

Curriculum Vitae

Name: Trees-Juen Chuang (莊樹諱)

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Education:

- 1988~1992: B.S., Department of Computer Science, Soochow University, Taiwan
- 1992~1998: Ph.D., Institute of Computer and Information Science, National Chiao Tung University, Taiwan (Ph.D. Thesis: "Compression, Encryption, and Hiding of Still Images")
- 1998~2003: Postdoctoral Fellow, Institute of Biomedical Sciences, Academia Sinica, Taiwan (military service)

Current position and relevant experience:

- 2003~2007: Assistant Research Fellow, Genomics Research Center, Academia Sinica
- 2007~2014: Associate Research Fellow, Genomics Research Center, Academia Sinica
- 2014~date: Research Fellow, Genomics Research Center, Academia Sinica

- Joint Professor, International Graduate Program for Biodiversity, National Taiwan Normal University
- Joint Professor, NTU-Academia Sinica Genomics and Systems Biology Degree Program, National Taiwan University
- Joint Professor, Department of Bioinformatics, Asia University
- Adjunct Professor, NYMU-Academia Sinica Genomics Science Degree Program, National Yang-Ming University
- Adjunct Professor, Graduate Institute of Life Sciences, National Defense Medical Center

Honors/Awards:

- Project for Excellent Junior Research Investigators Award, Ministry of Science and Technology, Taiwan, 2014-2018.
- Pius XI Medal, the Pontifical Academy of Sciences, Vatican, 2012.
- Academia Sinica Research Award for Junior Research Investigators, 2007.
- Wu Ta-Yuo Memorial Award, National Science Council, 2007.
- Post-doctoral Research Award of National Health Research Institutes (NHRI, Taiwan), 2001.
- Academia Sinica Post-doctoral Fellowship, 1999-2000.
- Academic Paper Awards from the Image Processing and Pattern Recognition (IPPR) Society, 1998.

Research evaluation:

- The best oral presentations, the 5th International Conference on Biological and Medical Sciences (ICBMS 2017), Kitakyushu, Japan, 2017.
- The top 5 most cited articles over the past two years in *WIREs RNA*, 2017.
- *Nature Reviews Genetics*, Feature Report, 2013.
- *Asia-Pacific International Molecular Biology Network (A-IMBN)*, Feature Report, 2012.
- Significant publications of Academia Sinica, 2004, 2006, 2010, and 2016.
- Editorial Board of *ISRN Bioinformatics*, Hindawi Publishing Corporation (2011~date)
- Associate Editor, *BMC Genomics*, BioMed Central, London (2010~date)
- Board member, Taiwan Society of Evolution and Computational Biology (2012~2014; 2016~2018)
- Supervisory Board, Bioinformatics Society Taiwan (2007~2009)

Research Interests:

Bioinformatics, Comparative and Evolutionary Genomics/Transcriptomics, Post-transcriptional Regulation, *Trans*-/back-splicing, Gene Fusion, DNA Methylation, Systems Biology, Pattern Recognition, Machine Learning

Referee for international journals

● Nature Reviews Genetics ● Nature Protocols ● Nature Communications ● PNAS ● Genome Biology ● Molecular Biology and Evolution ● Nucleic Acids Res. ● RNA Biology ● WIREs RNA ● Scientific Reports ● PLoS Computational Biology ● Human Molecular Genetics ● Frontiers in Neuroscience ● PLoS One ● BMC Genomics ● BMC Bioinformatics ● BMC Evol. Biol. ● BMC Plant Biol. ● Gene ● J. Bioinform. Comput. Biol. ● Nucleic Acid Therapeutics ● Cell Biology and Toxicology ● Genes, Chromosomes and Cancer ● Int. J. of Evol. Biol.

Referee for international project

The START project (Y 1204-B), the Austrian Science Fund, 2018.

Publication List: (*corresponding author)

PART 1. Publications at GRC

1. Te-Lun Mai and **Trees-Juen Chuang*** (2019) A-to-I RNA editing contributes to the persistence of predicted damaging mutations in populations. *Genome Research*. In press. (**Corresponding author; SCI impact factor: 9.944; Rank (Biotechnology & Applied Microbiology): 6/162; Q1**)
2. Chia-Ying Chen and **Trees-Juen Chuang*** (2019) Comment on “A comprehensive overview and evaluation of circular RNA detection tools”. *PLoS Comput Biol.*, 15: e1006158. (**Corresponding author; SCI impact factor: 4.428; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 5/59; Q1**)
3. Lien-Szu Wu, Wei-Cheng Cheng, Chia-Ying Chen, Ming-Che Wu¹, Yi-Chi Wang⁴, Yu-Hsiang Tseng, **Trees-Juen Chuang***, C-K James Shen* (2019) Transcriptopathies of Pre- and Post-Symptomatic Frontotemporal Dementia-like Mice with TDP-43 Depletion in Forebrain Neurons. *Acta Neuropathologica Communications*, 7:50. (**Corresponding author; SCI impact factor: 5.883; Rank (NEUROSCIENCES): 33/267; Q1**)
4. Chia-Ying Chen and **Trees-Juen Chuang*** (2019) NCLcomparator: systematically post-screening non-co-linear transcripts (circular, trans-spliced, or fusion RNAs) identified from various detectors. *BMC Bioinformatics*, 20:3. (**Corresponding author; SCI impact factor: 2.511; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 9/59; Q1**)
5. **Chuang Trees-Juen***, Yen-Ju Chen, Chia-Ying Chen, Te-Lun Mai, Yi-Da

- Wang, Chung-Shu Yeh, Min-Yu Yang, Yu-Ting Hsiao, Tien-Hsien Chang, Tzu-Chien Kuo, Hsin-Hua Cho, Chia-Ning Shen, Hung-Chih Kuo, Mei-Yeh Lu, Yi-Hua Chen, Shan-Chi Hsieh, and Tai-Wei Chiang (2018) Integrative transcriptome sequencing reveals extensive alternative *trans*-splicing and *cis*-backsplicing in human cells. *Nucleic Acids Research*, 46(7): 3671-3691. **(Corresponding & first author; SCI impact factor: 11.147; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY): 14/298; Q1)**
6. Li-Yuan Hung, Yen-Ju Chen, Te-Lun Mai, Chia-Ying Chen, Min-Yu Yang, Tai-Wei Chiang, Yi-Da Wang, and **Trees-Juen Chuang*** (2018) An evolutionary landscape of A-to-I RNA editome across metazoan species. *Genome Biology and Evolution*, 10(2):521-537. **(Corresponding author; SCI impact factor: 3.726; Rank (GENETICS & HEREDITY - SCIE): 46/173)**
 7. **Trees-Juen Chuang***, Yu-Hsiang Tseng, Chia-Ying Chen, Yi-Da Wang (2017) "Assessment of imprinting- and genetic variation-dependent monoallelic expression using reciprocal allele descendants between human family trios", *Scientific Reports*, 7:7038. **(Corresponding & first author; SCI impact factor: 4.011; Rank (MULTIDISCIPLINARY SCIENCES): 15/69; Q1)**
 8. Chia-Ying Chen, Li-Yuan Hung, Chan-Shuo Wu, and **Trees-Juen Chuang*** (2016) Purifying selection shapes the coincident SNP distribution of primate coding sequences. *Scientific Reports*, 6:27272. **(Corresponding author; SCI impact factor: 4.011; Rank (MULTIDISCIPLINARY SCIENCES): 15/69; Q1)**
 9. **Trees-Juen Chuang***, Chan-Shuo Wu, Chia-Ying Chen, Li-Yuan Hung, Tai-Wei Chiang, and Min-Yu Yang (2016) NCLscan: accurate identification of non-co-linear transcripts (fusion, *trans*-splicing, and circular RNA) with a good balance between sensitivity and precision. *Nucleic Acids Research*, 44(3), e29. **(Corresponding & first author; SCI impact factor: 11.147; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY): 14/298; Q1) → collected in 2016 significant publications of Academia Sinica.**
 10. Iju Chen, Chia-Ying Chen and **Trees-Juen Chuang*** (2015) Biogenesis, identification, and function of exonic circular RNAs. *WIREs RNA*, 6(5):563-79. **(Corresponding author; SCI impact factor: 4.928; Rank (CELL BIOLOGY): 55/193; Q2) → the top 5 most cited articles over the past two years in WIREs RNA.**
 11. **Trees-Juen Chuang***, Min-Yu Yang, Chuang-Chieh Lin, Ping-Hom Hsieh and Li-Yuan Hung (2015) Comparative genomics of grass EST libraries

- reveals previously uncharacterized splicing events in crop plants. *BMC Plant Biology*, 2015, 15:39. **(Corresponding & first author; SCI impact factor: 3.670; Rank (PLANT SCIENCES): 30/228; Q1)**
12. Chun-Ying Yu, Hsiao-Jung Liu, Li-Yuan Hung, Hung-Chih Kuo* and **Trees-Juen Chuang*** (2014) Is an Observed Non-co-linear RNA Product Spliced in *trans*, in *cis*, or just *in vitro*? *Nucleic Acids Research*, 42(14), 9410-9423. **(Corresponding author; SCI impact factor: 11.147; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY): 14/298; Q1)**
 13. Feng-Chi Chen*, **Trees-Juen Chuang***, Hsuan-Yu Lin and Min-Kung Hsu (2014) The evolution of the coding exome of the Arabidopsis species - the influences of DNA methylation, relative exon position, and exon length. *BMC Evolutionary Biology*, 2014, 14:145. **(Corresponding author; SCI impact factor: 3.045; Rank (GENETICS & HEREDITY): 71/173; Q2)**
 14. **Trees-Juen Chuang*** and Tai-Wei Chiang (2014) Impacts of Pre-transcriptional DNA Methylation, Transcriptional Transcription Factor and Post-transcriptional microRNA Regulations on Protein Evolutionary Rate. *Genome Biology and Evolution*, 6(6), 1530-1541. **(Corresponding & first author; SCI impact factor: 3.726; Rank (GENETICS & HEREDITY - SCIE): 46/173; Q2)**
 15. Chan-Shuo Wu, Chun-Ying Yu, Ching-Yu Chuang, Michael Hsiao, Cheng-Fu Kao, Hung-Chih Kuo* and **Trees-Juen Chuang*** (2014) Integrative transcriptome sequencing identifies *trans*-splicing events with important roles in human embryonic stem cell pluripotency. *Genome Research*. 24(1), 25-36. **(Corresponding author; SCI impact factor: 9.944; Rank (Biotechnology& Applied Microbiology): 6/162; Q1) → [highlighted in Nature Reviews Genetics 14, 822, 2013.](#)**
 16. **Trees-Juen Chuang*** and Feng-Chi Chen* (2014) DNA methylation is associated with an increased level of conservation at nondegenerate nucleotides in mammals. *Molecular Biology and Evolution*. 31(2), 387-396. **(Corresponding & first author; SCI impact factor: 14.797; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY): 5/298; Q1)**
 17. **Trees-Juen Chuang**, Shian-Zu Wu and Yao-Ting Huang* (2013) A Novel Framework for the Identification and Analysis of Duplicons between Human and Chimpanzee. *BioMed Research International (formerly titled Journal of Biomedicine and Biotechnology)*, 2013 (2013). **(First author; SCI impact factor: 2.197; Rank (BIOTECHNOLOGY & APPLIED MICROBIOLOGY): 94/162)**
 18. Yi-Ching Chen, Jen-Hao Cheng, Zing Tsung-Yeh Tsai, Huai-Kuang Tsai*

- and **Trees-Juen Chuang*** (2013) The Impact of *Trans*-Regulation on the Evolutionary Rates of Metazoan Proteins. *Nucleic Acids Research*, 13 (41), 6371-6380. **(Corresponding author; SCI impact factor: 11.147; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY): 14/298; Q1)**
19. **Trees-Juen Chuang***, Feng-Chi Chen*, Yen-Zho Chen (2012) Position-dependent correlations between the level of DNA methylation and the evolutionary rates of mammalian coding exons. *P Natl Acad Sci USA*, 109(39), 15841-15846. **(Corresponding & first author; SCI impact factor: 9.580; Rank (MULTIDISCIPLINARY SCIENCES): 7/69; Q1) → highlighted in A-IMBN (Asia-Pacific International Molecular Biology Network) Research**
 20. Jean-Christophe Gelly, Hsuan-Yu Lin, Alexandre G. de Brevern*, **Trees-Juen Chuang***, and Feng-Chi Chen* (2012) Selective Constraint on Human Pre-mRNA Splicing by Protein Structural Properties. *Genome Biology and Evolution*, 4(9): 842–851. **(Corresponding author; SCI impact factor: 3.726; Rank (GENETICS & HEREDITY - SCIE): 46/173; Q2)**
 21. Ming-Chih Wang, Feng-Chi Chen*, Yen-Zho Chen, Yao-Ting Huang and **Trees-Juen Chuang*** (2012) LDGIdb: a database of gene interactions inferred from long-range strong linkage disequilibrium between pairs of SNPs. *BMC Research Note* 2012, 5:212. **(Corresponding author)**
 22. Sean Chun-Chang Chen, **Trees-Juen Chuang**, Wen-Hsiung Li* (2011) The relationships among microRNA regulation, intrinsically disordered regions, and other indicators of protein evolutionary rate. *Molecular Biology and Evolution*, 28(9), 2513-20. **(Co-author; SCI impact factor: 14.797; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY - SCIE): 5/298; Q1)**
 23. Kong-Bung Choo, **Trees-Juen Chuang**, Wan-Yi Lin, Che-Ming Chang, Yao-Hui Tsai and Chiu-Jung Huang (2010) Evolutionary expansion of *SPOP* and associated *TD/POZ* gene family: Impact of evolutionary route on gene expression pattern. *Gene*, 460(1-2), 39-47. **(Co-author; SCI impact factor: 2.638; Rank (GENETICS & HEREDITY): 82/173)**
 24. Feng-Chi Chen, Chueng-Jong Chen, Wen-Hsiung Li, and **Trees-Juen Chuang*** (2010) Gene family size conservation is a good indicator of evolutionary rates. *Molecular Biology and Evolution*, 27(8), 1750-8. **(Corresponding author; SCI impact factor: 14.797; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY - SCIE): 5/298; Q1) → collected in 2010 significant publications of Academia Sinica.**

25. Fan-Kai Lin, Chia-Lin Pan, Jinn-Moon Yang, Trees-Juen Chuang* and Feng-Chi Chen* (2009) CAPIH: A Web interface for comparative analyses and visualization of host-HIV protein-protein interactions. *BMC Microbiology* 2009, **9**:164. **(Corresponding author; SCI impact factor: 3.287; Rank (MICROBIOLOGY): 49/133; Q2)**
26. Chun-Hsi Chen#, Trees-Juen Chuang#, Ben-Yang Liao, and Feng-Chi Chen (2009) Scanning for the signatures of positive selection for human-specific insertions and deletions. *Genome Biology and Evolution*. Vol. 2009:415. # Equal contribution. **(Co-first author; SCI impact factor: 3.726; Rank (GENETICS & HEREDITY - SCIE): 46/173; Q2)**
27. Feng-Chi Chen, Yen-Zho Chen, and Trees-Juen Chuang* (2009) CNVdb: a database of copy number variations across vertebrate genomes. *Bioinformatics* 25(11), 1419-1421. **(Corresponding author; SCI impact factor: 4.531; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 4/59; Q1)**
28. Yao-Ting Huang, Feng-Chi Chen*, Chiuan-Jung Chen, Hsin-Liang Chen and Trees-Juen Chuang* (2008). Identification and analysis of ancestral hominoid transcriptome inferred from cross-species transcript and processed pseudogene comparisons. *Genome Research* 18(7), 1163-1170. **(Corresponding author; SCI impact factor: 9.944; Rank (Biotechnology& Applied Microbiology): 6/162; Q1)**
29. Feng-Chi Chen and Trees-Juen Chuang* (March 2008). Nucleotide Sequence Divergence between Humans and Chimpanzees. In: ENCYCLOPEDIA OF LIFE SCIENCES. John Wiley & Sons, Ltd: Chichester <http://www.els.net/> [DOI: 10.1002/9780470015902.a0020751], Invited review article. **(Corresponding author)**
30. Feng-Chi Chen and Trees-Juen Chuang* (2007). Different alternative splicing patterns are subject to opposite selection pressure for protein reading frame preservation. *BMC Evolutionary Biology*, 7(1):179. **(Corresponding author; SCI impact factor: 3.045; Rank (GENETICS & HEREDITY): 71/173; Q2)**
31. Feng-Chi Chen, Shu-Miaw Chaw, Yun-Huei Tzeng, Sheng-Shun Wang, and Trees-Juen Chuang* (2007). Opposite Evolutionary Effects between Different Alternative Splicing Patterns. *Molecular Biology and Evolution*, 24(7), 1443-6. **(Corresponding author; SCI impact factor: 14.797; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY - SCIE): 5/298; Q1)**
32. Feng-Chi Chen, Chueng-Jong Chen, and Trees-Juen Chuang* (2007). INDELSCAN: a web server for comparative identification of

- species-specific and non-species-specific insertion/deletion events, *Nucleic Acids Research*, 35 (Web Server issue):W633-8. **(Corresponding author; SCI impact factor: 11.147; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY): 14/298; Q1)**
33. Feng-Chi Chen, Chueng-Jong Chen, Wen-Hsiung Li*, and **Trees-Juen Chuang*** (2007). Human-specific insertions and deletions inferred from mammalian genome sequences. *Genome Research*, 17(1), 16-22. **(Corresponding author; SCI impact factor: 9.944; Rank (Biotechnology& Applied Microbiology): 6/162; Q1)**
 34. Feng-Chi Chen, Sheng-Shun Wang, Shu-Miaw Chaw, Yao-Ting Huang, and **Trees-Juen Chuang*** (2007). Plant Gene and Alternatively Spliced Variant Annotator. A Plant Genome Annotation Pipeline for Rice Gene and Alternatively Spliced Variant Identification with Cross-Species Expressed Sequence Tag Conservation from Seven Plant Species. *Plant Physiology*, 143(3), 1086-1095. **(Corresponding author; SCI impact factor: 6.305; Rank (PLANT SCIENCES): 10/228; Q1)**
 35. Lin YC, Diccianni MB, Kim Y, Lin HH, Lee CH, Lin RJ, Joo SH, Li J, **Chuang TJ**, Yang AS, Kuo HH, Tsai MD, Yu AL (2007). Human p16^{INK4A}, a novel transcriptional variant of p16^{INK4A}, coexpresses with p16^{INK4A} in cancer cells and inhibits cell-cycle progression. *Oncogene*, 26(49):7017-27. **(Co-author; SCI impact factor: 6.634; Rank (GENETICS & HEREDITY): 15/173; Q1)**
 36. Yun-Huei Tzeng, Wen-Hsiung Li, **Trees-Juen Chuang*** (2007). Mathematical Properties of Some Measures of Evolutionary Distance. *Journal of Theoretical Biology*, 245(4), 790-792. **(Corresponding author; SCI impact factor: 1.875; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 25/59)**
 37. Feng-Chi Chen and **Trees-Juen Chuang*** (2006). The effects of multiple features of alternatively spliced exons on the *Ka/Ks* ratio test. *BMC Bioinformatics*, 7:259. **(Corresponding author; SCI impact factor: 2.511; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 9/59; Q1)**
 38. Feng-Chi Chen, Sheng-Shun Wang, Chuang-Jong Chen, Wen-Hsiung Li and **Trees-Juen Chuang*** (2006). Alternatively and Constitutively Spliced Exons are Subject to Different Evolutionary Forces. *Molecular Biology and Evolution*, 23(3), 675–682. **(Corresponding author; SCI impact factor: 14.797; Rank (BIOCHEMISTRY & MOLECULAR BIOLOGY - SCIE): 5/298; Q1) → collected in 65 significant publications of Academia Sinica, 2005~2006.**

39. Feng-Chi Chen, Chuang-Jong Chen, Jar-Yi Ho, and **Trees-Juen Chuang*** (2006). Identification and evolutionary analysis of novel exons and alternative splicing events using cross-species EST-to-genome comparisons in human, mouse and rat. *BMC Bioinformatics*, 7:136. **(Corresponding author; SCI impact factor: 2.511; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 9/59; Q1)**
40. Feng-Chi Chen, and **Trees-Juen Chuang*** (2005). ESTviewer: a web interface for visualizing mouse, rat, cattle, pig and chicken conserved ESTs in human genes and human alternatively spliced variants. *Bioinformatics* 21, 2510-2513. **(Corresponding author; SCI impact factor: 4.531; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 4/59; Q1)**
41. **Trees-Juen Chuang***, Feng-Chi Chen, and Meng-Yuan Chou (2004). A comparative method for identification of gene structures and alternatively spliced variants. *Bioinformatics* 20, 3064-3079. **(Corresponding & first author; SCI impact factor: 4.531; Rank (MATHEMATICAL & COMPUTATIONAL BIOLOGY): 4/59; Q1)** → collected in 30 significant publications of Academia Sinica, 2004~2005.

PART 2. Publications before joining GRC (before Oct. 2003)

(A) Bioinformatics or Computing Biology

1. **Trees-Juen Chuang**, Wen-Chang Lin, Hurng-Chun Lee, Chi-Wei Wang, Keh-Lin Hsiao, Zi-Hao Wang, Danny Shieh, Simon C. Lin, and Lan-Yang Ch'ang* (2003) "A Complexity Reduction Algorithm for Analysis and Annotation of Large Genomic Sequences," *Genome Research*, 13(2), 313-322. **(First author; SCI impact factor: 9.944; Rank (Biotechnology& Applied Microbiology): 6/162; Q1)**
2. Patent: **T.J. Chuang** and L.Y. Ch'ang (2003) "A Complexity Reduction Algorithm for Analysis and Annotation of Large Genomic Sequences" (Patent no: TW238854).

(B) Computer Image & Vision

3. **T.J. Chuang**, J.C. Lin, and W.H. Tsai, "A New Efficient Approach to Image Hiding by Digit Number Transformation," *Pattern Recognition and Image Analysis*, Vol. 10, No. 3, pp.309-314, **2000**.

4. **T.J. Chuang** and J.C. Lin, "On the Multiresolution Encryption of Still Image," *Pattern Recognition and Image Analysis*. Vol.9, No.3, pp. 431-436, **1999**.
5. **T.J. Chuang** and J.C. Lin, "A New Algorithm for Lossless Still Image Compression," *Pattern Recognition*, Vol. 31, No. 9, pp.1343-1352, **1998**. **(First author; SCI impact factor: 5.898; Rank (ENGINEERING, ELECTRICAL & ELECTRONIC): 25/265; Q1)**
6. **T.J. Chuang** and J.C. Lin, "A New Approach to Image Encryption," *Journal of Electronic Imaging*, Vol. 7, No. 2, pp. 350-356, **1998**. **(First author; SCI impact factor: 0.924; Rank (ENGINEERING, ELECTRICAL & ELECTRONIC): 220/265)**
7. **T.J. Chuang** and J.C. Lin, "Lossy Compression by Base Switching (BS)," *Pattern Recognition and Image Analysis*, Vol. 7, No. 4, pp. 423-430, **1997**.