

# Stanford

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## Nilotpal Sanyal

Postdoctoral Research Fellow, Biomedical Informatics

### Bio

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#### BIO

Nilotpal Sanyal completed his PhD in Statistics from University of Missouri, Columbia with dissertation titled 'Bayesian fMRI data analysis and Bayesian optimal design'. He worked in the Indian Statistical Institute, Kolkata for a year as visiting scientist following which he started his postdoctoral career in USA by joining Texas A&M University as a postdoctoral associate working on high-dimensional variable selection methods. Later, he joined the Radiology department at the University of California, San Diego as a postdoctoral scholar working on Genome wide association study (GWAS) analysis. Currently, he is a postdoctoral scholar in the Biomedical Informatics division under the Department of Medicine at the Stanford University. Presently, his research topics include gene by environment interaction analysis in case-control studies and screening strategies for lung cancer.

#### PROFESSIONAL EDUCATION

- Master of Science, University Of Calcutta (2007)
- Bachelor of Science, University Of Calcutta (2004)
- Doctor of Philosophy, University of Missouri Columbia (2012)

#### STANFORD ADVISORS

- Summer Han, Postdoctoral Faculty Sponsor
- Summer Han, Postdoctoral Research Mentor

### Publications

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#### PUBLICATIONS

- **Tobacco Smoking and Risk of Second Primary Lung Cancer.** *Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer*  
Aredo, J. V., Luo, S. J., Gardner, R. M., Sanyal, N. n., Choi, E. n., Hickey, T. P., Riley, T. L., Huang, W. Y., Kurian, A. W., Leung, A. N., Wilkens, L. R., Robbins, H. A., Riboli, et al  
2021
- **A robust test for additive gene-environment interaction under the trend effect of genotype using an empirical Bayes-type shrinkage estimator** *American Journal of Epidemiology*  
Sanyal, N., Napolioni, V., de Rochemonteix, M., Belloy, M. E., Caporaso, N. E., Landi, M. T., Greicius, M. D., Chatterjee, N., Han, S. S.  
2021
- **A Likelihood Ratio Test for Gene-Environment Interaction Based on the Trend Effect of Genotype Under an Additive Risk Model Using the Gene-Environment Independence Assumption.** *American journal of epidemiology*  
de Rochemonteix, M., Napolioni, V., Sanyal, N., Belloy, M. E., Caporaso, N. E., Landi, M. T., Greicius, M. D., Chatterjee, N., Han, S. S.  
2020

- **Identification of genetic heterogeneity of Alzheimer's disease across age** *NEUROBIOLOGY OF AGING*  
Lo, M., Kauppi, K., Fan, C., Sanyal, N., Reas, E. T., Sundar, V. S., Lee, W., Desikan, R. S., McEvoy, L. K., Chen, C., Alzheimer's Dis Genetics  
2019; 84: 243.e1–243.e9
- **PREDICTING ANTIPSYCHOTIC RESPONSE COMBINING POLYGENIC RISK WITH PROTEIN-PROTEIN NETWORKS**  
Kauppi, K., Gani, O., Sanyal, N., Bettella, F., Smeland, O., Andreassen, O., Chen, C.  
ELSEVIER.2019: S27
- **GWASinlps: non-local prior based iterative SNP selection tool for genome-wide association studies** *BIOINFORMATICS*  
Sanyal, N., Lo, M., Kauppi, K., Djurovic, S., Andreassen, O. A., Johnson, V. E., Chen, C.  
2019; 35 (1): 1–11
- **Revisiting Antipsychotic Drug Actions Through Gene Networks Associated With Schizophrenia** *AMERICAN JOURNAL OF PSYCHIATRY*  
Kauppi, K., Rosenthal, S., Lo, M., Sanyal, N., Jiang, M., Abagyan, R., McEvoy, L. K., Andreassen, O. A., Chen, C.  
2018; 175 (7): 674–82
- **Modeling prior information of common genetic variants improves gene discovery for neuroticism** *HUMAN MOLECULAR GENETICS*  
Lo, M., Wang, Y., Kauppi, K., Sanyal, N., Fan, C., Smeland, O. B., Schork, A., Holland, D., Hinds, D. A., Tung, J. Y., Andreassen, O. A., Dale, A. M., Chen, et al  
2017; 26 (22): 4530–39
- **Leveraging genome characteristics to improve gene discovery for putamen subcortical brain structure** *Scientific Reports*  
Chen, C., Wang, Y., Lo, M., Schork, A., Fan, C., Holland, D., Kauppi, K., Smeland, O. B., Djurovic, S., Sanyal, N., Hibar, D. P., Thompson, P. M., Thompson, et al  
2017; 7 (1)
- **Bayesian Wavelet Analysis Using Nonlocal Priors with an Application to fMRI Analysis** *Sankhya B*  
Sanyal, N., Ferreira, M. A.  
2017; 79: 361–388
- **Identification of Genetic Heterogeneity of Alzheimer's Disease Across Age** *Genetic Epidemiology*  
Lo, M., Fan, C., Kauppi, K., Sanyal, N., Desikan, R. S., Farrer, L. A., Haines, J. L., Mayeux, R., Pericak-Vance, M., Schellenberg, G. D., Chen, C.  
2017; 41 (7): 706–707
- **Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders** *NATURE GENETICS*  
Lo, M., Hinds, D. A., Tung, J. Y., Franz, C., Fan, C., Wang, Y., Smeland, O. B., Schork, A., Holland, D., Kauppi, K., Sanyal, N., Escott-Price, V., Smith, et al  
2017; 49 (1): 152–56
- **Bayesian optimal sequential design for nonparametric regression via inhomogeneous evolutionary MCMC** *STATISTICAL METHODOLOGY*  
Ferreira, M. R., Sanyal, N.  
2014; 18: 131–41
- **Bayesian hierarchical multi-subject multiscale analysis of functional MRI data** *NEUROIMAGE*  
Sanyal, N., Ferreira, M. R.  
2012; 63 (3): 1519–31