**Noteworthy Cancer Papers from the Previous Year**

E Khurana, Y Fu, D Chakravarty, F Demichelis, MA Rubin, M Gerstein (2016). “Role of non-coding sequence variants in cancer.” *Nat Rev Genet* **17**: 93-108 (2016).

A review of the role of noncoding variation in cancer, and computational and experimental methods for noncoding variant discovery and analysis.

LT Fang, PT Afshar, A Chhibber, M Mohiyuddin, Y Fan, JC Mu, G Gibeling, S Barr, NB Asadi, MB Gerstein, DC Koboldt, W Wang, WH Wong, HY Lam. “An ensemble approach to accurately detect somatic mutations using SomaticSeq.” *Genome Biol* **16**: 197 (2015).

A discussion on a combination of five different somatic variant callers that together achieve improved accuracy of somatic variant calls, outperforming any of the individual methods.

L Lochovsky, J Zhang, Y Fu, E Khurana, M Gerstein. “LARVA: an integrative framework for large-scale analysis of recurrent variants in noncoding annotations.” *Nucleic Acids Res* **43**: 8123-34 (2015).

A computational framework for determining somatic mutation burdens in noncoding elements using a background somatic mutation model that properly accounts for factors influencing whole genome mutation heterogeneity.

**Summary**

In the past year, we have worked on a number of TCGA projects that have resulted in the publication of a couple of large-scale genome analyses of prostate carcinoma and papillary renal-cell carcinoma. Additionally, we have built upon our analyses of cancer somatic single nucleotide variants (SNVs) and released LARVA, a computational framework that aims to address the relative lack of noncoding cancer driver analysis. LARVA is designed to identify somatic mutation burdens in noncoding elements using a novel background somatic mutation model that accurately reflects the variable mutation rate of different genome regions. Followups to LARVA include the development of NIMBus, which uses a more robust background model with many additional factors that influence mutation rate, and MOAT, a software tool that offers several empirical, nonparametric methods for determining mutation burdens. Furthermore, we have worked on producing an ensemble of complementary somatic mutation callers that enables higher accuracy in somatic mutation calls than would otherwise be possible.