JUSTIN THOMAS REESE

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SUMMARY

I am a biologist with experience in all aspects of research and teaching. I am a native English speaker with excellent communication skills. I am seeking a position that will allow me to apply these skills and contribute meaningfully to cross-cultural projects involving Thai and foreign nationals.

EXPERIENCE

2014 - 2015   **Khon Kaen University**

Research Professor

- Developed computational biology projects to aid in treatment of cholangiocarcinoma and nasopharyngeal carcinoma in coordination with Khon Kaen University faculty
- Advised Khon Kaen University faculty and students dealing with computational biology data related to existing projects
- Assisted faculty and students in preparation of scientific manuscripts and presentations

2010 – 2015   **Genformatic, LLC**

Chief Operating Officer

- Managed bioinformatics team that performed genome variant detection and bespoke bioinformatics analyses for Genformatic, LLC, generating revenue and producing several peer-reviewed research papers
- Led development of several bioinformatic products, including novel software for improving genome variant detection, custom SNP and indel calling pipeline and genome variant annotation pipeline
- Assisted in business development

2012 – 2013   **University of Missouri**

Assistant Research Professor

- Lead developer of bovinegenome.org and hymenopteragenome.org, web portals to display information pertaining to the *Bos taurus* and hymenopteran genomes (e.g. *Apis mellifera*, *Nasonia vitropennis*) genomes, respectively
- Developed novel software and designed/maintained IT infrastructure for the annotation of genes in three genomes: *Apis mellifera, Nasonia vitripennis, Bos taurus*
- Developed scientific software for research and analysis of several newly sequenced genomes, including *Apis mellifera, Bos taurus, Strongylocentrotus purpuratus, Nasonia vitripennis, Tribolium castaneum, Atta cephalotes, Pogomyrmex barbatus, Linepithema humile and Pediculus humanus.*
- Lectured on bioinformatics and scientific programming

2006 – 2012   **Georgetown University**

Affiliate Research Professor

- Lead developer of bovinegenome.org and hymenopteragenome.org, web portals to display information pertaining to the *Bos taurus* and hymenopteran genomes (e.g. *Apis mellifera, Nasonia vitropennis*) genomes, respectively
- Developed novel software and designed/maintained IT infrastructure for the annotation of genes in three genomes: *Apis mellifera, Nasonia vitripennis, Bos taurus*
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- Lectured on bioinformatics and scientific programming

2004 – 2006   **Texas A&M University**

Research Associate

- Lead developer of hymenopteragenome.org, web portals to display information pertaining hymenopteran genomes (e.g. *Apis mellifera, Nasonia vitropennis*) genomes, respectively
- Training of graduate students and postdoctoral staff as required

2004 – 2005   **First Global Community College, Nong Khai, Thailand**

Lecturer/Director of Science (Part-time Volunteer)

- Set up and administered a science and IT program consisting of six teachers
- Taught science and computer classes

1998 – 2004   **University of Virginia (Laboratory of William Pearson)**

Graduate student

- Investigated the evolution of repeated sequences in protein and DNA
- Developed a mathematical model to explain the evolution of proteins in bacterial genomes
- Developed formula for optimal gap penalties for sequence alignment and database searching, improving sensitivity and selectivity of sequence analysis tools (FASTA, BLAST)
- Acquired a broad range of computer skills, including proficiency in several computer languages

EDUCATION

Ph.D.	**University of Virginia**	**May 2004**
Expertise: Computational biology and bioinformatics		
M.S.	**University of Georgia**	**August 1997**
Expertise: Immunology		
B.S.	**Clemson University**	**December 1994**
Major: Biochemistry (*cum laude*)		

SKILLS

- Excellent communication skills
- Experienced in manuscript preparation, editing and review
- Experienced in undergraduate and graduate teaching and training
- Proficient in several programming languages (PERL, Ruby, C, Java, R, S-Plus, shell scripting)

LANGUAGES

- English: native speaker, excellent speaking and writing skills
- Thai: fluent in spoken Thai, intermediate reading and writing skills
- Lao: elementary knowledge of spoken and written Lao
- Spanish: elementary knowledge of spoken and written Spanish

PUBLICATIONS

Cantarel, B., Weaver, D., McNeill, N., Zhang, Jianhua, Z., Mackey, A., **Reese, J.** (2014). BAYSIC: a Bayesian method for combining sets of genome variants with improved specificity and sensitivity. *BMC Genomics,* 15(1), 104.

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Elsik, C., Worley, K., Bennett, A., Beye, M., Camara, F., Childers, C., de Graff, Debyser, G., Deng, J., Devreese, B., Elhaik, E., Evans, J., Foster, L., Graur, D., Guigo, R., Hoff, K., Holder, M., Hudson, M., Hunt, G., Jiang, H., Joshi, V., Khetani, R., Kosarev, P., Kovar, C., Ma, J., Maleskzka, R., Moritz, R., Muñoz-Torres, M., Murphy, T., Muzny, M., Newsham, F., **Reese, J.**, Robertson, M., Robinson, G., Rueppel, O., Solovyev, V., Stanke, M., Stolle, E., Tsuruda, J., Van Vaerenbergh, M., Waterhouse, R., Weaver, D., Whitfield, C., Wu., Y., Zdobnov, E., Lan, Z., Zhu, D. and Gibbs., R. (2014). Finding the missing honey bee genes: lessons learned from a genome upgrade. *BMC Genomics, 15*(1), 86.

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Lee., E., Helt., G., **Reese, J.**, Muñoz-Torres, M., Childers, C., Buels, R., Stein, L., Holmes, I., Elsik, C. and Lewis, S. (2013). Web Apollo: A Web-based Genomic Annotation Editing Platform. *Genome Biology,* 14, R93.

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Saha, S., Hunter, W. B., **Reese, J.**, Morgan, J. K., Marutani-Hert, M., Huang, H., and Lindeberg, M. (2012). Survey of endosymbionts in the Diaphorina citri metagenome and assembly of a Wolbachia wDi draft genome. *PloS One, 7*(11), e50067.

Smith, C.D., Abouheif, E., Benton, R., Croset, V., Currie, C.R., Elhaik, E., Elsik, C.G., Fave, M-J, Fernandes, V., Gadau, J., Gibson, J.D., Graur, D., Hagen, D.E., Helmkampf, M., Holt, C., Hu, H., Johnson, B.R., Johnson, R.M., Abderrahman, K., Kim, J.K., Mathis, K.A., Munoz-Torres, M.C., Murphy, M.C., Nakamura, R., Nigam, S., Overson, R., Placek, J., Rajakumar, R., **Reese, J.T.**, Robertson, H.M., Smith, C.R., Suen, G., Tao, S., Torres, C.W., van Wilgenburg, E., Viljakainen, L., Vinniegra, A-S. I., Walden, K.K.O., Yandell, M.D., Zimin, A. & N.D. Tsutsui (2011). The Genome of the Globally Widespread and Invasive Argentine Ant (*Linepithema humile*). *Proceedings of the National Academy of Sciences USA.* 108:5667-5672.

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Munoz-Torres, M.,* **Reese, J.**,* Childers, C.,* Bennett, A., Sundaram, J., Childs, K., Anzola, J., Milshina, N. and Elsik, C. (2010) Hymenoptera Genome Database: integrated community resources for insect species of the order Hymenoptera. *Nucleic Acids Res.* 39:D658-662.

Reese, J.,* Childers, C.,* Sundaram, J.,* Dickens, M., Childs, K., Vile, D. and Elsik, C. (2010) Bovine Genome Database: supporting community annotation and analysis of the *Bos taurus* genome. *BMC Genomics.* 11:645.

Reese, J., as member of The *Nasonia* Genome Working Group (2010) Functional and Evolutionary Insights from the Genomes of Three Parasitoid *Nasonia* Species. *Science.* 327:343 – 348.

Reese, J., as member of Tribolium Genome Sequencing Consortium (2008) The genome of the model beetle and pest Tribolium castaneum. *Nature.* 2008 452:949-55

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Reese, J. as member of the Honeybee Genome Sequencing Consortium (2006) Insights into social insects from the genome of the honeybee *Apis mellifera. Nature.* 443:931-949.

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