Publications
Sheila M. Gaynor

Peer-Reviewed

1. **Gaynor, S.M.**, Schwartz, J., and Lin, X. (2019). Mediation analysis for common binary outcomes. Statistics in Medicine, 38(4), 512-529.

2. **Gaynor, S.M.***, Sun, R.*, Lin, X., and Quackenbush, J. (2019). Identification of differentially expressed gene sets using the Generalized Berk–Jones statistic. Bioinformatics.

3. Borrelli, B., **Gaynor, S.**, Tooley, E., Armitage, C. J., Wearden, A., & Bartlett, Y.K. (2018). Identification of three different types of smokers who are not motivated to quit: Results from a latent class analysis. Health Psychology, 37(2), 179.

4. **Gaynor, S.**, and Bair, E. (2017). Identification of relevant subtypes via preweighted sparse clustering. Computational Statistics and Data Analysis, 116, 139-154.

5. Bair, E., **Gaynor, S.**, Slade, G.D., Ohrbach, R., Fillingim, R.B., Greenspan, J.D., Dubner, R., Smith, S.B., Diatchenko, L., and Maixner, W. (2016). Identification of clusters of individuals relevant to temporomandibular disorders and other chronic pain conditions: the OPPERA study. Pain, 157(6), 1266.

6. Kallogjeri, D., **Gaynor, S.M.**, Piccirillo, M.L., Jean, R.A., Spitznagel Jr, E.L., & Piccirillo, J.F. (2014). Comparison of comorbidity collection methods. Journal of the American College of Surgeons, 219(2), 245-255.

7. Raffield, L.M., Iyengar, A.K., Wang, B., **Gaynor, S.M.**, Spracklen, C.N., Kowalski, M.H., Salimi, S., Polfus, L.M., Benjamin, E.J., Bis, J.C., Bowler, R.,Cade, B.E., Comellas. A.P., Correa, A., Durda, P., Gogarten, S., Jain, D., Kral, B.G., Lange, L.A., Larson, M.G., Laurie, C., Lee, J., Lewis, J.P., Mitchell, B., Pankratz, N., Rich, S.S., Rotter, J.I., Ryan, K., Tracy, R.P., Yanek, L.R., Zhao, L.P., Lin, X., Li, Y., Dupuis, J., Reiner, A.P., Mohlke, K.L., Auer, P.L., TOPMed Inflammation Working Group, and NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium. Allelic heterogeneity at CRP locus identified by whole-genome sequencing in multi-ancestry cohorts. *To appear, American Journal of Human Genetics.*

Submitted and Preprints

1. **Gaynor, S.M.**, Fagny, M., Lin, X., Platig, J., and Quackenbush, J. Connectivity of variants in eQTL networks dictates reproducibility and functionality. bioRxiv 515551 [Preprint].

2. **Gaynor, S.M.**, Lin, X., and Quackenbush, J. Spectral clustering in regression-based biological networks. bioRxiv 651950 [Preprint].

3. **Gaynor, S.M.**, Fillingim, R.B., Zolnoun, D.A., Slade, G.D., Ohrbach, R., Greenspan, J.D., Maixner, W., and Bair, E. Association between craniofacial pain and hormonal contraceptive use: The OPPERA study.

4. **Gaynor, S.M.**, Bortsov, A., Maixner, W., and Smith, S.B. Pragmatic patient profile clustering identifies diagnostically and prognostically informative subgroups.

5. McCaw, Z.R., **Gaynor, S.M.**, Sun, R., and Lin, X. Cross-tissue eQTL Calling via Surrogate Expression Analysis.

6. Sun, R.*, Xu, M.*, Li, X., **Gaynor, S.M.**, Zhou, H., Bosse, Y., Lam, S., Tsao, M., Tardon, A., Chen, C., Doherty, J., Goodman, G., Egil Bojesen, S., Teresa, M.T., Johansson, M., Field, J.K., Bickeboller, H, Wichmann, H., Risch, A., Rennert, G., Arnold, S., Wu, X., Melander, O., Brunnstrom, H., Marchand, L.L., Zong, X., Liu, G., Andrew, A., Duell, E., Kiemeney, L.A., Shen, H., Haugen, A., Johansson, M., Grankvist, K., Caporaso, N., Woll, P., Teare, M.D., Scelo, G., Hong, Y., Yuan, J., Lazarus, P., Schabath, M.B., Aldrich, M.C., Albanes, D., Brennan, P., Barbie, D., Mak, R., Hung, R.J., Amos, C.I., Christiani, D.C and Lin, X. Identification of inflammation and immune-related risk variants associated with squamous cell lung cancer.

7. Li, X.*, Li, Z.*, Zhou, H., **Gaynor, S.M.**, Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D.K., Aslibekyan, S., Ballantyne, C.M., Bielak, L.F., Blangero, J., Boerwinkle, E., Bowden, D.W., Broome, J.G., Conomos, M.P., Correa, A., Curran, J.E., Cupples, L.A., Freedman, B.I., Guo, X., Kardia, S.L.R., Kathiresan, S., Khan, A.T.,

Kooperberg, C.L., Irvin, M.R., Laurie. C.C., Manichaikul, A.W., Mahaney, M.C., Mathias, R.A., Morrison, A.C., Martin, L.W., McGarvey, S.T., Mitchell, B.D., Montasser, M.E., Moore, J., O'Connell, J.R., Palmer, N.D., Pampana, A., Peralta, J.M., Peyser, P.A., Psaty, B.M., Vasan, R.S., Redline, S., Rice, K.M., Rich, S.S., Smith, J.A., Tsai, M., Tiwari, H.K., Wang, F.F., Weeks, D.E., Weng, Z., Wilson, J.G., Yanek, L.R., NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Neale, B.M., Sunyaev, S.R., Abecasis, G.R., Rotter, J.I., Willer, C.J., Peloso G.M., Natarajan, P., and Lin, X. Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis of large whole genome sequencing studies at scale. *In revision, Nature Genetics.*

* Indicates equal contribution as first authors