterlinden AG, Hernández MC, Van der Brug M, Van der Lugt A, Van der Wee NJ, Van Duijn CM, Van Haren NE, Van T Ent D, Van Tol MJ, Vardarajan BN, Veltman DJ, Vernooij MW, Völzke H, Walter H, Wardlaw JM, Wassink TH, Weale ME, Weinberger DR, Weiner MW, Wen W, Westman E, White T, Wong TY, Wright CB, Zielke HR, Zonderman AB, Deary IJ, DeCarli C, Schmidt H, Martin NG, De Craen AJ, Wright MJ, Launer LJ, Schumann G, Fornage M, Franke B, Debette S, Medland SE, Ikram MA, Thompson PM. Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature neuroscience. 2016 December;19(12):1569-1582. PubMed PMID: 27694991; PubMed Central PMCID: PMC5227112.
Complete	Kochunov P, Ganjgahi H, Winkler A, Kelly S, Shukla DK, Du X, Jahanshad N, Rowland L, Sampath H, Patel B, O'Donnell P, Xie Z, Paciga SA, Schubert CR, Chen J, Zhang G, Thompson PM, Nichols TE, Hong LE. Heterochronicity of white matter development and aging explains regional patient control differences in schizophrenia. Human brain mapping. 2016 December;37(12):4673-4688. PubMed PMID: 27477775; PubMed Central PMCID: PMC5118078.
Unpublished	
In Process at NIHMS	Unpublished
Complete	Chiappelli J, Kochunov P, Savransky A, Fisseha F, Wisner K, Du X, Rowland LM, Hong LE. Allostatic load and reduced cortical thickness in schizophrenia.

	Psychoneuroendocrinology. 2017 March;77:105-111. PubMed PMID: 28027496; PubMed Central PMCID: PMC5336512.
In Process at NIHMS	Unpublished

C.2 WEBSITE(S) OR OTHER INTERNET SITE(S)

Nothing to report

C.3 TECHNOLOGIES OR TECHNIQUES

NOTHING TO REPORT

C.4 INVENTIONS, PATENT APPLICATIONS, AND/OR LICENSES

Have inventions, patent applications and/or licenses resulted from the award during the reporting period?

No

C.5 OTHER PRODUCTS AND RESOURCE SHARING

NOTHING TO REPORT

D. PARTICIPANTS

D.1 WHAT INDIVIDUALS HAVE WORKED ON THE PROJECT?

Commons ID	S/K	Name	Degree(s)	Role	Cal	Aca	Sum	Foreign Org	Country	SS
KOCHUNOV	Y	KOCHUNOV, PETER V	MS,MS,PHD	PD/PI	EFFORT					NA

Glossary of acronyms:
S/K - Senior/Key
DOB - Date of Birth
Cal - Person Months (Calendar)
Aca - Person Months (Academic)
Sum - Person Months (Summer)
Foreign Org - Foreign Organization Affiliation
SS - Supplement Support
RE - Reentry Supplement
DI - Diversity Supplement
OT - Other
NA - Not Applicable

D.2 PERSONNEL UPDATES

D.2.a Level of Effort

Will there be, in the next budget period, either (1) a reduction of 25% or more in the level of effort from what was approved by the agency for the PD/PI(s) or other senior/key personnel designated in the Notice of Award, or (2) a reduction in the level of effort below the minimum amount of effort required by the Notice of Award?

No

D.2.b New Senior/Key Personnel

Are there, or will there be, new senior/key personnel?

No

D.2.c Changes in Other Support

Has there been a change in the active other support of senior/key personnel since the last reporting period?

No

D.2.d New Other Significant Contributors

Are there, or will there be, new other significant contributors?

No

D.2.e Multi-PI (MPI) Leadership Plan

Will there be a change in the MPI Leadership Plan for the next budget period?

No

E. IMPACT

E.1 WHAT IS THE IMPACT ON THE DEVELOPMENT OF HUMAN RESOURCES? Not Applicable
E.2 WHAT IS THE IMPACT ON PHYSICAL, INSTITUTIONAL, OR INFORMATION RESOURCES THAT FORM INFRASTRUCTURE? NOTHING TO REPORT
E.3 WHAT IS THE IMPACT ON TECHNOLOGY TRANSFER? Not Applicable
E.4 WHAT DOLLAR AMOUNT OF THE AWARD'S BUDGET IS BEING SPENT IN FOREIGN COUNTRY(IES)? NOTHING TO REPORT

F. CHANGES

F.1 CHANGES IN APPROACH AND REASONS FOR CHANGE

Not Applicable

F.2 ACTUAL OR ANTICIPATED CHALLENGES OR DELAYS AND ACTIONS OR PLANS TO RESOLVE THEM

NOTHING TO REPORT

F.3 SIGNIFICANT CHANGES TO HUMAN SUBJECTS, VERTEBRATE ANIMALS, BIOHAZARDS, AND/OR SELECT AGENTS

F.3.a Human Subjects

No Change

F.3.b Vertebrate Animals

No Change

F.3.c Biohazards

No Change

F.3.d Select Agents

No Change

G. SPECIAL REPORTING REQUIREMENTS

G.1 SPECIAL NOTICE OF AWARD TERMS AND FUNDING OPPORTUNITIES ANNOUNCEMENT REPORTING REQUIREMENTS

NOTHING TO REPORT

G.2 RESPONSIBLE CONDUCT OF RESEARCH

Not Applicable

G.3 MENTOR'S REPORT OR SPONSOR COMMENTS

Not Applicable

G.4 HUMAN SUBJECTS

G.4.a Does the project involve human subjects?

No

G.4.b Inclusion Enrollment Data

Not Applicable

G.4.c ClinicalTrials.gov

Does this project include one or more applicable clinical trials that must be registered in ClinicalTrials.gov under FDAAA?

G.5 HUMAN SUBJECTS EDUCATION REQUIREMENT

Are there personnel on this project who are newly involved in the design or conduct of human subjects research?

G.6 HUMAN EMBRYONIC STEM CELLS (HESCS)

Does this project involve human embryonic stem cells (only hESC lines listed as approved in the NIH Registry may be used in NIH funded research)?

No

G.7 VERTEBRATE ANIMALS

Does this project involve vertebrate animals?

No

G.8 PROJECT/PERFORMANCE SITES

Organization Name:	DUNS	Congressional District	Address
Primary: University of Maryland, Baltimore	188435911	MD-07	PO Box 21247 Baltimore MD 21228
University of Maryland, Baltimore	188435911	MD-007	UNIVERSITY OF MARYLAND BALTIMORE Office of Research and Development Baltimore MD 212011508
University of Texas Health Science Center at San Antonio	800772162	TX-021	7703 Floyd Curl Drive, Mail Code 7828 San Antonio TX 782293900

University of Warwick	231745683	00-000	University House Kirby Corner Road Coventry, West Midlands
University of Maryland Baltimore	188435911	MD-007	Maryland Psychiatric Research Center Grounds of Spring Grove Hospital Center Baltimore MD 212284663

G.9 FOREIGN COMPONENT

No foreign component

G.10 ESTIMATED UNOBLIGATED BALANCE

G.10.a Is it anticipated that an estimated unobligated balance (including prior year carryover) will be greater than 25% of the current year's total approved budget?

No

G.11 PROGRAM INCOME

Is program income anticipated during the next budget period?

No

G.12 F&A COSTS

Is there a change in performance sites that will affect F&A costs?

No

QVR *NIH Business System (NBS) Accounting Details*

PRINT DOWNLOAD CLOSE

PI: KOCHUNOV, PETER V FY: 2017

Total IMPACII Award Amt: $400,000

Obligation Details for Project:

5R01EB015611-05

External Organization:

UNIVERSITY OF MARYLAND BALTIMORE

Accounting System Totals

PMS Account Type:	Subaccount:domestic(P)	
Award Document Number:	REB015611B	*Click hyperlink for accounting details for all projects with this document number*

TIMING INFORMATION: QVR gathers disbursement data from NBS/nVision on a nightly basis, however, PMS data in NBS may lag as much as 2 weeks.

Accounting System

IC	CAN	Budget FY	Obligated Dt	Last Disburse. Dt	NBS Obligated $	NBS Disbursed $	Obligated Balance
EB	8015183	2017	2017-07-19	2019-08-01	$ 400,000.00	$ 127,912.00	$ 272,088.00

Accounting System Transactions

Accounting System Transactions

IC	CAN	OCC	NBS Doc Num	NBS Transact. Dt	Obligation Amt	Disbursement Amt
EB	8015183	414E	380REB015611B	2019-08-01	$ 0.00	$ 108,035.64
EB	8015183	414E	380REB015611B	2019-05-01	$ 0.00	$ 19,876.36
EB	8015183	414E	380REB015611B*10001	2017-07-19	$ 400,000.00	$ 0.00
				Grand Totals:	$ 400,000.00	$ 127,912.00