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**RE: Principal Scientist: Computational Biologist  
(ID: 1014981)**

July 2, 2015

Dear Dr. Brockel and associates:

I am writing concerning the posted position of Principal Scientist: Computational Biologist (ID: 1014981). I recently informed my former colleague Dr. William Gordon that I was interested in exploring positions at Pfizer after hearing how much he respected the company and how positively he regards his experiences there. I am thrilled that he made me aware of this position as I feel that there is a considerable intersection between my experience, personal career goals, and the challenges of this professional opportunity.

I have developed expertise that particularly positions me to excel at the interface of biology and its computational interpretation. My training as a molecular biologist combined with both my formal and self-driven training and experience in applying computational solutions to biological questions allow me to think in both "languages" and make me a strong communicator with practitioners of both disciplines.

I have applied data mining methods to multiple large-scale, multidimensional data sets, both during my doctoral work at the University of California, Irvine and in my current postdoc at Yale University. During my doctoral work, I both generated and analyzed RNA-seq transcriptomics data from four distantly related disease-vector mosquitoes by integrating phylogenetic, comparative genomic, and functional annotation data from disparate database sources using network graphs to generate testable hypotheses regarding the shared regulatory mechanisms of transcription related to the management of the bloodmeal by the midgut. I developed an internal pipeline and infrastructure for high throughput sequencing analysis in my lab whereby both computationally experienced and inexperienced colleagues could process and analyze the data we were generating. At Yale I am analyzing genome-wide SNP-based population genetics of tsetse fly populations in Uganda. Most recently, I devised and implemented a Bayesian filtering method for analyzing linkage disequilibrium values of SNP-pairs binned by separation distance to prioritize pairs for further analysis while managing varying amounts of data per bin. Further, I am fluent in dataframe-based analysis workflows and habitually maintain IPython executable notebooks which enable sharable, documented, *repeatable* work.

I am excited about the prospect of working with the Computational Sciences Center of Emphasis as well as within the context of Pfizer and am eager to apply my knowledge to human translational/medical research. I believe that the Computational Sciences Center of Emphasis and your group will provide me with a rich environment for professional growth and new computational challenges through its access to varied data-sources with real-world, translational implications. Furthermore, the ability to work within and continue to learn from a group of other bioinformatically-minded professionals is very important to me. Finally, the conversations I have had with Dr. Gordon in particular, as well as my exploration of Pfizer more broadly, have convinced me that this is a spectacular environment within which to do science.

Thank you for your time regarding my interest in this position. Please feel free to contact me if you need additional information; I am also happy to provide a list of references at your request.

Sincerely,

**W. Augustine Dunn, III**