

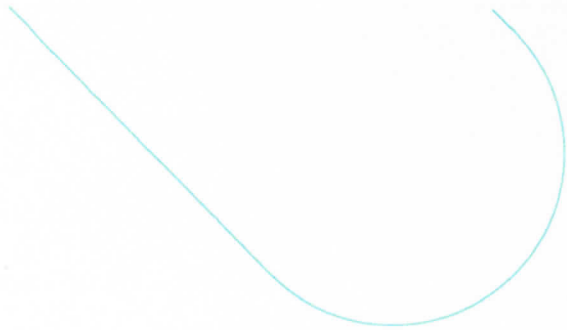


ChunLab Company Introduction

www.chunlab.com

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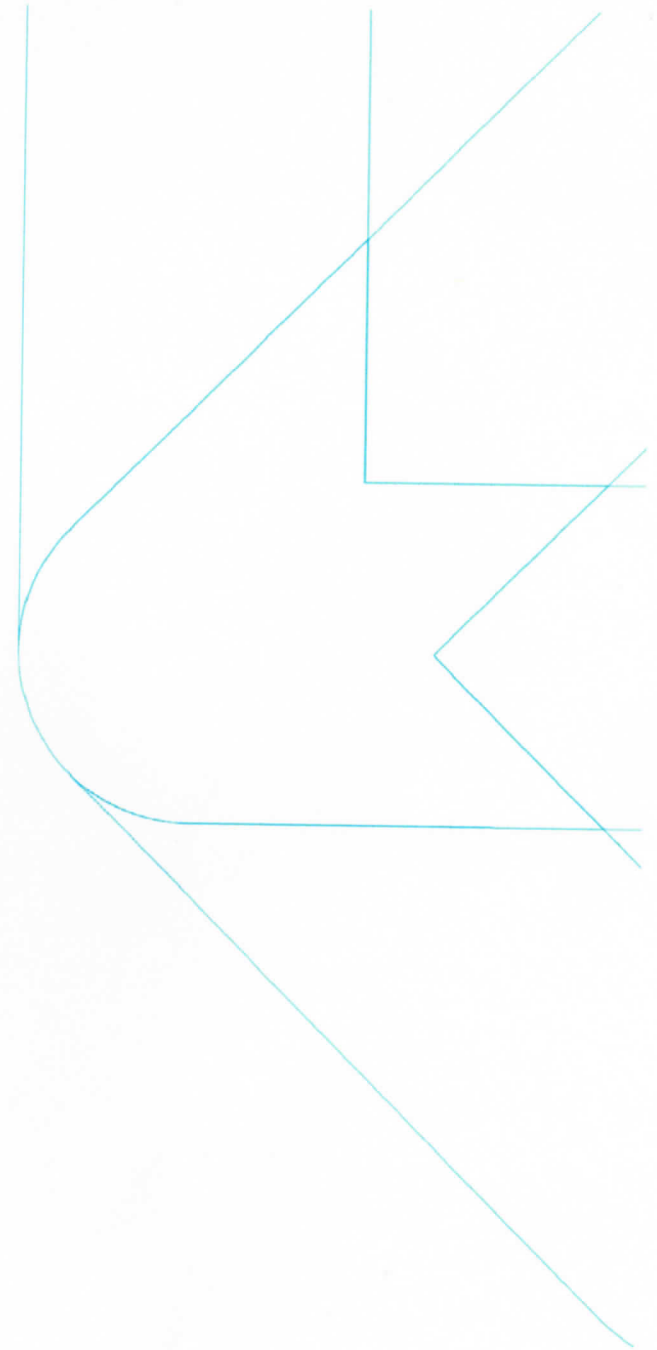
CHUNLAB
Bioinformatics Made Easy



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About ChunLab



About ChunLab

- ChunLab is a next-generation sequencing (NGS) and bioinformatics service provider offering an end to end solution from sample to discovery
- Established in Dec. 2009 by Dr. Jongsik Chun of Seoul National University

About Dr. Jongsik Chun

- Full tenured professor, School of Biological Sciences, Seoul National University (SNU) (2000~Present)
 - Trustee, Bergey's Manual Trust
 - Associate Editor, IJSEM (2002~2014)
 - Editorial Board , Antonie van Leeuwenhoek (1999~present); Microb. Environ. (2005~Present)
 - Founding Director, Bioinformatics Institute, Seoul National University (2010)
- Headquarters in Seoul, Korea with a satellite office in Rockville, MD

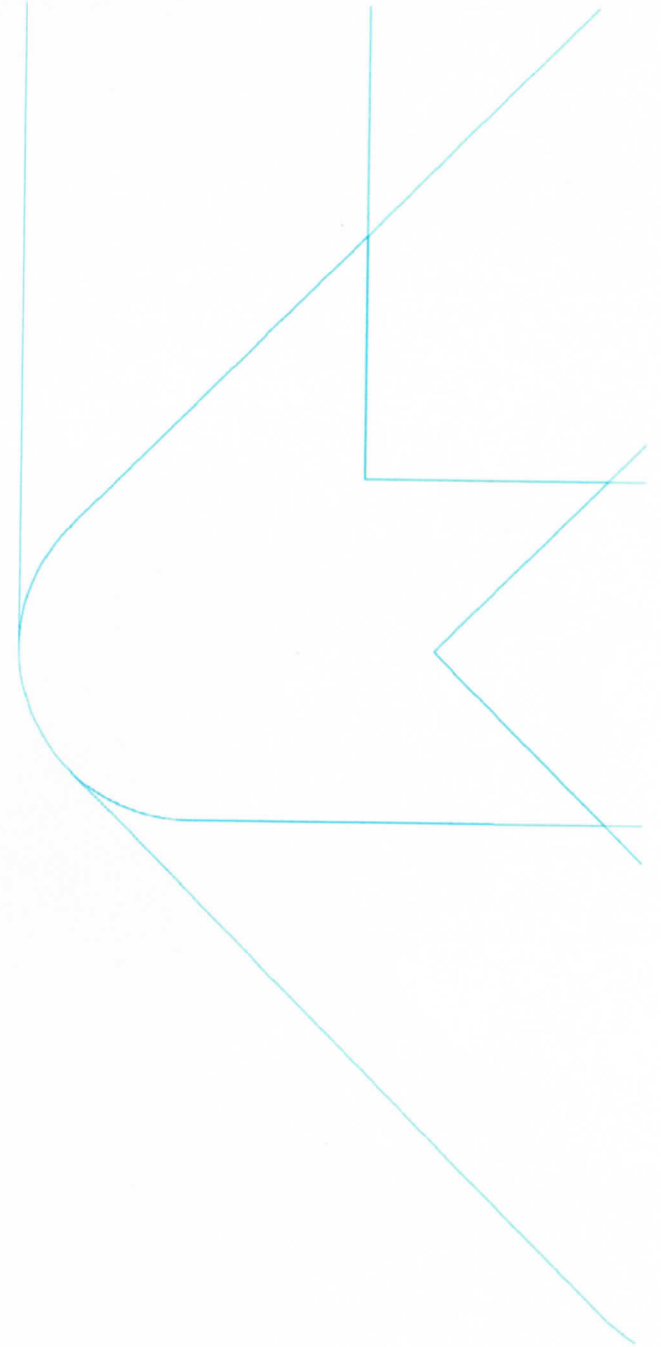
Our Mission

ChunLab's mission is to simplify bioinformatics to enable clients to easily perform high-end analytics of their NGS data

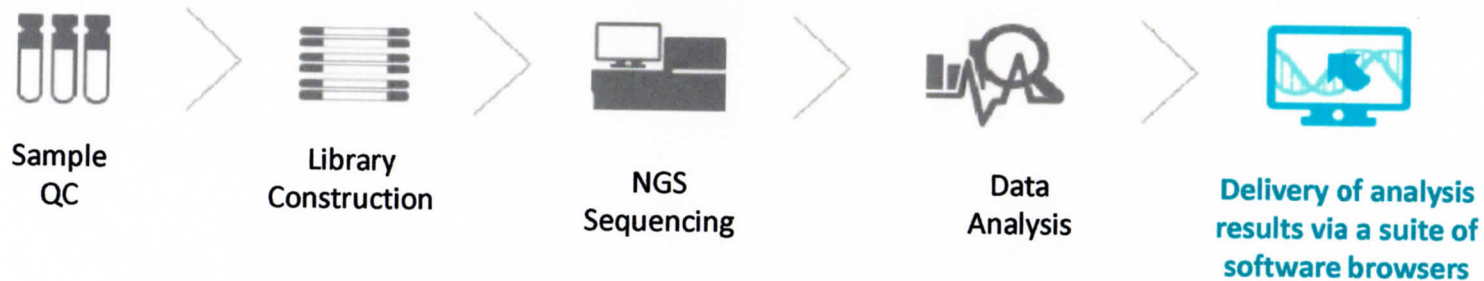
To achieve this mission, we have designed optimized bioinformatics pipelines for various research disciplines (metagenomics, genomics and transcriptomics) using carefully chosen, tested algorithms and biostatistical techniques.

Furthermore, we have designed a suite of point and click software tools that enable researchers to easily perform large-scale sophisticated visualizations, secondary analysis and comparative analysis.

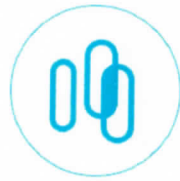
Why ChunLab?



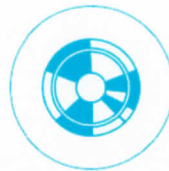
One-Stop Solution from Sample to Discovery



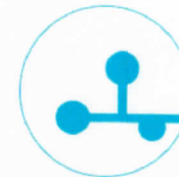
Suite of software tools designed for specific research disciplines



CLcommunity™
for Microbial Community Analysis



CLgenomics™
for Whole Genome Analysis



CLRNASeq™
for Transcriptomics Analysis

- ✓ Intuitive point & click user interfaces with advanced visualization and analytical tools
- ✓ Standalone Windows and Mac based applications
- ✓ No expertise in Linux and programming languages required
- ✓ Data results provided in sophisticated publication-ready visualizations
- ✓ Exportation of data into Excel, text or FASTA formats for further downstream analyses

Why ChunLab?

List of highly curated proprietary reference databases

EzTaxon

- Database of 16S rRNA gene sequences of species type strains for valid and invalid names
- 63,000+ 16S rRNA gene sequences for Bacteria & Archaea
- 10,000+ users world wide
- >2,600 citations (Jan 2015)

EzGenome

- Database of manually curated prokaryote genomes
- > 25,000 prokaryote genomes

EzFungi

- Database of highly curated fungal strains using the ITS region
- >17,000 fungi species

EzRNASeq

- Database of a wide selection of RNA Seq data (based on SRA) formatted to be viewed and compared using ChunLab's CLRNAseq software
- Includes human, mouse, *Arabidopsis*, *C. elegans*, *Drosophila* and other model organisms

EzEcology

- Database of microbial communities, includes data from the Human Microbiome Project (expected to be launched 2Q of 2015)

For more information visit <http://www.ezbiocloud.net>

Why ChunLab?

Composed of Ph.D. and master level bio scientists, bioinformaticians and software engineers

To provide...

- Consultation on the best platform(s) and study design for a success research project
- NGS and bioinformatics training (through workshops and webinars)



Why ChunLab?

Equipped with State-of-the-Art Facilities and Platforms



Illumina HiSeq 2500



Illumina MiSeq



Roche 454 Junior



Ion Torrent PGM



Bionano Irys System



Nanostring nCounter



Roche 454 GS FLX+

Why ChunLab?

Over 350 government and research agencies, medical centers, companies and universities using ChunLab's services worldwide



What Our Clients Are Saying

“It has been a pleasure working with ChunLab. At every step of the way, ChunLab members assisted with shipping/customs, sample preparation, and data generation. Their knowledge of microbial systems, in particular, sets this group apart from other genomic facilities. The resulting publication would not have been possible without the extra input and analysis of results by ChunLab team members. ”

Dr. Shana K. Goffredi

Asst. Professor | Occidental College (USA)

“We are very happy with the genome sequencing and analysis results ChunLab provided us with and we would certainly recommend ChunLab to our colleagues. I do not have any genome-sequencing projects planned for next year, but ChunLab will definitely be my first choice when I next want a bacterial genome sequenced. ”

Dr. Paul Meyers

Professor | University of Cape Town (South Africa)

“Yes I was able to download all the software and use it to analyze my data. It is very user-friendly. Overall we are very satisfied with your service and quality of the data. ”

Dr. Jing Wang

Researcher | Instit. of Molecular and Cell Biology (Singapore)