HSUAN PU CHEN

4F.-1, No.128, Xinhu 2nd Rd., Neihu Dist.
Taipei City 114, Taiwan
(011886) 0976102358
albertkimforest@gmail.com

OBJECTIVE   A position where I can use my creativity and analytical skill to drive the value of new products in your lab.

EXPERIENCE

2011-Present   **Kimforest, Gene Biodesign Ltd. Co**   **Taipei, Taiwan**
Bioinformatics Researcher (Head of Bioinformatics Team)
- In charge of the demonstration and pre-sales and post-sale services for Golden Helix and DNAStar, both are bioinformatics software for analyzing GWAS, CNV and tertiary NGS data.
- Provide analytical support to an affiliate's micro array data analysis arm, Gene Biodesign, which is located at Mackay Memorial Hospital
- Conducting a cell-based high-throughput drug screening product, DiscoveRX
- Collaborating Bioinformatics projects with National Taiwan Medical University on breast cancer study and Taipei Veterans General Hospital on stem cell research

2010-2011   **Institute of Statistical Science Academia Sinica**   **Taipei, Taiwan**
Principal Investigator: Dr. Ker Chau Li, Ph.D
Postdoctoral Scholar
- Conducted a study to identify possible fusion genes in cancer tissue by using public exon array data.

2008-2010   **UNIVERSITY of CALIFORNIA, SAN FRANCISCO (UCSF)**   **San Francisco, CA**
Principal Investigator: Dr. Sergio E Baranzini, Ph.D
Postdoctoral Scholar
Project leader in a longitudinal research on Multiple Sclerosis. Responsible for generating both transcript- and exon-level expression profiles, providing an unprecedented level of resolution in the analysis of gene activity patterns in Multiple Sclerosis.

- Generated longitudinal genome-wide transcriptional profiles from peripheral blood cells in 500 MS patients and 100 well-matched controls. All profiles are generated using Affymetrix Exon 1.0 ST arrays, thus interrogating over 1 million exons genome-wide.
- Completed a GWAS study on gene expression level to identify expression quantitative trait loci (eQTL) that causes gene expression variation in Humans across two time points
- Conducted a GWAS study on exon level to find out the roles of SNP in alternative splicing for Multiple Sclerosis patients.
- Investigated the alternative splicing isoforms by high-throughput approach using exon arrays between cases and controls.
- Performed a network analysis for both in gene expression and exon expression level.

1997-1999   **TRI-SERVICE GENERAL MILITARY HOSPITAL**   **Taipei, Taiwan**
Physical Therapist Supervisor
- Managed Rehabilitation Department; supervised 4 staff physical therapists.
- Purchased equipments to increase capacity, which raised yearly average patient visit volume by 30%
- Recruited staff and conducted in-house training for staff physical therapists

EDUCATION

12/04-12/07   UNIVERSITY of CALIFORNIA, LOS ANGELES (UCLA)   Los Angeles, CA
Principal Investigator: Desmond Smith, MD. Ph.D
Ph.D, Biomedical Engineering
Worked for my Doctoral degree on the thesis entitled: "**Screening Reveals Conserved and On-Conserved Regulatory Elements Including an E3/E4 Allele Dependent *APOE* Coding Region Enhancer**".

- Performed a high-throughput approach to identify novel regulatory elements of a 157 kb BAC that contain seven genes
- Developed a high-throughput mapping method for human and mouse genome by combining transcript analysis (from radiation hybrid cell lines) using cDNA array technology and available data from classical radiation hybrid mapping
- Completed basic bioinformatics projects by using C++ programming language, including global sequence alignment, multiple sequence alignment, and hierarchical clustering analysis

Bioinformatics Courses Taken or Audited
- Statistics:
  - Introduction to probability
  - Applied statistics and regression analysis
  - Applied Bayesian statistical analysis
  - Applied multivariate quantitative methods
- Programming:
  - Introduction to c++
  - c++ and data structure
- Bioinformatics:
  - Microarray data analysis (dChip, SAM, Bioconductor, WGCNA networking analysis)
  - eQTL analysis and GWAS study
  - Bioinformatics algorithm

09/01-12/04   UNIVERSITY of CALIFORNIA, LOS ANGELES (UCLA)   Los Angeles, CA
MS, Biomedical Engineering
Worked for my Master's degree on the thesis entitled: "**High-Throughput Deletion Mapping of Mammalian Promoters**".

- Conducted a promoter deletion analysis to identify the regulatory elements regions of EWS gene.
- Investigated hundreds of genes regulatory regions and their functions by using a new in-vivo technique named cell array.

09/93-06/97   NATIONAL TAIWAN UNIVERSITY   Taipei, Taiwan
BS, Physical Therapy
- GPA: 3.3/4.0

LABORATORY SKILLS
- Cell culture techniques, PCR, Real time quantitative PCR, Cloning and sub-cloning.
- Design and print of cDNA/Oligo array chips, and their analysis using RNA from mouse/human tissue and cell RNA.
- Isolation and purification of Genomic/Plasmid DNA, RNA, Lymphocytes and proteins
- Protein and Enzymatic Assay, TLC, Gel Filtration, Ion-Exchange & Affinity Chromatography

BIOINFORMATICS SKILLS
- GWAS: PLINK (3rd party) , MatrixEQTL (R), haplo.stats (R), Golden Helix (Commercial)

- Gene expression and CNV: Bioconductor (R), Limma (R), WGCNA (R), PluriTest (R), Brb-arraytool (3rd party), Netrork-based classification (3rd party), JMP (SAS)

- Pathway analysis: GOstats (R), Cytoscape (ClueGO, Reactcome FI, 3rd party), PathVisio (3rd party), GSEA (3rd party), IPA (Commercial)

- Little experience in Perl, AMOS and WinBUGS

PUBLICATION

- Screening reveals conserved and non-conserved regulatory elements including an E3/E4 allele dependent APOE coding region enhancer. **Genomics** Volume 92, Issue 5, November 2008, Pages 292-300
- Association of SELE genotypes/haplotypes with sE-selectin levels in Taiwanese individuals: interactive effect of MMP9 level. BMC Med Genet. 2012 Nov 29;13:115. doi: 10.1186/1471-2350-13-115.
- Two other additional papers are on the process

OTHER DATA

- Fluency in Mandarin Chinese.
- Elected as the President of Taiwanese Association in UCSF.