# Curriculum Vitae

## Achal Neupane

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## Education

- PhD (Bioinformatics), August 2017-December 2019
  *South Dakota State University, Brookings, South Dakota, USA,*

- Master of Science (Bioinformatics), August 2011-May 2013
  *South Dakota State University, Brookings, South Dakota, USA.*

- Bachelor of Science (Biological Science), August 2005-December 2009
  *University of the District of Columbia (UDC), Washington, DC, USA.*

## Professional Summary

I have been working on computational and statistical genetics focused projects for more than 10 years. I have extensive experience in academic, clinical and industry collaborations with researchers in the US and Australia. I have gained key expertise in the analysis of large clinically focused datasets and developed genotyping algorithms using various statistical models to analyze these data. Since the beginning of my graduate program, I have taken several "data-heavy" courses from Statistics and Computer Science departments in order to develop my skills for big-data analysis, algorithm development, and scientific computing, including analysis of large genome data. Additionally, I have been writing computer programs in R, python, Perl, JavaScript, and also have been working on Linux/Unix system with extensive use of shell (bash) and PBS scripts for nearly 10 years of my career. I am interested in big data analysis, algorithm development, scientific computing and data visualization.

## Computer Skills

- Programming languages: R, Python, JavaScript, Perl, PHP, ASP.NET, MySQL
- Operating systems: Linux/Unix, Linux based high performance computing (HPC) cluster and command lines (Shell, awk, sed, PBS, git)
- Machine learning, including Deep Neural Networks (LSTM and RNN), and statistical modeling and algorithm development with R and python
- Tensorflow/keras, sklearn, pandas, including customizing or designing neural networks
- ARIMA, exponential smoothing, ARCH/GARCH, and testing for seasonality, lags, hetero-skedasticity, and multicollinearity
- GitHub/Bitbucket: achalneupane

## Statistical Analyses

- Simple and multiple linear regressions, ANOVA for one or multiple factors, Design of experiments, Linear models with categorical data, and Models with categorical response variable

- Logistic Regression I, Generalized Linear Models, Density Estimation, Recursive Partitioning, Generalized Additive Models and Spline Models, Survival Analysis, Longitudinal Data Analysis and Mixed Models, Multiple Comparisons, False Discovery Rates, Simultaneous Inference and Meta-Analysis
- Classification, Resampling Methods, Model Selection, Moving Beyond Linearity", Tree-Based Methods, Support Vector Machines, ROC curves, and Clustering/Unsupervised Learning

## Graduate level courses in Computer Science and Statistics

- Data Structures and Algorithms (Python; 3 credits)
- Perl Programming for Biological Applications (3 credits)
- Statistical Methods II (3 credits)
- Statistical Programming (R and SAS; 3 credits)
- Modern Applied Statistics I (3 credits)
- Modern Applied Statistics II (3 credits)

## Experience

- **Computational Biologist/Research Assistant (PhD candidate)**
  South Dakota State University, USA (Aug 2017- present)
    - Studying the effects of hypovirulence-associated DNA virus 1(SsHADV-1) and Sclerotinia sclerotiorum hypovirus 2 Lactuca (SsHV2L) on white mold fungus pathogen *Sclerotinia sclerotiorum* analyzing small RNAseq and RNAseq data
    - Studying the evidence/effect of RNAi by induction of virus in *Sclerotinia sclerotiorum* using bioinformatics approaches.
    - Studying the roles of dicers and argonautes on *Sclerotinia sclerotiorum* antiviral Small RNA Processing.
    - Analyzing metatranscriptomic data to study novel mycoviruses infecting arbuscular mycorrhizal fungus *Rhizophagus* spp and other pathogenic fungi.
    - Studying the effect of crop rotation in soil microbiome diversity affecting the overall yield from Illinois-Urbana sites.
    - Studying the effects of soil salinity in microbiome diversity by analyzing 16S and ITS data from South Dakota.

- **Data Scientist**
  University of Queensland, Translational Research Institute (TRI), Brisbane, Australia (Jan 2015- Jun 2016)
    - Studied and characterized the genetic landscape of Acute Myeloid Leukemia (AML) by analyzing sequence genotyped SNP data from 480 exomes and 150 whole genomes from AML samples.
    - Analyzed a cohort of 900 control exomes and 600 whole genomes to perform gene discovery for both somatic and germline risk variants using sophisticated statistical genetics algorithms that identify both protective and deleterious variants.
    - Validated and compared genotyping algorithms and sequencing technologies using pathology, cytogenetic and Sequenom genotyping data to refine and calibrate these algorithms.

- Discovered AML related genes using SKAT and burden like statistics. Used several variant calling methods to characterize germline, copy number and structural variants in AML and control samples in whole exome sequenced samples.
- Developed algorithms to identify sample contamination, identity and ethnicity for quality control of Next Generation Sequencing (NGS) data.

- **Computational Biologist**
  School of Biological Sciences, University of Nebraska-Lincoln, Nebraska, USA (Aug 2013- May 2014)
  - Studied the modes of pathogenesis and impacts of western corn rootworm (WCR) in corn roots by analyzing gene expression of gustatory receptors using larval/egg transcriptome data.
  - Identified several gamma-aminobutyric acid type A (GABAA) receptor and gustatory receptors from the WCR transcriptome.
  - Performed bioinformatics analysis to study the conservation of gene structure and function of chemoreceptor protein family across insect genome.
- **Bioinformatics Researcher**
  Department of Biology and Microbiology, South Dakota State University, USA (Aug 2011- Jul 2013)
  - Identified all three families of mitogen-activated protein kinases (MAPKs), and characterized the legume specific MAPK genes involved in *Rhizobium*-legume interaction.
  - Identified MAPK and MAPKK gene members in soybean, *Lotus*, *Medicago* and *Phaseolous* and studied their evolutionary relationships with respect to their counterparts in different non-legume species.
  - Used approaches in bioinformatics and comparative genomics to study functional and evolutionary divergence of MAPK genes in legumes.
  - Performed MAPK silencing and hairy root transformation using RNAi constructs in soybean.
  - Performed time-course expression analysis of MAPKs in root nodulation of mock and *Rhizobium* inoculated soybean seedlings using RT-PCR and Microarray analysis.
  - Mentored undergraduate researchers.

# Publications

### Peer- reviewed journal articles

- **Neupane**, **A**., Feng, C., Mochama, PK., Saleem H., and Lee Marzano SY. (2019). Roles of Argonautes and Dicers on Sclerotinia sclerotiorum Antiviral RNA Silencing. *Frontiers in Plant Science*; 10:976.
- SY., Marzano, **Neupane**, **A**., Domier, L. (2018). Transcriptional and Small RNA Responses of the White Mold Fungus *Sclerotinia sclerotiorum* to Infection by a Virulence-Attenuating Hypovirus. *Viruses*; 10 (12), 713.
- **Neupane, A.**, Feng, C., Feng, J., Kafle, A., Bücking, H., and Marzano, SY. (2018) Metatranscriptomic Analysis and In Silico Approach Identified Mycoviruses in the Arbuscular Mycorrhizal Fungus *Rhizophagus* spp. *Viruses* 10 (12), 707.

- Neupane, S., Schweitzer, SE., **Neupane**, **A**., Andersen, EJ., Fennell, A., Zhou and Nepal, MP. (2019). Identification and Characterization of Mitogen-Activated Protein Kinase (MAPK) Genes in Sunflower (*Helianthus annuus* L.). *Plants (Basel)* 8.
- Neupane, S., Andersen, E., **Neupane**, **A**., and Nepal, M. (2018) Genome-Wide Identification of NBS-Encoding Resistance Genes in Sunflower (*Helianthus annuus* L.). *Genes* 9 (8), 384.
- Mochama, P., Jadhav, P., **Neupane**, **A**., Marzano, SY. (2018) Mycoviruses as Triggers and Targets of RNA Silencing in White Mold Fungus *Sclerotinia sclerotiorum*. *Viruses* 10 (4).
- S. Piya, **Neupane**, **A**., Butler, J., Larson, GE., and Nepal, MP. (2014) Genetic Diversity and Population Structure of Sickleweed (*Falcaria vulgaris* L.) in the Upper Midwest USA Midwest USA. *Biological Invasions* 2014:1-11.
- **Neupane**, **A**., Nepal, MP., Benson, BV., MacArthur, KJ., and Piya, S. (2013). Mitogen-Activated Protein Kinase Genes and their Evolutionary History in *Lotus*, *Medicago* and *Phaseolus*. *Plant Signaling & Behavior*; 8:e27189.
- **Neupane**, **A**., Piya, S., Subramanian, S., Rohila, JS., Reese, N., and Nepal, MP. (2013). Identification, Nomenclature, and Evolutionary Relationships of Mitogen-Activated Protein Kinase (MAPK) Genes in Soybean. *Evolutionary Bioinformatics*; 9:363-86.
- Piya, S., **Neupane**, **A**., Butler, J., Larson, GE., and Nepal, MP. (2012)**.** Inferring the introduction history of sickleweed (*Falcaria vulgaris* L.) in the United States. *Proceedings of the South Dakota Academy of Science*; 91:113-129.

## Presentations

- **Neupane**, **A**., and Marzano, S. Profiling the Classes of the RNA Editing in Virus-derived small RNAs in White Mold *Sclerotinia sclerotiorum*. *American Society for Virology*, 2019, 20-24 July, Minneapolis, USA (Oral).
- **Neupane**, **A**., Mochama, P., Saleem, H., Marzano, S. Roles of Dicers and Argonautes on *Sclerotinia sclerotiorum* Antiviral Small RNA Processing. *Plant and Animal Genome Conference XXVII*, 2019, 12-16 January, San Diego, CA, USA (Poster).
- Smith, A., **Neupane**, **A**., Ellis, J., Afrin, S., Burow, R., Stinson, C., Leo, P., Cristino, A., Moore, A. MEK inhibitor resistance in acute myeloid leukaemia. *New Direction in Leukaemia Research*, 2016, 16-19 March, Peppers Noosa, Australia (Poster)
- Leo, P., **Neupane**, **A**., Bassal, M., Maung, Z., Newell, F., Ellis, M., Boxall, G., Smith, A., Marlton, P., D'Andrea, R., Gonda, T., Brown, M., Saal, R., Moore, A. Gene Discovery in Acute Myeloid Leukaemia: somatic and germline mutations. *International Congress of Immunology*, 2016, 21-26 August, Melbourne, Australia (Oral).
- Moore, A., Leo, P., **Neupane**, **A**., Bassal, M., Newell, F., Ellis, M., Boxall, G., Smith, A., Marlton, P., D'Andrea, R., Gonda, T., Brown, M., Saal, R, Anderson, L. Sensitivity of Whole Exome Sequencing for the Detection of FLT3-ITD and NPM1 Mutations in Acute Myeloid Leukaemia. *European School of Hematology (ESH)*. 2015, 10-12 September, Budapest, Hungary (Oral).
- **Neupane**, **A**., Eyun, S., Wang, H., Siegfried, BD., and Moriyama, EN. Transcriptome analysis of western corn rootworm larvae and eggs. *IWGO & International Conference of Diabrotica Genetics*. 2014, 14-17 April. Chicago, IL, USA (Poster).

- **Neupane**, **A**., Piya, S., Reese, N., Rohila, JS., Subramanian, S., and Nepal, MP. Identification of Mitogen Activated Protein Kinase Family members in Soybean. *Botanical Society of America Conference* 2012, 7-11 July. Columbus, OH, USA (Poster).
- Piya, S., **Neupane**, **A**., Butler, J., Larson, GE., and Nepal, MP. Population Genetics of *Falcaria vulgaris* (Sickleweed) in North America. *Botanical Society of America Conference* 2012, 7 -11 July. Columbus, OH, USA (Poster).
- Piya, S., **Neupane**, **A**., Butler, J., Larson, GE., and Nepal, MP. Introduction history and spread of *Falcaria vulgaris* Bernh. (Apiaceae) in the United States based on herbarium records. *South Dakota Academy of Science* 2012, 13-14 April. Vermillion, SD, USA (Oral).
- **Neupane**, **A**., Piya, S., Subramanian, S., Rohila, JS., Reese, N., and Nepal, MP. A Nomenclatural Conundrum: Applying Existing Nomenclature to the Identification of Soybean (*Glycine max*) MAP Kinase Genes. *ASPB Midwestern Sectional Society* 2012, 24-25 March. Lincoln, NE, USA (Poster).
- **Neupane**, **A**., Anjorin, C., Song, X., and Kumar, D. Anticancer Activity of Novel Ionic Triorganotin Derivatives against MDA-MB 231 Breast Cancer Cells. *HBCU-UP National Research Conference* 2009, October 29-November 1. Washington, DC, USA (Poster).

## Research Grants

- University of Nebraska-Lincoln travel grants ($1500, FY 2014)
- Center for Excellence in Drought Tolerance Research (CEDTR)-USDA/NIFA (#SA1100029): Identification and characterization of mitogen-activated protein kinases (MAPKs) involved in root nodulation in *Glycine max*. ($4000, FY 2012/2013).
- MERCK/ AAAS: Anticancer activity of novel ionic triorganotin derivatives against MDA-MB 231 breast cancer cells. ($5000, FY2009).

## Membership in Professional Organizations

- Associate member, Sigma XI
- Member, American Association for the Advancement of Science (AAAS)

## Awards and Achievements

- Sigma Xi Masters Research Paper, South Dakota State University, (2012)
- Dean's List Honoree, University of the District of Columbia, Washington DC (2006-2009)
- United Nations Mission in Nepal (UNMIN) Scholarship (2002)

## References

**Available upon request**