Company Brochure · 2023

Read Data, Lead Big

Bio Big Data Leader, Insilicogen

INSILICOGEN

www.insilicogen.com

Contents

Upgraded Bioinformatics service with AI

Insilicogen is a company, specializes in Bioinformatics. Our company provides a platform to share and execute various biological data analysis effectively.

Insilicogen is preparing for the future and is motivated by our new slogan “make the data come alive.” Insilicogen will provide the standards of big data and ensure that various data worldwide is evolved ceaselessly by being deeply involved with data collection, data storage, and data analysis.

We, 人Co, will actively learn and adopt AI, state-of-the-art technology, and quickly provide new values to our customers. Our overarching goal is to design the future of our clients with one-step-ahead suggestions.

Bio Big Data Leader

Insilicogen has continuously constructed the bio big data for the past 20 years.
We have and are constructing Omics big data system for government administrations such as the Ministry of Science and ICT, the Ministry of Health and Welfare, the Ministry of Agriculture, Food and Rural Affairs, Korea Disease Control and Prevention Agency and the Rural Development Administration.
BIGBIGHUG, BLIMS, CODA, CRIS, CowScan, KAHIS, MAGIC, MBDC, MEE, NABIC, ODFM, OREO, RRM are the representatives.

Constructing a database is an opportunity to learn where the raw data comes from, flows into and what the hidden implications are.
Our country and many corporations have produced bio-data with massive investments for a very long period of time and are still producing them. However, there will be no meaning in creating larger data unless data is standardized and managed systematically.

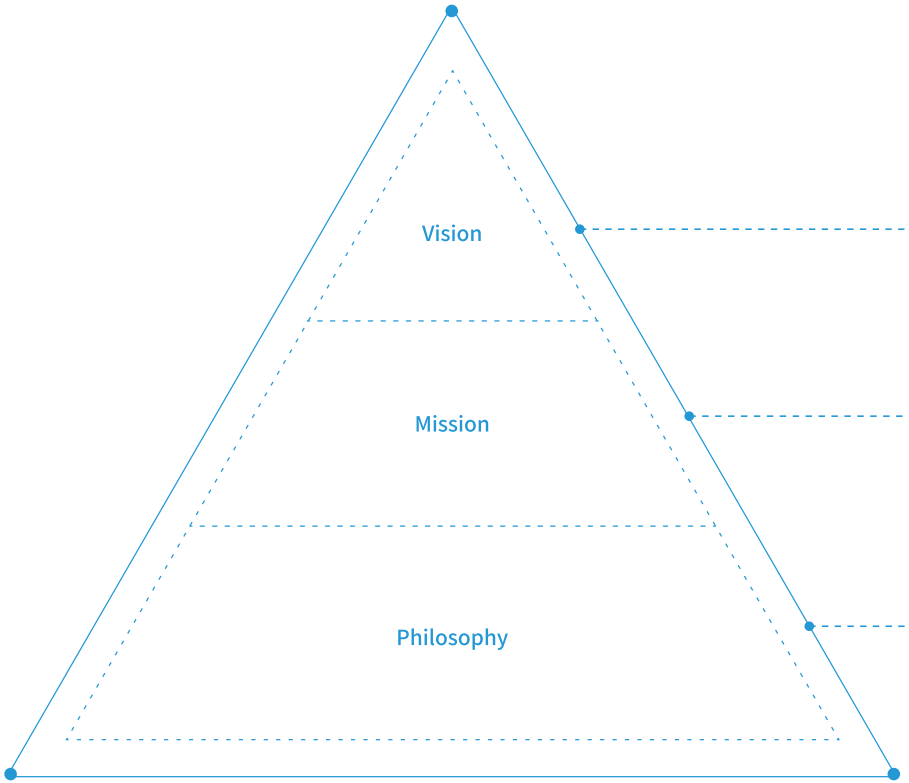
We 人Co will go one step deeper into this trend. Insilicogen will be the headstone of big data and will provide the most productive and effective process with the know-how that has been acquired through the development of data production, archiving, modeling and analysis.

As always, insillicogen will always put people first and leap forward to make the technical advancement.
We greatly appreciate your interest and support.

CEO of Insilicogen, Namwoo Choi.

Value Pyramid

人Co is an Insilicogen's core brand value. It represents our aim to create our own corporate culture with the help of people, computer technology, and through considerate communication.

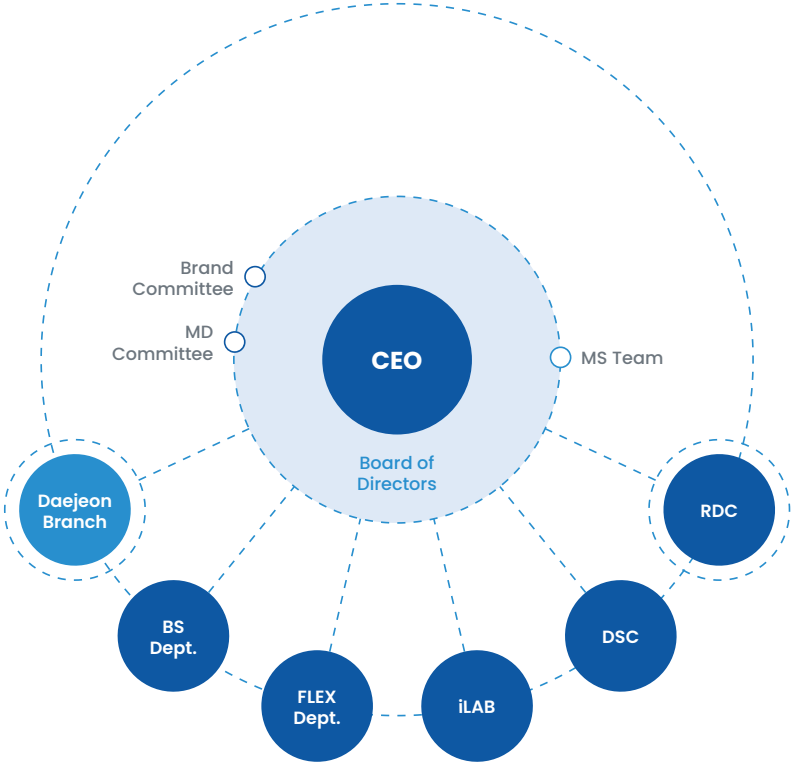


Professional Bioinformatics company

Creation of new value through sharing biological information and communication.

A dream you dream alone is only a dream.
A dream you dream together becomes a reality.

Horizontal communication and creative culture guarantee diversity



iLAB

insilico Lab

iLAB, your customized bioinformatics partner, provides everything you need in the lab using our techniques and know-how obtained from years of experience and consulting various solutions.

RDC

R&D Center

(Excellent research institute selected from the Military Manpower Administration)

Beyond the combination of coded biological data and algorithms, RDC is providing the consultation for the Bioinformatics analysis of NGS-related data for animals, plants, and microbes.

BS

Bioinformatics System Department

BS leads knowledge informatization by blowing life into information and putting it into the system.

FLEX

FLEX Department

FLEX will offer practical customer values utilizing a successful digital business model by integrating planning, marketing, UX/UI, Front-end and Back-end.

DSC

Data Science Center

DSC provides practical values for the basic science, medical science, plant/animal breeding and microbiome. DSC provides integrated data science services from professional consulting to data analysis and platform development.

We will continue to transform for our business growth

2004

10 Insilicogen's distributed business established

2005

08 Insilicogen, Inc. Bioinformatics Consulting Firm established

2006

02 Joint research on the development of alternative materials for malachite green derived from natural materials

06 Win a contract on constructing 'Animal Genome Information System' for the National Livestock Research Institute (Formerly Livestock Research Institute)

2007

06 Certified R&D center, Insilicogen, Inc. as a research institute

07 Win a contract on constructing 'Breeding Information Linkage Utilization System' for the National Institute of Agricultural Science and Technology

2008

04 Selected as the supervision institution to participate on National Research project organized from Ministry of Environment (Construction of environmentally harmful substance-genome knowledge database and development of technology-based on semantics, 2008 ~ 2010)

05 Moved the office to Suwon High-Tech Venture Valley

06 Signed MOU on joint research projects and technical cooperation with Biomax Informatics AG

07 Win a contract on the development of DB analysis tool for early detection pathogen, posted from KCDC

09 Build an Ancient Genetic Resource Database for National Institute of Cultural Heritage

2009

02 Registered LabKM® trademark

05 Developed a genetic information system to identify fallen soldiers from the Korean War(Ministry of National Defense Inspection Headquarters)

10 Insilicogen, Inc. Daejeon branch established

2010

01 Completed analysis of the Korean cow's entire genomic sequence analysis on its single mutation with Yeungnam University, Department of Animal Science, Chungbuk National University, CLC bio A / S, Solgent

03 Signed Plant Genomics MOU with three organization (Insilicogen, Inc., CLC bio A/S, Seoul National Univ.)

05 Participated in establishment of LIMS(Laboratory Information Management System) for Livestock Products Quality Assurance Service

09 Win a contract on Bioinformatics analysis of cabbage SNP marker from National Horticultural Research Institute

12 Registered Glter® trademark

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2011

- 01 Ontle™(Web-based Ontology Editing), international patent registered
- 01 Signed MOU on cultivating prospective bioinformaticians(School of Life Systems, Soongsil Univ.)
- 06 Selected as a Management Innovation Certification Company
- 12 Selected as a technology innovation business by Ministry of Knowledge Economy(2011~2016)

2012

- 01 Patent for Ontle™(Web-based Ontology Editing) registered
- 11 Signed academic exchange agreement with 6 Universities(Yeungnam, Hanyang, Chungbuk, Chonbuk, Sungkyunkwan, Sangmyung)

2013

- 07 Patent for KinMatch™ (DNA search method) registered
- 10 Selected as a special research center from military manpower administration for those who need alternative military service
- 11 Executed ICT fusion contents utilization system and information standardization project based on traditional food history of KFRI and scientific evidences (Bio Big Data Business)

2014

- 01 Joint registered pepper gene sequencing analysis on 'Nature Genetics'(The Next Generation Bio-Green 21, organized by the RDA)
- 03 Registered as a research and development service
- 08 Selected as a prospective public data providing company
- 12 Moved to Heungdeok IT Valley

2015

- 01 Certified as a small-giant company by Ministry of Employment and labor
- 09 Incorporated Insilicogen's Daejeon branch
- 10 Organized Hanwoo Genome Symposium (sponsored by the Ministry of Agriculture, Forestry and Fisheries Technology Planning and Evaluation, Gyeongsangbuk-do)
- 11 Increased capital to 200 million won
- 12 Opened 人CoFLEX

2016

- 02 Selected as an excellent management company designated by the Military Manpower Administration (Awarded from Small and Medium Business Administration in Gyeonggi province)
- 07 Registered a domestic patent on developing traitchemical network-based model for providing personalized trait-specific dietary information

2017

- 03 Selected as a sincere taxpayer in the year of 2017
- 08 Selected as the best-service company by Korean Credit Guarantee Fund
- 11 Registered trademark iF(insilico Food)

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2018

- 01 Selected as a youth-friendly small company in the year 2018(Ministry of Employment and Labor)
- 03 Signed MOU on building a big-data based, customized service platform(Kwangdong Pharmaceutical Co.,Ltd.)
- 12 Received a certified award from Ministry of Oceans and Fisheries(Business on building National Fisheries Biointegration System)

2019

- 01 Signed MOU on building the ecosystem of healthcare healing convergence business((Re)GSIPA)
- 04 Proceeded a workshop on animal genetic big data platform based on IncoGWAS at the RDA & NIAS (Opened Event)
- 11 Registered domestic patent for a target gene screening method and device for multi-omics data and survival analysis
- 12 Received a certified award from Ministry of Oceans and Fisheries

2020

- 01 Selected as a youth-friendly small company(Excellence in work life balance)
- 03 Registered a domestic patent for human body type and metabolic susceptibility SNP marker and diagnostic information provision method
- 12 Received a minister award (Ministry of Agriculture, Food and Rural Affairs)

2021

- 01 Selected as a youth-friendly company (Above-average Salaries in the industry/ Excellence in Work-life Balance)
- 06 Selected as an excellent corporation R&D Center in 2021 (Value creation through outstanding R&D competencies)
- 06 Selected as an outstanding small and medium sized company in 2021 (Contributing to the growth of the industry)

2022

- 01 Selected as a youth-friendly company (Above-average Salaries in the industry)
- 04 Signed a contract on digital breeding technology development business with Korea Institute of Planning and Evaluation for Technology in Food (Ministry of Agriculture, Food and Rural Affairs)

2023

- 01 Selected as a youth-friendly company (Above-average Salaries in the industry)

Beyond collaboration, we build partnership for mutual growth!

By building a real-time collaborative work system with global Bioinformatics companies, we enhance the product development and its service.

Data Production

DNA Link
LabGenomics
Macrogen
BioCore
Seoul Clinical Laboratories
Celemics
Seasun Biomaterials
CJ Bioscience
Ajou University Medical Center
Weedahm Oriental Hospital
Bioto
SFC

Database & Hardware

BethesdaSoft
Mutecsoft
Daewon CTS
ThinkTek
Zinion
Misoinfo
Naver
Dell Korea
Oracle Korea
Intel Korea
IBM Korea
Lenovo Korea
Amazon Korea

Data Analysis

Biobase(QIAGEN)
BioBam Bioinformatics S.L.
Biomax Informatics AG
CLC bio(QIAGEN)
Gene Codes Corporation
geneXplain GmbH
Ingenuity(QIAGEN)
OmicSoft Corporation(QIAGEN)
Petagene
ThermoFisher Scientific Korea
Agilent Technologies Korea

Sales & Marketing

Qiagen Korea
ThermoFisher Scientific Korea
HanDok
Bioplus
Ventech Science
Dawinbio
Pigenomics
Eloombio
Hanall
Bion-tech

Education

Gachon Univ.
Kangwon National Univ.
Konkuk Univ.
Kyung Hee Univ.
Sangmyung Univ.
Seoul Women's Univ.
Sungkyunkwan Univ.
Sejong Univ.
Sookmyung Women's Univ.
Soonchunhyang Univ.
Soongsil Univ.
Ajou Univ.
Yeungnam Univ.
Chung-Ang Univ.
Chonnam National Univ.
Jeonbuk National Univ.
Chungnam National Univ.
Chungbuk Univ.
Hanyang Univ.

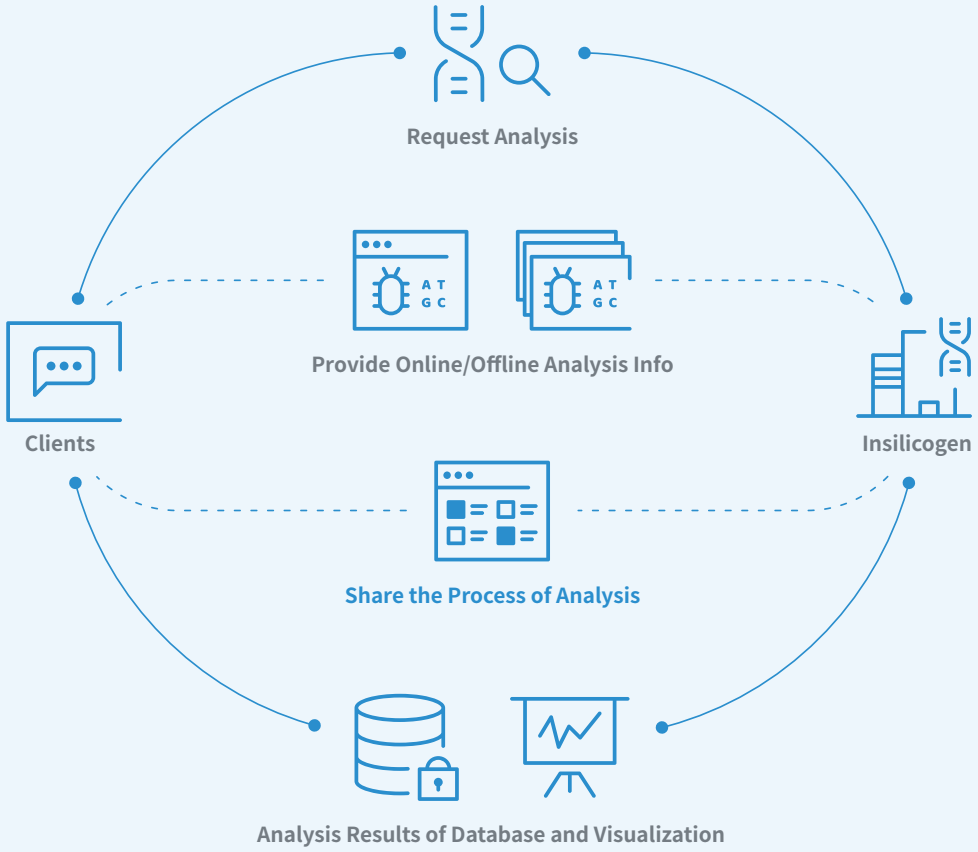
Together with the highly-skilled foreign and domestic professionals, provide fast, reliable, and personalized Bioinformatics services

Insilicogen is a professional Bioinformatics company.
We suggest methodologies to satisfy clients' needs and purpose, and communicate based on the results. Next-Generation Sequencing(NGS) becomes a universally used research method in all fields, including Genomics, Transcriptome, and Variant analysis.

Insilicogen provides customized service with 60 Bioinformatics professionals and Bioinformatics analysis pipeline and knowledge developed by foreign partners for years. Experience all-in-one service that allows from production to analysis of data difficult to interpret and specialize in the new studies.

Analysis of 500TB raw data in decoding 30 genomes

Korean beef, abalone, flatfish, rockfish, red pepper, sweet potato, cucumber, red seabream, mushroom, etc.



Human

- Variant analysis (WES, Targeted)
  CLC Genomics Workbench
  QIAGEN Clinical Insight Interpret(QCII)
- Gene expression & network analysis (RNA-seq)
  CLC Genomics Workbench Premium
  Ingenuity Pathway Analysis(IPA)
  OmicSoft Land Explorer

Animal·Plants

- Functional variant analysis
  CLC Genomics Workbench
- Gene expression profile (RNA-seq)
  CLC Genomics Workbench
  OmicsBox Transcriptomics Module

Microbe

- Gene structure and function annotation
  OmicsBox Genomics Module
  OmicsBox Functional Analysis Module
- Metagenome analysis
  CLC Microbial Genomics Module
  OmicsBox Metagenomics Module

Transcriptome

- Gene Expression profiling
- DEG/Pattern analysis
- GSEA analysis
- Pathway analysis
- Association study between promoters and transcripts
- WGCNA

Genome

- Genome size estimation
- De novo genome assembly
- Repeat elements analysis
- Structure gene prediction (Ab initio gene + Evidenced gene)
- Protein function annotation
- Long non-coding RNA analysis
- Promoter prediction
- Linkage map construction using GBS data

Variation

- Potential SNPs detection
- Potential SSRs analysis
- Lineage marker development
- Genetic marker development for breeding
- Hereditary/disease associated SNP marker
- Population structure analysis
- Selective sweep analysis
- Genomic selection analysis
- Effective population size analysis
- GWAS analysis
- Marker development based on ML

Comparative Genomics

- Ortholog analysis
- Phylogeny analysis
- Gene gain & loss analysis
- Gene duplication analysis
- Synteny analysis
- Pangenome analysis

Epigenome

- Epigenome analysis based on array/sequencing
- Methylation/histone mark/miRNA analysis
- DMR and pattern analysis
- GSEA and pathway analysis
- Comprehensive analysis of expression & regulation

Transcriptome

01 Initial response on protein medicine in human PBMC
02 Transcriptome profiling for human sepsis
03 Human brain tumor & senescence transcriptional association study
04 Transcriptome and Pathway analysis on the 'Korean beef'
05 Genetically modified mouse(GEM) RNA-sequencing
06 Discovery marker from *Equus ferus caballus* Transcriptome analysis
07 Comparative transcriptomics between two *Haliotis discus* subspecies
08 *De novo* transcriptome assembly of *Frankliniella occidentalis*
09 piRNA/miRNA/small RNA Expression profile of Chicken
10 Establishment of the EST information of Korean domestic canine
11 Transcriptome analysis and discovery of novel AMP on *Scolopendra subspinipes*
12 Discovery novel AMP and transcriptome analysis on the cockroach
13 *De novo* transcriptome and DEG/pathway analysis on *Valeriana fauriei*
14 Transcriptome profiling for marine fish with bacterial infection
15 *De novo* transcriptome and functional DEGs/pathway analysis on the grass
16 Leaf color gene expression profile on the rice
17 Gene expression profile of the radiation effect on *Arabidopsis thaliana*
18 *Panax ginseng* ESTs analysis
19 *De novo* transcriptome assembly and DEG analysis on the *Bostrychia*
20 Gene expression profile of *Pleurotus ostreatus* by developmental stage
21 Gene expression difference between asexsual and sexual reproduction of the *Fusarium* sp

Variation

01 Discovery of the genetic factor and mechanism for Papaver petal color
02 Comparative genomics for HIV
03 Identification of prediction markers for *Platycodon grandiflorus*
04 Discovery of early diagnostic markers of degenerative disease of a house dog
05 Korean breast cancer WES analysis
06 Discovery of breed-classification markers of Chestnut
07 *Haliotis discus hannai*(abalone) population study
08 *Undaria pinnatifida* population study
09 Discovery of Functional Gene and variant on 'Korean beef'
10 Variant analysis among Traditional chicken strains

11 *Coturnix japonica* variant analysis among subspecies
12 *Caenorhabditis elegans* comparative genome analysis using variants
13 Methylation/mRNA/miRNA chip analysis on the breast and stomach cancer
14 Variant analysis on Rice strains and novel gene discovery
15 Cabbage SNP marker selection
16 Variant analysis among Chili pepper strains
17 Discovery of the strain identification marker of Lettuce
18 Discovery of the origin identification marker of milk vetch root
19 Discovery of the species identification marker of *Brucella*

Genome

01 Senna tora genome analysis
02 8 fishes genome project (*Epinephelus akaara, Thamnaconus modestus, Misgurnus mizolepis, Anguilla japonica, Hypomesus nipponensis,Theragra Chalcogramma, Platichthys stellatus,* and Amphiprioninae)
03 Powdery mildew mtDNA analysis
04 Development of liquid biopsy NGS pipelines and clinical reporting system
05 Seawater/Freshwater *Bivalvia* genome project
06 *Haliotis discus hannai* genome analysis
07 *Trombiculidae,* factor of Scrub typhus, genome analysis
08 *Coturnix japonica* genome analysis
09 Minke whale genome analysis
10 Analysis of the genomic sequence of Chili pepper, Cabbage genome analysis
11 *Gracilariopsis chorda*(red algae) genome analysis, *Gelidium vagum*(red algae) genome analysis, *Undaria pinnatifida* genome analysis
12 *Xylaria*(fungi) genome analysis
13 *Cochliobolus miyabeanus*(Brown spot disease) genome analysis
14 *Phellinus linteus*(Fungi) genome analysis
15 Genome analysis for Hansenula polymorpha
16 Comparative genomics among *Fusarium* subspecies
17 *Oplegnathus fasciatus, Sebastes schlegelii, Pagrus major and Chelon haematocheilus* genome analysis
18 *Scolopendra subspinipes* genome analysis

Comparative genomics

01 Genome-enabled discovery of anthraquinone biosynthesis in *Senna tora*
02 Expansion of alginate, ferredoxin, and transporter related gene families led to the evolution of brown algae in the Stramenopiles.
03 Chromosome-Scale Genome Assemblies of Two Korean Cucumber Inbred Lines.
04 Pangenome analysis with Enterococcus

Epigenome

01 Epigenetic response for heat stress in *Haliotis discus hannai*
02 The multi-omics analysis on 'Korean beef' (RNA/MBD-seq)
03 The multi-omics analysis to discover a genetic effect of the Chinese medicine (RNA/Epic850k)
04 Cancer Stem Cell(CSC) Histone CHIP-seq analysis
05 Mouse WGBS analysis

Our education programs drive the growth of Bioinformatics

For the latest Bioinformatics education demanded from a domestic research institute, we provide onsite human resource training and the best bioinformatic solution to develop their skills required for biological research and development.

Insilicogen has experts in various fields, such as data processing, genomics & transcriptomics analysis, and programming. With the help of experts, we come up with a suitable curriculum for our target education group and have the best educational results.

50 institutions, Training 10,000 talented individuals

人CoSEMINAR

- Basic educational program for Bioinformatics
- Education on utilizing Bioinformatics solution and its theory

人CoWORKSHOP

- Personalized education for enhancement of Bioinformatic analysis
- Provide example centered education for the work

New-Generation BI Educational Workshop

- Collaborate with KOBIC
- Proceed an education on overall Bioinformatics

人CoACADEMY

- Online education center
- Provide various educational contents using Bioinformatics solutions and support Bioinformatics analysis

人CoINTERNSHIP

- Program for educating prospective bioinformaticians
- Provide opportunities to understand a basic concept of research development and life in the company via practices

In the process of transforming data into knowledge, our AI will assist you

In Bioinformatics, Artificial Intelligence plays a significant role.
Through machine-learning, we discover unknown matters.
Recently, persistent technological advancements of big data and deep-learning elevate the possibility.

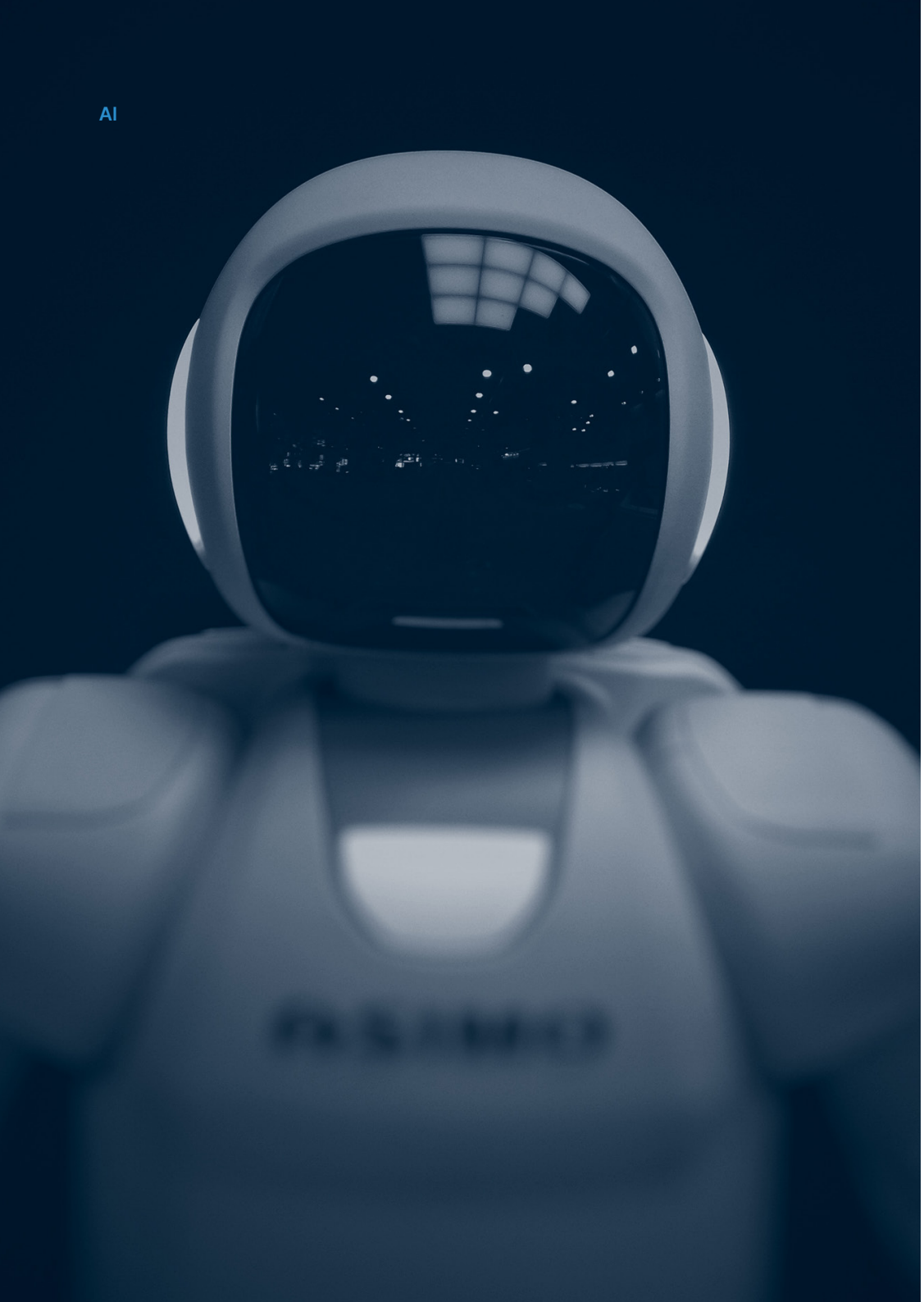
AI technology unveils and discovers meanings and values of complicated data not only from multi-omics but also from documents, videos, and networks.

Insilicogen's AI technology handles character data, sequential data, video imaging, and unstructured big data to discover hidden knowledge and implements techniques such as structuring, interconnecting, machine-learning, feature selection, and extraction to support integrated understanding.

Multiple big data analysis, machine learning task execution

Beef quality estimation by image analysis, selection of genetic markers for agricultural, forestry and fishery economic traits, analysis of pottery microelements

AI



Semantic Modeling

- Through semantic modeling, we integrate the clients' complex data and open sources for continuous data accumulation and creation, and find insight.

Machine Learning

- EDA (Exploratory data analysis)
- Analysis of data structure and reduction of dimension
- Data refinement, transformation and preprocessing
- Feature selection and extraction
- An optimized machine-learning model Development and assessment

Deep Learning

- Deep Learning
- Extract pattern map using DNN(Deep Neural Network), create a deep learning model by applying the architecture
- Classification, detection, segmentation, and model development for biological and medical image
- Complex network construction by NLP (Natural language processing) based literature data analysis

Tailored Knowledge

- Visualize web-based analysis results
- Provide data result of real-time dynamic programming, which is available online
- Web application and mobile app development
- Development of artificial intelligence and analysis algorithms at mobile edge

Research Projects

[Korea Disease Control and Prevention Agency] Building a large-scale computing-based AI pipeline and visualization
[Rowan] Establishment of a personalized content-based recommendation system for dementia
[National Institute of Fisheries Science] Establishment of flatfish growth prediction model based on machine learning
[Korea Institute for Animal Products Quality Evaluation] Establishment of a mechanized quality evaluation system for Korean beef based on artificial intelligence
[D.iF] Food object detection and classification by deep learning
[National Research Institute of Cultural Heritage] Establishment of machine learning model to predict termite damage of wooden cultural heritage
[Korea Institute for Animal Products Quality Evaluation] Beef quality estimation by image analysis (Deep Learning) and machine learning
[National Institute of Animal Science] Maker selection for degenerative disease by machine learning
[National Institute of Fisheries Science] Development of machine learning model for prediction of high temperature tolerance for abalone
[Ministry of Environment] Construction of environmentally hazardous material-genomics knowledge-based and Development of semantics-based technology
[Ministry of Environment] Excavation of indicators for heavy metal toxicology using toxicogenomics
[Food Industry Technology Support Center] Coordination analysis among health function, culture, excellence geographic location of Korean food and Korean food ingredient
[Korea Food Research Institute] Traditional food semantics database construction and analysis program
[Korea Food Research Institute] Construction of semantics database and korean food specialized ontology
[Pusan National University] Construction of anti-aging molecular network of aging Database
[Korea Food Research Institute] Development of InsilicoFood pilot system through the integrated analysis of food information
[Kwang Dong] Development of iF DB based dry complex system DB and h-pilot system

Patent and Program Registration

[Patent Registration 10-2021-0168283] System for risk prediction of osteoporosis
[Patent Registration 10-2118103] Method for measuring the fineness of marbling using ribeye image of Korean beef
[Patent Registration 10-2067076] Biomarker composition for prediction or diagnosis of canine patellar lunation
[Patent Registration 10-2018-0156903] Biomarker composition for prediction or diagnosis of canine patellar lunation
[Patent Application 10-2019-0023081] Biomarker composition for diagnosing lung cancer comprising peptide nucleic acid
[Patent Application 10-2019-0025109] High sensitive genetic variation detection and reporting system based on barcode sequence
[Patent Application 10-2019-0155754] Biomarker composition for prediction or diagnosis of canine degenerative Diseases
[Patent Registration 10-1107582] Web-based ontology editing operation system
[Program Registration 2011-01-121-005389] Smart-TGM heavy metals toxicity-index excavating tools
[Program Registration 2011-01-129-001569] WeightViz by weight visualization tool
[Program Registration C-2014-030421] Personal genomics-based obesity risk computing program
[PCT Application pct110125] Web-based ontology editing operation system
[Patent Application 10-2014-0163505] Customized personal traits dietary ingredients for information character-chemical agent network system and providing methods
[Patent Application 10-2014-0170397] Personal genomics-based obesity risk analysis system and method
[Patent Application 10-2015-0156844] Customized food information recommendation system considering personal genotype and phenotype information

Reduce your time with scientific results!

We provide internationally well recognized Bioinformatics software.
Through online education center and various education consulting, we foster a pleasant environment for researchers to analyze biological information.

120 institutions · acquisition of 100,000 clients

Human Genetic Variation Analysis

CLC Genomics Workbench
OmicSoft Suite
HGMD® Professional
HSMD
COSMIC
QCI™ Interpret
Sequencher

Animal·Plant Genome Analysis

CLC Genomics Workbench
OmicsBox Genome/Functional Analysis
FGENESH
Pedant-Pro™ Sequence Analysis Suite

Transcriptome Analysis

CLC Genomics Workbench Premium
OmicSoft Suite
OmicSoft OncoLand / DiseaseLand / Single-CellLand
Ingenuity® Pathway Analysis
OmicsBox Transcriptomics
Genevestigator®

Microbial Genome Analysis

CLC Genomics Workbench Premium
OmicsBox Genome/Functional Analysis
OmicsBox Metagenomics

Lab Management

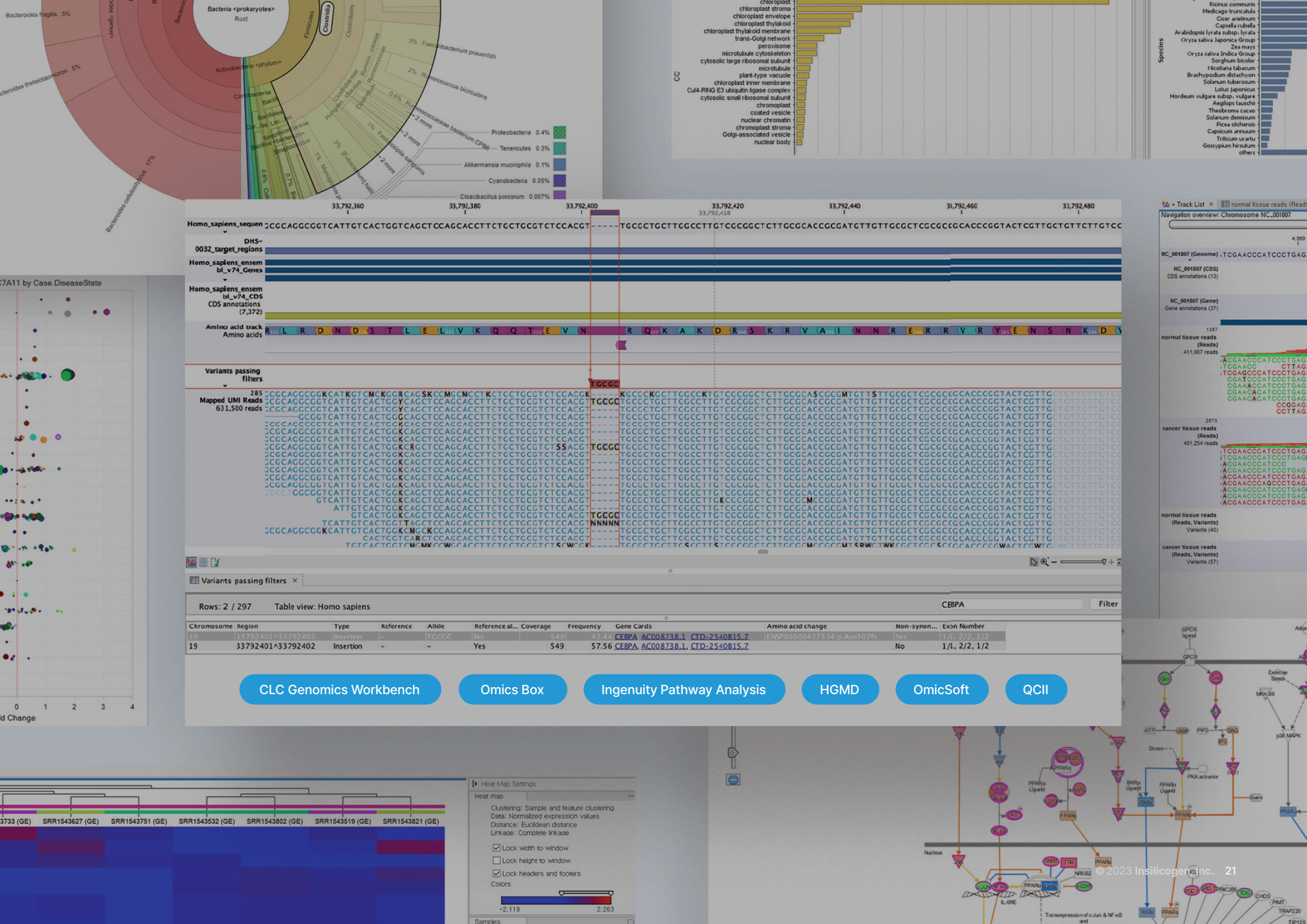
LabCollector

Hardware

Intel Select Solution - GATK Best Practice
Dell OEM Workstation

Lab Customized Solution

incoFIT Basic
incoFIT Advanced
incoFIT Professional
incoFIT Rental



Lead knowledge informatization by blowing life into information and put it into the system

Insilicogen's System Integration(SI) business provides the latest BIO DB management and analysis solutions that researchers need based on 20 years of experience in building and analyzing biometric information systems, making it easier and more convenient to produce useful data and analyze large amounts of biological information data.

Insilicogen will always work in all areas that require basic genetic resource management, such as species, genes, and samples, laboratory information management, omics data and large-capacity data analysis and management, and even data-breeding to develop new varieties using big data and artificial intelligence.

과학기술정보통신부 · 농림축산검역본부 · 농촌진흥청 · 보건복지부 · 환경부
산업통상자원부 · 중소벤처기업부 · 통일부 · 해양수산부 · 행정안전부 · 질병관리본부 KCDC
농촌진흥청 국립농업과학원 · 환경부 국립생물자원관 · 해양수산부 국립수산과학원 · 경찰청 · 대한민국 국방부
국립해양생물자원관 · 국방부조사본부 · 보훈공단 중앙보훈병원 · 축산물품질평가원
KISTI 한국과학기술정보연구원 · 한국생명공학연구원 · KFRI 한국식품연구원 · KAERI 한국원자력연구원

30 institutions, 60 system development

CODA, NABIC, MAGIC, Dementia Big Data Platform AIzNAVI,
Genetic Retrieval System for 6.25 war dead and missing children, etc

Construction of an Integrated Information System

[Korea Centers for Disease Control and Prevention] Establishment of Clinical Genetic Management System for Rare Diseases
[Korea Bioinformation Center] Establishment of Quality Management System for Bio data
[National Marine Biodiversity Institute of Korea] Development of Marine Bio Data Center Platform
[National Institute of Fisheries Science] Establishment of national fisheries biological zone integration system
[Korea Atomic Energy Research Institute] Standardization of food and quarantine radiation response data and establishment of management system
[Centers for Disease Control & Prevention] Clinical Omics Data Archive(CODA)
[National Institute of Agricultural Sciences] Agricultural biotechnology-information system(NABIC)
[National Research Institute of Cultural Heritage] Ancient genetic information system
[National Institute of Animal Science] Livestock genetic resource total management system
[National Institute of Animal Science] Animal genetic information system
[National Research Institute of Cultural Heritage] Ancient human bone traits integration information system

Omics Analysis and Management System Development

[Korea Centers for Disease Control and Prevention] Establishment of a multi-omics information analysis system for COVID-19 confirmed patients
[National Research Institute of Cultural Heritage] Ancient life genetics big data DB system
[KISTI - Korean Institute of Science and Technology Information] Web-based multi-omics integration analysis interface
[KISTI - Korean Institute of Science and Technology Information] Next-generation bio research analysis technology for International cooperation research support
[KISTI - Korean Institute of Science and Technology Information] User-customized next-generation genetics data integration analysis system

Genetic Resource Management and DB Development

[Gachon University Medical Campus] Establishment of a medical database for intermediary research related to COVID-19 rest
[Korea Bioinformation Center] Establishment of Genetic Registration and Management System
[Centers for Disease Control & Prevention] Integrated database construction of Kor-GLASS
[Ministry of Food and Drug Safety] Food poisoning bacteria integration information DB system
[Centers for Disease Control & Prevention] Virus gene DB acceleration
[Centers for Disease Control & Prevention] Food poisoning virus surveillance operation system and genetic analysis module development
[Centers for Disease Control & Prevention] Nervous system virus gene DB function improvement and extension
[Animal and Plant Quarantine Agency] Genetic variation management system
[National Institute of Fisheries Science] Marine life single nucleotide information management system
[Centers for Disease Control & Prevention] System for real-time acute diarrhea disease-causing agent DB operation
[Animal and Plant Quarantine Agency] Genetic analysis results and DB management system
[National Institute of Fisheries Science] Life resources integration DB
[National Research Institute of Cultural Heritage] Ancient human skeleton Y-SNP and ancient life genetic information DB system
[Korea Research Institute of Bioscience & Biotechnology] Genetically modified mouse data collecting computing system

Bio-bank System

[VHS Medical Center] Establishment of BioBank and genetic information management system

Record Management System Development

[Shinan-gun, Jeollanamdo] Production traceability management system for Shinan Bay salt prestige
[Namwon Environmentally-Friendly Black Pork Cluster Enterprise Organization] Environmentally-friendly Gowon black pork record management tracking system
[Hankyong National University] Evergreen Hongcheon Korean-beef RFID record information management system
[Korea Institute for Animal Products Quality Evaluation] Smart beef record system advancement
[Chonnam National University] Green Korean-beef population management system
[Hankyong National University] Jangsu country population management system

Analysis and Development of a Large Volume of DB

[KISTI - Korean Institute of Science and Technology Information] Integrated analysis system for biodegradable network big data
[Agency for Defense Development] Unknown agent integrated verification system
[KISTI - Korean Institute of Science and Technology Information] Alzheimer data network navigation program and integrated analysis platform
[KISTI - Korean Institute of Science and Technology Information] Astronomical space data analysis cloud user interface
[KISTI - Korean Institute of Science and Technology Information] Protein interaction and computer simulation integration management system

[KISTI - Korean Institute of Science and Technology Information] Interface for managing virtual cluster
[KISTI - Korean Institute of Science and Technology Information] Resource management portal system for brain imaging information extraction application analysis
[National Marine Biodiversity Institute of Korea] National marine fishery resources genetics information management system

Genetic Inspection System Development

[Ministry of the Interior and Safety] Compulsory mobilization victim DNA identity validation DB
[Ministry of Unification] Genetic information of separated families DB
[KISTI - Korean Institute of Science and Technology Information] Web-based multi-omics integrated analysis interface
[Korea Institute for Animal Products Quality Evaluation] Beef-record laboratory information management system
[Criminal Investigation Command] Genetic information identification system of fallen soldiers from the Korean War(6.25)
[National Forensic Service] Genetic information search system for finding missing children

Sample Management and Genetic Barcode

[National Institute of Biological Resources] Wildlife integrated genetic information system
[National Institute of Fisheries Sciences] Marine life sample-securing DB and management system
[Chungnam National University] Marine life resource donation registry agency Integration management system
[RDA-Genebank Information Center] Agricultural genetic resources barcoding system

Certifications

01 Certificate of professional research business operator (order research: engineering research and development business)
From Ministry of Science and ICT 2022.06.27 ~ 2024.10.20

02 Direct production certificate(Big-data analysis)
From Korea Federation of SMEs 2021.03.17 / 2023.03.16

03 Direct production certificate(Software development)
From Korea Federation of SMEs 2021.03.17 / 2023.03.16

04 Confirmation letter of Innovative business management in small and medium sized company(MAIN-BIZ)
From Small and Medium Business Administration 2020.06.27 / 2023.06.26

05 Selected as the best service company
From Korea Credit Guarantee Fund 2017.08.04

06 Certified youth-friendly small and medium sized company
From Ministry of Employment and Labor 2016.04.17 ~ Present

07 Approved as a research Institute
From KOITA 2007.06.18

Patent Registration

01 Human body type and metabolic susceptibility SNP marker and diagnostic information provision method (10-2093453) 2020.03.19

02 Prediction and diagnosis method of canine degenerative joint disease(10-2067076) 2020.01.10

03 Network system between traits and chemicals, and provision method for personalized dietary information(10-1645206) 2016.07.28

04 DNA search method(10-1287400) 2013.07.12

05 Web-based ontology editing operation system(10-1107582) 2012.01.12

Awards

01 Official commendation of contribution on marine fishery industry development
From the Minister of Oceans and Fisheries 2019.12

02 Official commendation on promoting experimental research of fishery
From Minister of Ocean and Fisheries 2018.12

03 Official commendation on excellence in management
From the Gyeonggi Provincial Small and Medium Business Administration 2016.02

Registered Marks

01 iF®(INSILICO FOOD)
2017.11.01

02 GLTER®
2011.01.05

03 LabKM®
2009.02.13

Program Registration

01 Registered 61 programs including KinMatch(Birth related information search system)

Applied Patent

01 A device provides gene expression information and 6 others

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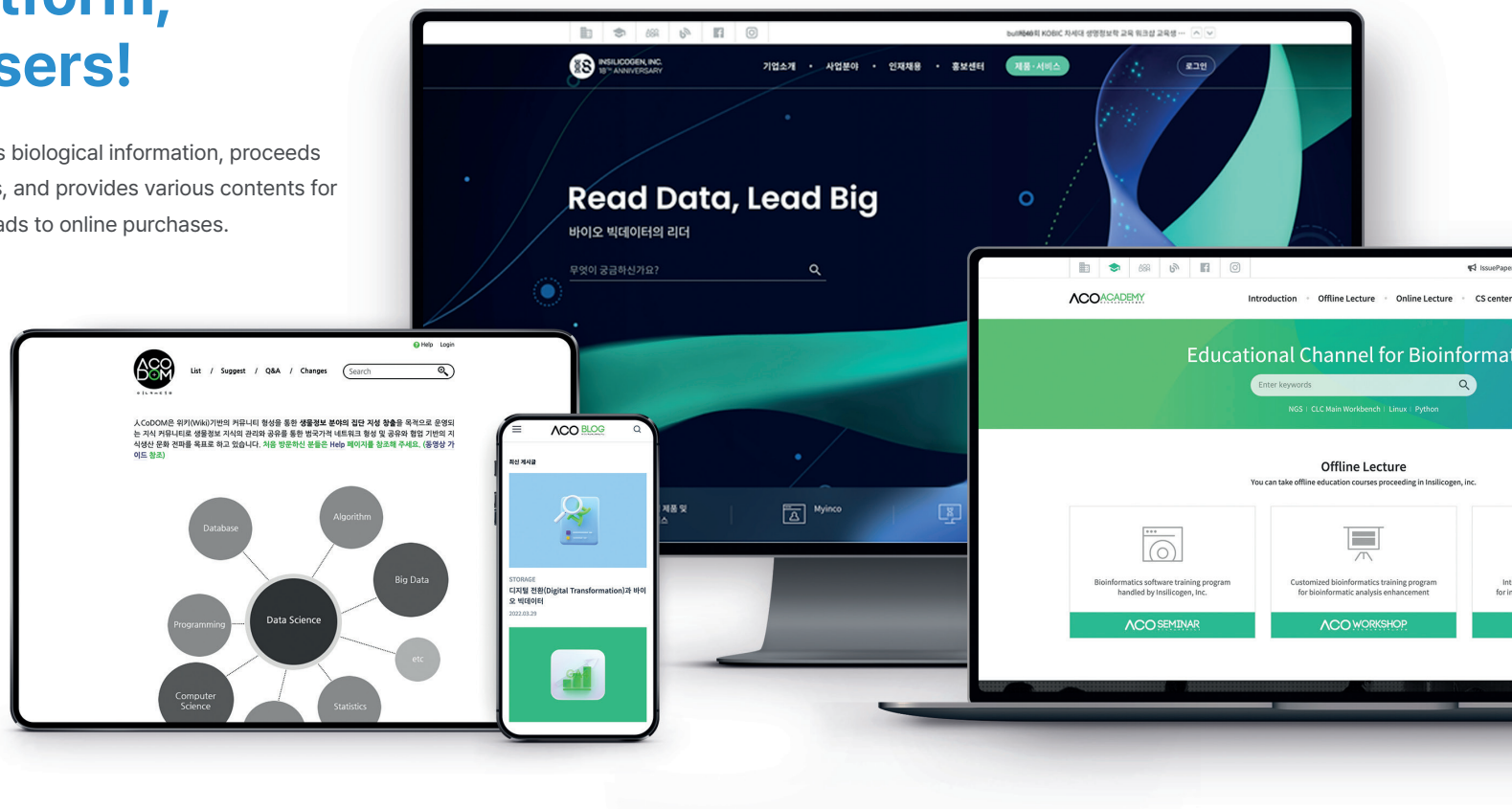


01 Malik A, Subramaniyam S, Kim CB, Manavalan B. SortPred: The first machine learning based predictor to identify bacterial sortases and their classes using sequence-derived information. Comput Struct Biotechnol J. 2021 Dec 14;20:165-174. doi: 10.1016/j.csbj.2021.12.014. PMID: 34976319; PMCID: PMC8703055.

02 Mi XJ, Tran THM, Park HR, Xu XY, Subramaniyam S, Choi HS, Kim J, Koh SC, Kim YJ. Immune-enhancing effects of postbiotic produced by Bacillus velezensis Kh2-2 isolated from Korea Foods. Food Res Int. 2022 Feb;152:110911. doi: 10.1016/j.foodres.2021.110911. PMID: 35181083.

03 Graf L, Shin YH, Yang JH, Hwang IK, Yoon HS. Transcriptome analysis reveals the spatial and temporal differentiation of gene expression in the sporophyte of Undaria pinnatifida. Algal Research. 2022 Nov;68, 102883. doi: 10.1016/j.algal.2022.102883.

04 Kim C, Kim JS , Lee HJ, Seong B, Seo SW, Son HJ , Jeon JH , Shin YH. Transcriptome analysis demonstrating the therapeutic effect of Tenodera angustipennis (Mantidis Ootheca) extracts on radiation-induced gonadal toxicity in mouse testis. Entomological Research. 2022 Jul 20; 52(7), 319-326. doi: 10.1111/1748-5967.12604.

05 Kwon YI, Lee JY, Park JH, Kim YM, Kim SH, Won YJ, Kim HY. Osteoporosis Pre-Screening Using Ensemble Machine Learning in Postmenopausal Korean Women. Healthcare. 2022 Jun 11; 10(6), 1107. doi: 10.3390/healthcare10061107. PMID: 35742158; PMCID: PMC9222287.

06 Lee CW, Cheon KS, Shin YJ, Oh HJ, Jeong YM, Jang H, Park YC, Kim KY, Cho HC, Won YJ, Baek JH, Cha YS, Kim SL, Kim KH, Ji HS. Development and Application of a Target Capture Sequencing SNP-Genotyping Platform in Rice. Genes. 2022 Apr 28;13(5), 794. doi: 10.3390/genes13050794. PMID: 35627177; PMCID: PMC9141132.

07 Shin GH, Hong JM, Park SW, Kang BC, Lee BM. Visualization for Integrated Analysis of Multi-Omics Data by Harmful Substances Exposed to Human. Journal of Korea Multimedia Society. 2022 Dec; 25:2.

08 Shin GH, Hong JM, Park SW. Novel data archival system for multi omics data of human exposure to harmful substances. Molecular & Cellular Toxicology. 2022 Feb 25;18.

09 Noh ES, Kang BC, Kim J, Jeon JH, Kim YO, Byun SG, Kim WJ, Nam BH. Draft Assembled Genome of Walleye Pollock (Gadus chalcogrammus). Front Marin. 2022 Feb 16; 9:744941. Doi: 10.3389/fmars.2022.744941.

10 Shin Y, Noh ES, Jeon JH, Shin GH, Kim EM, Kim YO, Kim H, Jung H, Nam BH. First Draft Genome of a Mud Loach (Misgurnus mizolepis) in the Family Cobitidae. Front Marin. 2022 Jan 3;8:1913. doi: 10.3389/fmars.2021.799148.

11 Jo S, Seo S, Jung K, Bai H. Radiation response data analysis using Bayesian nonparametric regression models with shape-restriction. J Kor Data & Infor. Sci. Soc. 2021; 32:1295.

12 Lee SC, Lee JW, Lee DH, Huh MJ, Nam I, Park JH, Jung M, Park IK. Identification of Sex Pheromone Components of Korean Dioryctria abietella (Lepidoptera: Pyralidae) Population and Synergism of Pheromone and Pine Cone Volatile Blends. J Econ Entomol. 2021 Dec 1:toab227. doi: 10.1093/jee/toab227. Epub ahead of print. PMID: 34865067.

13 Song K, Shin Y, Jung M, Subramaniyam S, Lee KP, Oh EA, Jeong JH, Kim JG. Chromosome-Scale Genome Assemblies of Two Korean Cucumber Inbred Lines. Front Genet. 2021 Nov 19;12:733188. doi: 10.3389/fgene.2021.733188. PMID: 34868208; PMCID: PMC8640492.

14 Xuan B, Park J, Choi S, You I, Nam BH, Noh ES, Kim EM, Song MY, Shin Y, Jeon JH, Kim EB. Draft genome of the Korean smelt Hypomesus nipponensis and its transcriptomic responses to heat stress in the liver and muscle. G3 (Bethesda). 2021 Sep 6;11(9):jkab147. doi: 10.1093/g3journal/jkab147. PMID: 33944944; PMCID: PMC8496316.

15 Shin Y, Subramaniyam S, Chun JM, Jeon JH, Hong JM, Jung H, Seong B, Kim C. Genome-Wide Differential Methylation Profiles from Two Terpene-Rich Medicinal Plant Extracts Administered in Osteoarthritis Rats. Plants (Basel). 2021 Jun 2;10(6):1132. doi: 10.3390/plants10061132. PMID: 34199631; PMCID: PMC8227118.

16 Yu GE, Shin Y, Subramaniyam S, Kang SH, Lee SM, Cho C, Lee SS, Kim CK. Machine learning, transcriptome, and genotyping chip analyses provide insights into SNP markers identifying flower color in Platycodon grandiflorus. Sci Rep. 2021 Apr 13;11(1):8019. doi: 10.1038/s41598-021-87281-0. PMID: 33850210; PMCID: PMC8044237.

17 Kim S, Subramaniyam S, Jung M, Oh EA, Kim TH, Kim JG. Genome Resource of Podosphaera xanthii, the Host-Specific Fungal Pathogen That Causes Cucurbit Powdery Mildew. Mol Plant Microbe Interact. 2021 Apr;34(4):457-459. doi: 10.1094/MPMI-11-20-0307-A. Epub 2021 Mar 3. PMID: 33264046.

18 Kang SH, Pandey RP, Lee CM, Sim JS, Jeong JT, Choi BS, Jung M, Ginzburg D, Zhao K, Won SY, Oh TJ, Yu Y, Kim NH, Lee OR, Lee TH, Bashyal P, Kim TS, Lee WH, Hawkins C, Kim CK, Kim JS, Ahn BO, Rhee SY, Sohng JK. Genome-enabled discovery of anthraquinone biosynthesis in Senna tora. Nat Commun. 2020 Nov 18;11(1):5875. doi: 10.1038/s41467-020-19681-1. Erratum in: Nat Commun. 2021 Mar 8;12(1):1665. PMID: 33208749; PMCID: PMC7674472.

19 Graf L, Shin Y, Yang JH, Choi JW, Hwang IK, Nelson W, Bhattacharya D, Viard F, Yoon HS. A genome-wide investigation of the effect of farming and human-mediated introduction on the ubiquitous seaweed Undaria pinnatifida. Nat Ecol Evol. 2021 Mar;5(3):360-368. doi: 10.1038/s41559-020-01378-9. Epub 2021 Jan 25. PMID: 33495590; PMCID: PMC7929912.

20 Seo D, Cho S, Manjula P, Choi N, Kim YK, Koh YJ, Lee SH, Kim HY, Lee JH. Identification of Target Chicken Populations by Machine Learning Models Using the Minimum Number of SNPs. Animals (Basel). 2021 Jan 19;11(1):241. doi: 10.3390/ani11010241. PMID: 33477975; PMCID: PMC7835996.

21 Lee JH, Jung M, Shin Y, Subramaniyam S, Kim IW, Seo M, Kim MA, Kim SH, Hwang J, Choi EH, Hwang UW, Hwang JS. Draft Genome of the Edible Oriental Insect Protaetia brevitarsis seulensis. Front Genet. 2021 Jan 13;11:593994. doi: 10.3389/fgene.2020.593994. PMID: 33519896; PMCID: PMC7838600.

22 Jeong GY, Park MK, Choi HJ, An HW, Park YU, Choi HJ, Park J, Kim HY, Son T, Lee H, Min KW, Oh YH, Le e JY, Kong G. NSD3-Induced Methylation of H3K36 Activates NOTCH Signaling to Drive Breast Tumor Initiation and Metastatic Progression. Cancer Res. 2021 Jan 1;81(1):77-90. doi: 10.1158/0008-5472.CAN-20-0360. Epub 2020 Sep 23. PMID: 32967925.

23 Chun JM, Lee AY, Nam JY, Lee MY, Choe MS, Lim KS, Kim C, Kim JS. Protective effects of Phlomis umbrosa extract on a monosodium iodoacetate-induced osteoarthritis model and prediction of molecular mechanisms using transcriptomics. Phytomedicine. 2021 Jan;81:153429. doi: 10.1016/j.phymed.2020.153429. Epub 2020 Dec 1. PMID: 33310311.

24 Kim JS, Shin IS, Shin NR, Nam JY, Kim C. Genome wide analysis of DNA methylation and gene expression changes in an ovalbumin induced asthma mouse model. Mol Med Rep. 2020 Sep;22(3):1709-1716. doi: 10.3892/mmr.2020.11245. Epub 2020 Jun 17. PMID: 32705270; PMCID: PMC7411290.

25 Hwang SD, Hwang JY, Sohn S, Kim SM, Kim SR, Kim KI, Kwon MG, Jung M, Lee KY, Kang BC, Seo JS. Genome data of shrimp acute hepatopancreatic necrosis disease causative Vibrio parahaemolyticus strains isolated from South Korea aquaculture farms. Data Brief. 2020 May 13;31:105697. doi: 10.1016/j.dib.2020.105697. PMID: 32509934; PMCID: PMC7264491.

26 Kim DH, Kim WD, Kim SK, Moon DH, Lee SJ. TGF-β1-mediated repression of SLC7A11 drives vulnerability to GPX4 inhibition in hepatocellular carcinoma cells. Cell Death Dis. 2020 May 29;11(5):406. doi: 10.1038/s41419-020-2618-6. PMID: 32471991; PMCID: PMC7260246.

27 Lee JE, Jung M, Lee SC, Huh MJ, Seo SM, Park IK. Antibacterial mode of action of trans-cinnamaldehyde derived from cinnamon bark (Cinnamomum verum) essential oil against Agrobacterium tumefaciens. Pestic Biochem Physiol. 2020 May;165:104546. doi: 10.1016/j.pestbp.2020.02.012. Epub 2020 Feb 19. PMID: 32359541.

28 Kim HY, Choi HJ, Lee JY, Kong G. Cancer Target Gene Screening: a web application for breast cancer target gene screening using multi-omics data analysis. Brief Bioinform. 2020 Mar 23;21(2):663-675. doi: 10.1093/bib/bbz003. PMID: 30698638.

29 Boopathi V, Subramaniyam S, Mathi yalagan R, Yang DC. Till 2018: a survey of biomolecular sequences in genus Panax. J Ginseng Res. 2020 Jan;44(1):33-43. doi: 10.1016/j.jgr.2019.06.004. Epub 2019 Jun 20. PMID: 32095095; PMCID: PMC7033366.

30 Kyeong D, Kim J, Shin Y, Subramaniyam S, Kang BC, Shin EH, Park EH, Noh ES, Kim YO, Park JY, Nam BH. Expression of Heat Shock Proteins in Thermally Challenged Pacific Abalone Haliotis discus hannai. Genes (Basel). 2019 Dec 23;11(1):22. doi: 10.3390/genes11010022. PMID: 31878084; PMCID: PMC7016835.

31 Subramaniyam S, Bae S, Jung M, Shin Y, Oh JH. The transcriptome data from the leaves of four Papaver species captured at the plant's three developmental life cycles. Data Brief. 2019 Dec 7;28:104955. doi: 10.1016/j.dib.2019.104955. PMID: 31890797; PMCID: PMC6926128.

32 Liyanage DS, Oh M, Omeka WKM, Wan Q, Jin CN, Shin GH, Kang BC, Nam BH, Lee J. First Draft Genome Assembly of Redlip Mullet (Liza haematocheila) From Family Mugilidae. Front Genet. 2019 Dec 3;10:1246. doi: 10.3389/fgene.2019.01246. PMID: 31850083; PMCID: PMC6902644.

33 Kim S, Jung M, Oh EA, Ho Kim T, Kim JG. Mitochondrial genome of the Podosphaera xanthii: a plant pathogen causes powdery mildew in cucurbits. Mitochondrial DNA B Resour. 2019 Nov 20;4(2):4172-4173. doi: 10.1080/23802359.2019.1618209. PMID: 33366368; PMCID: PMC7687534.

34 Choi HJ, Jin S, Cho H, Won HY, An HW, Jeong GY, Park YU, Kim HY, Park MK, Son T, Min KW, Jang KS, Oh YH, Lee JY, Kong G. CDK12 drives breast tumor initiation and trastuzumab resistance via WNT and IRS1-ErbB-PI3K signaling. EMBO Rep. 2019 Oct 4;20(10):e48058. doi: 10.15252/embr.201948058. Epub 2019 Aug 30. PMID: 31468695; PMCID: PMC6776914.

35 Kang MJ, Shin AY, Shin Y, Lee SA, Lee HR, Kim TD, Choi M, Koo N, Kim YM, Kyeong D, Subramaniyam S, Park EJ. Identification of transcriptome-wide, nut weight-associated SNPs in Castanea crenata. Sci Rep. 2019 Sep 11;9(1):13161. doi: 10.1038/s41598-019-49618-8. PMID: 31511588; PMCID: PMC6739505.

36 Kim HY, Choi BH, Oh T, Kang BC. SNP marker selection for dog breed identification from genotypes of high-density SNP array and machine learning. J Agri Lif Sci. 2019 Aug 6;53:(4)93-101. Doi:10.14397/jals.201953.4.93.

37 Lee SC, Kwon JH, Cha DJ, Kim DS, Lee DH, Seo SM, Lee HR, Huh MJ, Jung M, Park IK. Effects of Pheromone Dose and Trap Height on Capture of a Bast Scale of Pine, Matsucoccus thunbergianae (Hemiptera: Margarodidae) and Development of a New Synthesis Method. J Econ Entomol. 2019 Aug 3;112(4):1752-1759. doi: 10.1093/jee/toz079. PMID: 31009531.

38 Lee JY, Joo HS, Choi HJ, Jin S, Kim HY, Jeong GY, An HW, Park MK, Lee SE, Kim WS, Son T, Min KW, Oh YH, Kong G. Role of MEL-18 Amplification in Anti-HER2 Therapy of Breast Cancer. J Natl Cancer Inst. 2019 Jun 1;111(6):609-619. doi: 10.1093/jnci/djy151. PMID: 30265336.

39 Boopathi V, Subramaniyam S, Malik A, Lee G, Manavalan B, Yang DC. mACPpred: A Support Vector Machine-Based Meta-Predictor for Identification of Anticancer Peptides. Int J Mol Sci. 2019 Apr 22;20(8):1964. doi: 10.3390/ijms20081964. PMID: 31013619; PMCID: PMC6514805.

40 Nam BH, Yoo D, Kim YO, Park JY, Shin Y, Shin GH, Park CI, Kim H, Kwak W. Whole genome sequencing reveals the impact of recent artificial selection on red sea bream reared in fish farms. Sci Rep. 2019 Apr 24;9(1):6487. doi: 10.1038/s41598-019-42988-z. Erratum in: Sci Rep. 2020 Jan 28;10(1):1625. PMID: 31019228; PMCID: PMC6482192.

41 Shin GH, Shin Y, Jung M, Hong JM, Lee S, Subramaniyam S, Noh ES, Shin EH, Park EH, Park JY, Kim YO, Choi KM, Nam BH, Park CI. First Draft Genome for Red Sea Bream of Family Sparidae. Front Genet. 2018 Dec 12;9:643. doi: 10.3389/fgene.2018.00643. PMID: 30619468; PMCID: PMC6299066.

42 Kim D,Jung M,Ha IJ, Lee MY, Lee SG, Shin Y, Subramaniyam S, Oh J. Transcriptional profiles of secondary metabolite biosynthesis genes and cytochromes in the leaves of four Papaver Species. Data 2018 Nov 28;3(4):55. Doi: 10.3390/data3040055.

43 Kim JY, Lim HY, Shin SE, Cha HK, Seo JH, Kim SK, Park SH, Son GH. Comprehensive transcriptome analysis of Sarcophaga peregrina, a forensically important fly species. Sci Data. 2018 Nov 6;5:180220. doi: 10.1038/sdata.2018.220. PMID: 30398471; PMCID: PMC6219405.

44 Baek SJ, Chun JM, Kang TW, Seo YS, Kim SB, Seong B, Jang Y, Shin GH, Kim C. Identification of Epigenetic Mechanisms Involved in the Anti-Asthmatic Effects of Descurainia sophia Seed Extract Based on a Multi-Omics Approach. Molecules. 2018 Nov 5;23(11):2879. doi: 10.3390/molecules23112879. PMID: 30400597; PMCID: PMC6278437.

45 Shin Y, Jung M, Shin GH, Jung HJ, Baek SJ, Lee GY, Kang BC, Shim J, Hong JM, Park JY, An CM, Kim YO, Noh JK, Kim JW, Nam BH, Park CI. First draft genome sequence of the rock bream in the family Oplegnathidae. Sci Data. 2018 Oct 23;5:180234. doi: 10.1038/sdata.2018.234. PMID: 30351299; PMCID: PMC6198749.

46 Oh J, Shin Y, Ha IJ, Lee MY, Lee SG, Kang BC, Kyeong D, Kim D. Transcriptome Profiling of Two Ornamental and Medicinal Papaver Herbs. Int J Mol Sci. 2018 Oct 16;19(10):3192. doi: 10.3390/ijms19103192. PMID: 30332811; PMCID: PMC6213990.

47 Jung D, Seo EY, Owen JS, Aoi Y, Yong S, Lavrentyeva EV, Ahn TS. Application of the filter plate microbial trap (FPMT), for cultivating thermophilic bacteria from thermal springs in Barguzin area, eastern Baikal, Russia. Biosci Biotechnol Biochem. 2018 Sep;82(9):1624-1632. doi: 10.1080/09168451.2018.1482194. Epub 2018 Jun 8. PMID: 29882485.

48 Lee HR, Lee SC, Lee DH, Jung M, Kwon JH, Huh MJ, Kim DS, Lee JE, Park IK. Identification of Aggregation-Sex Pheromone of the Korean Monochamus alternatus (Coleoptera: Cerambycidae) Population, the Main Vector of Pine Wood Nematode. J Econ Entomol. 2018 Aug 3;111(4):1768-1774. doi: 10.1093/jee/toy137. PMID: 29788181.

49 Lee J, Yang EC, Graf L, Yang JH, Qiu H, Zelzion U, Chan CX, Stephens TG, Weber APM, Boo GH, Boo SM, Kim KM, Shin Y, Jung M, Lee SJ, Yim HS, Lee JH, Bhattacharya D, Yoon HS. Analysis of the Draft Genome of the Red Seaweed Gracilariopsis chorda Provides Insights into Genome Size Evolution in Rhodophyta. Mol Biol Evol. 2018 Aug 1;35(8):1869-1886. doi: 10.1093/molbev/msy081. PMID: 29688518.

50 Manavalan B, Subramaniyam S, Shin TH, Kim MO, Lee G. Machine-Learning-Based Prediction of Cell-Penetrating Peptides and Their Uptake Efficiency with Improved Accuracy. J Proteome Res. 2018 Aug 3;17(8):2715-2726. doi: 10.1021/acs.jproteome.8b00148. Epub 2018 Jul 2. PMID: 29893128.

51 Lee AY, Park W, Kang TW, Cha MH, Chun JM. Network pharmacology-based prediction of active compounds and molecular targets in Yijin-Tang acting on hyperlipidaemia and atherosclerosis. J Ethnopharmacol. 2018 Jul 15;221:151-159. doi: 10.1016/j.jep.2018.04.027. Epub 2018 Apr 23. PMID: 29698773.

52 Choi HJ, Joo HS, Won HY, Min KW, Kim HY, Son T, Oh YH, Lee JY, Kong G. Role of RBP2-Induced ER and IGF1R-ErbB Signaling in Tamoxifen Resistance in Breast Cancer. J Natl Cancer Inst. 2018 Apr 1;110(4). doi: 10.1093/jnci/djx207. PMID: 29028222.

53 Oh JH, Lee YJ, Byeon EJ, Kang BC, Kyeo ung DS, Kim CK. Whole-genome resequencing and transcriptomic analysis of genes regulating anthocyanin biosynthesis in black rice plants. 3 Biotech. 2018 Feb;8(2):115. doi: 10.1007/s13205-018-1140-3. Epub 2018 Feb 7. PMID: 29430376; PMCID: PMC5801106.

54 Thulasitha WS, Umasuthan N, Wan Q, Nam BH, Kang TW, Lee J. A proto-type galectin-2 from rock bream (Oplegnathus fasciatus): Molecular, genomic, and expression analysis, and recognition of microbial pathogens by recombinant protein. Dev Comp Immunol. 2017 Jun;71:70-81. doi: 10.1016/j.dci.2017.01.023. Epub 2017 Jan 25. PMID: 28131766.

55 Kim J, Jun KM, Kim JS, Chae S, Pahk YM, Lee TH, Sohn SI, Lee SI, Lim MH, Kim CK, Hur Y, Nahm BH, Kim YK. RapaNet: A Web Tool for the Co-Expression Analysis of Brassica rapa Genes. Evol Bioinform Online. 2017 Jun 19;13:1176934317715421. doi: 10.1177/1176934317715421. PMID: 28680265; PMCID: PMC5484627.

56 Nam BH, Kwak W, Kim YO, Kim DG, Kong HJ, Kim WJ, Kang JH, Park JY, An CM, Moon JY, Park CJ, Yu JW, Yoon J, Seo M, Kim K, Kim DK, Lee S, Sung S, Lee C, Shin Y, Jung M, Kang BC, Shin GH, Ka S, Caetano-Anolles K, Cho S, Kim H. Genome sequence of pacific abalone (Haliotis discus hannai): the first draft genome in family Haliotidae. Gigascience. 2017 May 1;6(5):1-8. doi: 10.1093/gigascience/gix014. PMID: 28327967; PMCID: PMC5439488.

57 Kim HY, Choi JW, Lee JY, Kong G. Gene-based comparative analysis of tools for estimating copy number alterations using whole-exome sequencing data. Oncotarget. 2017 Apr 18;8(16):27277-27285. doi: 10.18632/oncotarget.15932. PMID: 28460482; PMCID: PMC5432334.

58 Umasuthan N, Bathige SDNK, Thulasitha WS, Jayasooriya RGPT, Shin Y, Lee J. Identification of a gene encoding a membrane-anchored toll-like receptor 5 (TLR5M) in Oplegnathus fasciatus that responds to flagellin challenge and activates NF-κB. Fish Shellfish Immunol. 2017 Mar;62:276-290. doi: 10.1016/j.fsi.2017.01.020. Epub 2017 Jan 19. PMID: 28111358.

59 Shin GH, Kang BC, Jang DJ. Metabol ic Pathways Associated with Kimchi, a Traditional Korean Food, Based on In Silico Modeling of Published Data. Genomics Inform. 2016 Dec;14(4):222-229. doi: 10.5808/GI.2016.14.4.222. Epub 2016 Dec 31. PMID: 28154515; PMCID: PMC5287128.

60 Seol YJ, Won SY, Shin Y, Lee JY, Chun JS, Kim YK, Kim CK. A Multilayered Screening Method for the Identification of Regulatory Genes in Rice by Agronomic Traits. Evol Bioinform Online. 2016 Nov 2;12:253-262. doi: 10.4137/EBO.S40622. PMID: 27840573; PMCID: PMC5094579.

61 Shin Y, Jung HJ, Jung M, Yoo S, Subra maniyam S, Markkandan K, Kang JM, Rai R, Park J, Kim JJ. Discovery of Gene Sources for Economic Traits in Hanwoo by Whole-genome Resequencing. Asian-Australas J Anim Sci. 2016 Sep;29(9):1353-62. doi: 10.5713/ajas.15.0760. Epub 2016 Mar 4. PMID: 26954201; PMCID: PMC5003998.

62 Lim D, Kim HY, Cho YM, Chai HH, Park JE, Lim KS, Lee SS. Construction of gene network system associated with economic traits in cattle. J Lif Sci. 2016 Aug 23;26(8):04-910. doi: 10.5353/JLS.2016.26.8.904.

63 Cheong JY, Kim YB, Woo JH, Kim DK, Yeo M, Yang SJ, Yang KS, Soon SK, Wang HJ, Kim BW, Park JH, Cho SW. Identification of NUCKS1 as a putative oncogene and immunodiagnostic marker of hepatocellular carcinoma. Gene. 2016 Jun 10;584(1):47-53. doi: 10.1016/j.gene.2016.03.006. Epub 2016 Mar 9. PMID: 26968889.

64 Nik-Zainal S, Davies H, Staaf J, Raakr ishna M, Glodzik D, Zou X, Martincorena I, et al. Stratton MR. Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature. 2016 Jun 2;534(7605):47-54. doi: 10.1038/nature17676. Epub 2016 May 2. Erratum in: Nature. 2019 Feb;566(7742):E1. PMID: 27135926; PMCID: PMC4910866.

65 Kim IW, Lee JH, Subramaniyam S, Yun EY, Kim I, Park J, Hwang JS. De Novo Transcriptome Analysis and Detection of Antimicrobial Peptides of the American Cockroach Periplaneta americana (Linnaeus). PLoS One. 2016 May 11;11(5):e0155304. doi: 10.1371/journal.pone.0155304. PMID: 27167617; PMCID: PMC4864078.

66 Morganella S, Alexandrov LB, Glodzik D, Zou X, Davies H, Staaf J, Sieuwerts AM, Nik-Zainal S, et al. The topography of mutational processes in breast cancer genomes. Nat Commun. 2016 May 2;7:11383. doi: 10.1038/ncomms11383. PMID: 27136393; PMCID: PMC5001788.

67 Park YJ, Li X, Noh SJ, Kim JK, Lim SS, Park NI, Kim S, Kim YB, Kim YO, Lee SW, Arasu MV, Al-Dhabi NA, Park SU. Transcriptome and metabolome analysis in shoot and root of Valeriana fauriei. BMC Genomics. 2016 Apr 23;17:303. doi: 10.1186/s12864-016-2616-3. PMID: 27107812; PMCID: PMC4842265.Q, Nam BH, Kang TW, Lee J. A proto-type galectin-2 from rock bream (Oplegnathus fasciatus): Molecular, genomic, and expression analysis, and recognition.

68 Kim I, Lee SH, Jeong J, Park JH, Yoo MA, Kim CM. Functional Profiling of Human MeCP2 by Automated Data Comparison Analysis and Computerized Expression Pathway Modeling. Healthc Inform Res. 2016 Apr;22(2):120-8. doi: 10.4258/hir.2016.22.2.120. Epub 2016 Apr 30. PMID: 27200222; PMCID: PMC4871842.

69 Nam BH, Jung M, Subramaniyam S, Yoo SI, Markkandan K, Moon JY, Kim YO, Kim DG, An CM, Shin Y, Jung HJ, Park JH. Transcriptome Analysis Revealed Changes of Multiple Genes Involved in Haliotis discus hannai Innate Immunity during Vibrio parahemolyticus Infection. PLoS One. 2016 Apr 18;11(4):e0153474. doi: 10.1371/journal.pone.0153474. PMID: 27088873; PMCID: PMC4835058.

70 Kim H, Kumar KS, Hwang SY, Kang BC, Moon HB, Shin KH. Utility of Stable Isotope and Cytochrome Oxidase I Gene Sequencing Analyses in Inferring Origin and Authentication of Hairtail Fish and Shrimp. J Agric Food Chem. 2015 Jun 10;63(22):5548-56. doi: 10.1021/acs.jafc.5b01469. Epub 2015 Jun 2. PMID: 25980806.

71 Lee JY, Won HY, Park JH, Kim HY, Choi HJ, Shin DH, Kang JH, Woo JK, Oh SH, Son T, Choi JW, Kim S, Kim HY, Yi K, Jang KS, Oh YH, Kong G. MEL-18 loss mediates estrogen receptor-α downregulation and hormone independence. J Clin Invest. 2015 May;125(5):1801-14. doi: 10.1172/JCI73743. Epub 2015 Mar 30. PMID: 25822021; PMCID: PMC4463188.

72 Kim CK, Seol YJ, Shin Y, Lim HM, Lee GS, Kim AR, Lee TH, Lee JH, Park DS, Yoo S, Kim YH, Kim YK. Whole-genome resequencing and transcriptomic analysis to identify genes involved in leaf-color diversity in ornamental rice plants. PLoS One. 2015 Apr 21;10(4):e0124071. doi: 10.1371/journal.pone.0124071. PMID: 25897514; PMCID: PMC4405343.

73 Seo DW, Oh JD, Jin S, Song KD, Park HB, Heo KN, Shin Y, Jung M, Park J, Jo C, Lee HK, Lee JH. Single nucleotide polymorphism analysis of Korean native chickens using next generation sequencing data. Mol Biol Rep. 2015 Feb;42(2):471-7. doi: 10.1007/s11033-014-3790-5. Epub 2014 Oct 11. Erratum in: Mol Biol Rep. 2015 Feb;42(2):567. PMID: 25304812.

74 Park JY, An YR, Kanda N, An CM, An HS, Kang JH, Kim EM, An DH, Jung H, Joung M, Park MH, Yoon SH, Lee BY, Lee T, Kim KW, Park WC, Shin DH, Lee YS, Kim J, Kwak W, Kim HJ, Kwon YJ, Moon S, Kim Y, Burt DW, Cho S, Kim H. Cetaceans evolution: insights from the genome sequences of common minke whales. BMC Genomics. 2015 Jan 22;16(1):13. doi: 10.1186/s12864-015-1213-1. PMID: 25609461; PMCID: PMC4311506.

75 Yang EC, Nam BH, Noh SJ, Kim YO, Kim DG, Jee YJ, Park JH, Noh JH, Yoon HS. Complete mitochondrial genome of Pacific abalone (Haliotis discus hannai) from Korea. Mitochondrial DNA. 2015;26(6):917-8. doi: 10.3109/19401736.2013.863289. Epub 2014 Jan 10. PMID: 24409885.

76 Mathiyalagan R, Subramaniyam S, Kim YJ, Kim YC, Yang DC. Ginsenoside compound K-bearing glycol chitosan conjugates: synthesis, physicochemical characterization, and in vitro biological studies. Carbohydr Polym. 2014 Nov 4;112:359-66. doi: 10.1016/j.carbpol.2014.05.098. Epub 2014 Jun 10. PMID: 25129755.

77 Rengaraj D, Lee SI, Park TS, Lee HJ, Kim YM, Sohn YA, Jung M, Noh SJ, Jung H, Han JY. Small non-coding RNA profiling and the role of piRNA pathway genes in the protection of chicken primordial germ cells. BMC Genomics. 2014 Sep 4;15(1):757. doi: 10.1186/1471-2164-15-757. PMID: 25185950; PMCID: PMC4286946.

78 Subramaniyam S, Mathiyalagan R, Nat arajan S, Kim YJ, Jang MG, Park JH, Yang DC. Transcript expression profiling for adventitious roots of Panax ginseng Meyer. Gene. 2014 Aug 1;546(1):89-96. doi: 10.1016/j.gene.2014.05.024. Epub 2014 May 13. PMID: 24831831.

79 Kim JH, Roh JY, Kwon DH, Kim YH, Yoon KA, Yoo S, Noh SJ, Park J, Shin EH, Park MY, Lee SH. Estimation of the genome sizes of the chigger mites Leptotrombidium pallidum and Leptotrombidium scutellare based on quantitative PCR and k-mer analysis. Parasit Vectors. 2014 Jun 20;7:279. doi: 10.1186/1756-3305-7-279. PMID: 24947244; PMCID: PMC4079623.

80 Yoo WG, Lee JH, Shin Y, Shim JY, Jung M, Kang BC, Oh J, Seong J, Lee HK, Kong HS, Song KD, Yun EY, Kim IW, Kwon YN, Lee DG, Hwang UW, Park J, Hwang JS. Antimicrobial peptides in the centipede Scolopendra subspinipes mutilans. Funct Integr Genomics. 2014 Jun;14(2):275-83. doi: 10.1007/s10142-014-0366-3. Epub 2014 Mar 21. PMID: 24652097.

81 Kim S, Park M, Yeom SI, Kim YM, Lee JM, Lee HA, Seo E, Choi D, et al. Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. Nat Genet. 2014 Mar;46(3):270-8. doi: 10.1038/ng.2877. Epub 2014 Jan 19. PMID: 24441736.

82 Kim KU, Park SK, Kang SA, Park MK, Cho MK, Jung HJ, Kim KY, Yu HS. Comparison of functional gene annotation of Toxascaris leonina and Toxocara canis using CLC genomics workbench. Korean J Parasitol. 2013 Oct;51(5):525-30. doi: 10.3347/kjp.2013.51.5.525. Epub 2013 Oct 31. PMID: 24327777; PMCID: PMC3857499.

83 Jeong IS, Yoon UH, Lee GS, Ji HS, Lee HJ, Han CD, Hahn JH, An G, Kim TH. SNP-based analysis of genetic diversity in anther-derived rice by whole genome sequencing. Rice (N Y). 2013 Mar 14;6(1):6. doi: 10.1186/1939-8433-6-6. PMID: 24280451; PMCID: PMC4883692.

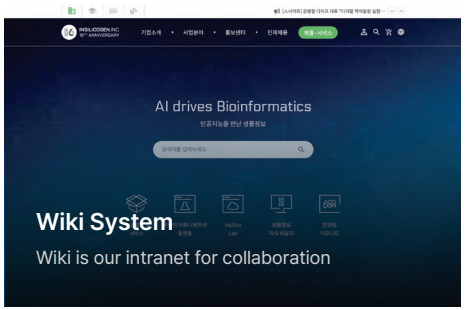
84 Kim DW, Kim DW, Yoo WG, Nam SH, Lee MR, Yang HW, Park J, Lee K, Lee S, Cho SH, Lee WJ, Park HS, Ju JW. SpiroESTdb: a transcriptome database and online tool for sparganum expressed sequences tags. BMC Res Notes. 2012 Mar 8;5:130. doi: 10.1186/1756-0500-5-130. PMID: 22397686; PMCID: PMC3329409.

85 Lim D, Lee SH, Cho YM, Yoon D, Shin Y, Kim KW, Park HS, Kim H. Transcript profiling of expressed sequence tags from intramuscular fat, longissimus dorsi muscle and liver in Korean cattle (Hanwoo). BMB Rep. 2010 Feb;43(2):115-21. doi: 10.5483/bmbrep.2010.43.2.115. PMID: 20193130.

86 Lee KT, Byun MJ, Lim D, Kang KS, Kim NS, Oh JH, Chung CS, Park HS, Shin Y, Kim TH. Full-length enriched cDNA library construction from tissues related to energy metabolism in pigs. Mol Cells. 2009 Dec 31;28(6):529-36. doi: 10.1007/s10059-009-0147-3. Epub 2009 Nov 19. PMID: 19937143.

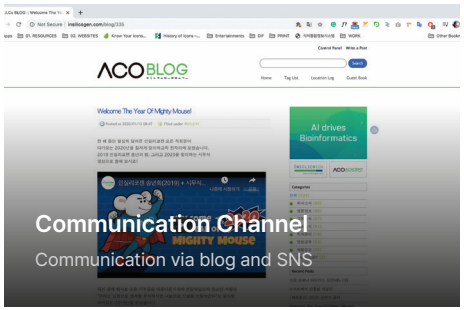
With creative and positive mind, discover new values and spread new culture

We build our competitiveness via our internal knowledge management system that includes reading, sharing ideas and tasks, and having a culture day and more. Seeking and developing our culture leads us to become a number-one company in the Bioinformatics field.



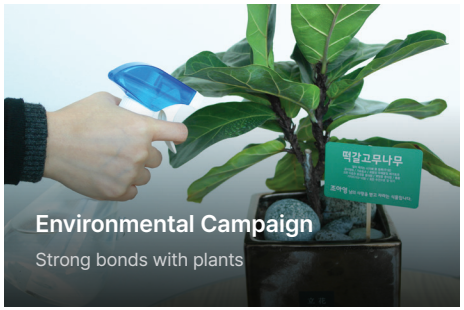
Wiki System

Wiki is our intranet for collaboration



Communication Channel

Communication via blog and SNS



Environmental Campaign

Strong bonds with plants

Culture Day

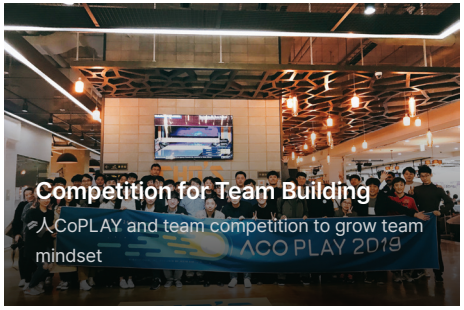
A culture day to enhance intellect & sensibility

Self-sustained Growth

Continuous improvements through seminar, blog, publishing, and reading

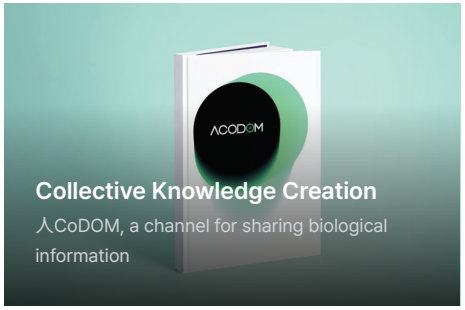
Health Enhancement

Health protector for a sound body and mind



Competition for Team Building

人CoPLAY and team competition to grow team mindset



Collective Knowledge Creation

人CoDOM, a channel for sharing biological information

Lead Future of Bioinformatics by putting AI and Big Data in the center!

Legacy of Bioinformatics Business

Based on 20 years of legacy and experiences, we will continue to provide solutions, customized system design for clients' environment, and the latest Bioinformatics education.

SI
Design customized system for clients

Education
The latest Bioinformatics education business

BI
The latest Bioinformatics education business

Solution
Provide solution

insilico Lab

Prefer 'customized Bioinformatics consulting' bases in silico(computer), leads in vivo, in vitro

Through long- accumulated biological information know-hows and knowledge, we are trying to contribute from designing experiments to coming up with optimized results.

AI Lab

Spearhead that will lead the future of Biology in the age of AI

By structuring, interconnecting, machine learning, selecting, and extracting data, we discover hidden knowledge and support integrated understanding.

iBREEDING

Data-Driven Breeding Company

Provide a platform that deals with a large volume of genotype and phenotype data, and detailed breeding based on environmental information.

D.iF

Data-Driven Food Company

Provide personalized food contents through network analysis that uses food related data and various personal data collected for a long time.

AIDX

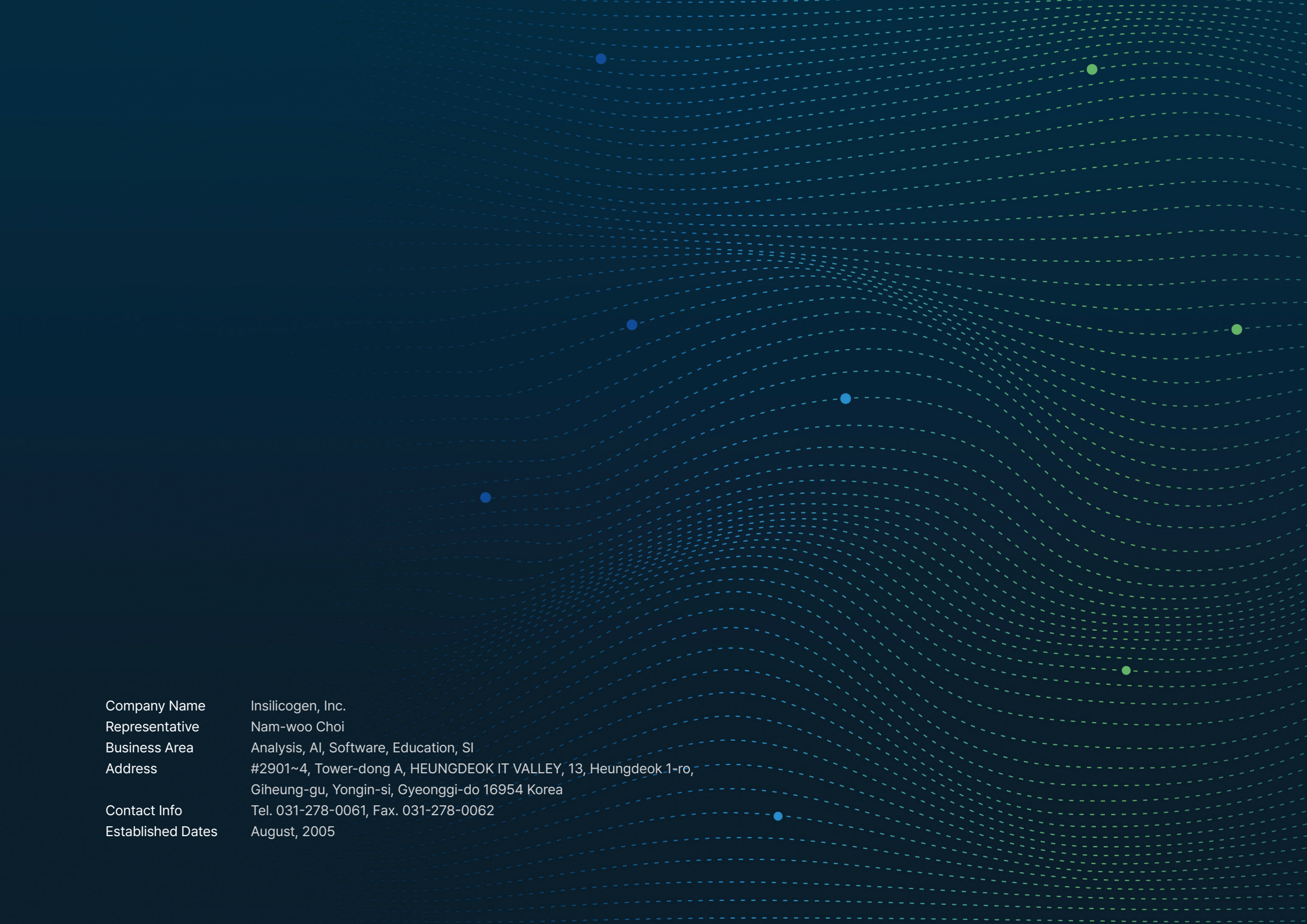
Data-Driven Diagnosis Company

We will create an AI based solution to provide diagnosis related recent knowledge which grounds public domain and onsite Information.

AIM

Data-Driven New Medicine Company

Based on BI and AI, already obtained, we contribute on repositioning drug and seeking new medicine lists.



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