CURRICULUM VITAE

- **NAME:**   **ALOK KUMAR MAITY**

- **MAILING ADDRESS:** CAS-MPG Partner Institute for Computational Biology,
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- **PERMANENT ADDRESS:** Vill- Rampur, P.O- Nandapur, P.S- Chandipur,
  Dist- Purbo Medinipur, Pin-721625,
  West Bengal, India.

- **DATE OF Birth: August 20, 1985**

- **Nationality: Indian**

- **EDUCATION:**

  B. Sc in Chemistry, University of Calcutta, India, 2007.

  M. Sc in Chemistry (Physical Chemistry major), University of Calcutta, India, 2009.

  Ph. D in Chemistry (Theoretical and computational Biology), University of Calcutta, Kolkata, India, 2016.

Standard	Institution/Board/ University	Year	Percentage of marks & Division/Class
10th Standard	West Bengal Board of Secondary Education	2001	75.25% (1st Division)
12th Standard	West Bengal Council of Higher Secondary Education	2003	72.2% (1st Division)
B.Sc. (Hons. in Chemistry)	University of Calcutta	2007	64% (1st Class)
M.Sc. (Chemistry; Spec. in Physical Chemistry)	University of Calcutta	2009	71.1% (1st Class)

- **PROFESSIONAL EMPLOYMENT:**

  1. Lecturer in Chemistry, Kingston Engineering College, Calcutta, India (March, 2010-June, 2011)

- **RESEARCH EXPERIENCE:**

  Doctoral Research: University of Calcutta, 92 A.P.C. Road, Kol-09, West Bengal, India (July, 2011 – August, 2016).

  1st Postdoctoral Research: University of California, Los Angeles, 611 Charles E Young Dr E, CA, USA (September, 2016 – August, 2019).

  2nd Postdoctoral Research: CAS-MPG Partner Institute for Computational Biology, Shanghai Institute of Nutrition and Health, Shanghai, P R China (November, 2019 - Present).

- **Ph.D THESIS TITLE:**

  Title: Stochastic Study Of Some Model Biochemical Networks.

  Supervisor: **Dr. Pinaki Chaudhury,**
  University Of Calcutta,
  92 A. P. C. Road, Kolkata-700009, INDIA.

  Joint Supervisor: **Dr. Suman Kumar Banik,**
  Bose Institute,
  93/1 A. P. C. Road, Kolkata-700009, INDIA.

- **RESEARCH INTEREST:**

  Systems Biology, Stochastic modeling of biochemical networks, Cellular signal transduction mechanism, Information encoding and decoding within a cell, Bioinformatics.

- **AWARD / FELLOWSHIP:**

  UGC fellowship (JRF and SRF from 2011 - 2016) (qualified on Dec, 2010 NET Examination).

  Qualified GATE-2010 examination with score 478 and 330 all India rank.

- **SYMPOSIUM / CONFERENCE ATTENDED:**

  1. Kolkata International School cum Conference on Systems Biology, "KOLSYSBIO", Dec 29, 2012-Jan 3, 2013. Jointly organized by Bose Institute and Saha Institute of Nuclear Physics, Kolkata, West Bengal, India.

  2. Kolkata International Conference on Statistical physics and Nonlinear dynamics, "STATPHYS-KOLKATA VIII", Dec 01-05, 2014. Organized by S. N. Bose Centre,

Kolkata, West Bengal, India. (**Presented a Poster**)

3. UCLA QCBio 4th Annual Retreat, Sept 25, 2018, Organized by Institute of Quantitative and Computational Biosciences, UCLA, CA, USA. (**Presented a Poster**).

4. Annual Meeting of CAS Key Lab of Computational Biology, Dec 10-11, 2019. Organized by CAS-MPG Partner Institute for Computational Biology, Shanghai, P R China.

- **TECHNICAL KNOWLEDGE:**

Theoretical expertise: I have a physical chemistry background. Thus, I have the knowledge of Thermodynamics, Chemical Kinetics, Statistical mechanics, Quantum mechanics and spectroscopic methods in general. During my PhD and postdoc, I have learned the nonlinear dynamical analysis, bifurcation and information theory. I have adopted several approximation theories for solving nonlinear stochastic differential equation (Langevin dynamics) such as linear noise approximation, naive perturbation theory, multiple time scale perturbation theory and direct method of time scale separation. Adopting these techniques, I have quantified fluctuations in intracellular components and mutual information between input and output signals in different biological network motifs. These studies pave the way for understanding the experimental results performed in single-cell regime. Leveraging scRNA-seq data, I estimated single-cell potency and pinpointed the cell-fate transitions stage. I also used DNAm data to characterize the switching stage from normal to cancerous cells (esophageal carcinoma).

Numerical expertise: I am familiar with the software **XPPAUT**, **Mathematica**, **MATLAB, R** and **Python**. I have also the experience of writing the code (in **Fortran** language) for stochastic simulation (Gillespie simulation).

Omics data analysis experience: Bulk and single-cell **RNA-seq** data, **DNAm** data.

- **List of Publications**

   1. **Quantification of noise in bifunctionality-induced post-translational modification**
      <u>**Alok Kumar Maity**</u>, Arnab Bandyopadhyay, Sudip Chattopadhyay, Jyotipratim Ray Chaudhuri, Ralf Metzler, Pinaki Chaudhury, and Suman K. Banik, **Phys Rev E 88, 032716 (2013).**

   2. **Role of functionality in two-component signal transduction: A stochastic study**
      <u>**Alok Kumar Maity**</u>, Arnab Bandyopadhyay, Pinaki Chaudhury, and Suman K. Banik, **Phys Rev E 89, 032713 (2014).**

   3. **Controlling mobility via rapidly oscillating time periodic stimulus,**
      Prasun Sarkar, <u>**Alok Kumar Maity**</u>, Anindita Shit, Sudip Chattopadhyay, Jyotipratim Ray Chaudhuri, Suman K. Banik, **Phys. Chem. Lett. 602, 4, (2014).**

   4. **Analysis of DevR regulated genes in *Mycobacterial tuberculosis***

Arnab Bandyopadhyay, Soumi Biswas, **Alok K. Maity** and Suman K. Banik, **Syst. Synth. Biol. 8, 3, (2014).**

5. **Role of Relaxation Time Scale in Noisy Signal Transduction,**
    <u>Alok Kumar Maity</u>, Pinaki Chaudhury, and Suman K. Banik, **PLOS ONE, 0123242, 1-26 (2015).**

6. **Information theoretical study of cross-talk mediated signal transduction in MAPK pathways**
    <u>Alok Kumar Maity</u>, Pinaki Chaudhury, and Suman K. Banik, **Entropy, 496, 19 (2017)**.

7. **Information transmission from NFkB signaling dynamics to gene expression**
    <u>Alok Maity</u>, Roy Wollman, **PLOS Computational Biology, 16(8), e1008011 (2020).**

8. **GATA3 Mediates a Fast, Irreversible Commitment to BMP4- Driven Differentiation in Human Embryonic Stem Cells**
    Alexandra Gunne-Braden, Adrienne Sullivan, Borzo Gharibi, Rahuman S.M. Sheriff, **Alok Maity**, Yi-Fang Wang, Amelia Edwards, Ming Jiang, Michael Howell, Robert Goldstone, Roy Wollman, Philip East and Silvia D.M. Santos, **Cell Stem Cell, 26, 1-14 (2020)**.

9. **Ultra-fast scalable estimation of single-cell differentiation potency from scRNA-Seq data**
    Andrew E. Teschendorff, **Alok K. Maity**, Xue Hu1, Chen Weiyan and Matthias Lechner, **Bioinformatics, 37(11), 1528-1534 (2021)**.

10. **Novel epigenetic network biomarkers for early detection of esophageal cancer**
    Alok K Maity, Timothy C. Stone, Vanessa Ward, Amy P. Webster, Zhen Yang, Aine Hogan, Hazel McBain, Margaraet Duku, Kai Man Alexander Ho, Paul Wolfson, David G. Graham, SPIT Study Group, Stephan Beck, Andrew Teschendorff, Laurence B. Lovat, **Clinical Epigenetics, 14, 23 (2022)**.

11. **Epigenetic fluctuations underlie gene expression timescales and variability**
    Ryan Lannan, **Alok Maity**, Roy Wollman, **Physiol Genomics, (2022).**

12. **Computational identification of preneoplastic cells displaying high stemness and risk of cancer progression**
    Tianyuan Liu, Shaosen Zhang, Yuan Lin, Qi Luo, Xuan Zhao, Yiyi Xi, Yamei Chen, Lin Lin, Wenyi Fan, Jie Yang, Yuling Ma, **Alok K. Maity**, Yanyi Huang, Jianbin Wang, Jiang Chang, Dongxin Lin, Andrew E. Teschendorff and Chen Wu, **Cancer Research**, (2022).

- **Papers Under Review**

1. **Extracellular Matrix Impairs Cellular Remodeling and Contributes to Stem Cell Dysfunction in Duchenne Muscular Dystrophy**
   Kristen M. Stearns-Reider, Katherine Hammond, Michael Hicks, **Alok Maity**, Yerbol Z. Kurmangaliyev, Jesse Chin, Roy Wollman, Kirk Hansen, April Pyle, and Rachelle H. Crosbie

2. **A distance covariance entropy measure for exploration of bifurcation dynamics in single-cell RNA-Seq data**
   Alok K Maity and Andrew E Teschendorff

3. **Identification of differentially abundant cell-type in scRNA-seq data using node-attributed community detection approach**
   Alok K Maity and Andrew E Teschendorff

4. **Inference of age-associated regulatory activity changes in single-cells reveals novel insights into age-related diseases**
   Alok K. Maity, Xue Hu, Tianyu Zhu and Andrew E. Teschendorff

- **REFERENCES:**

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