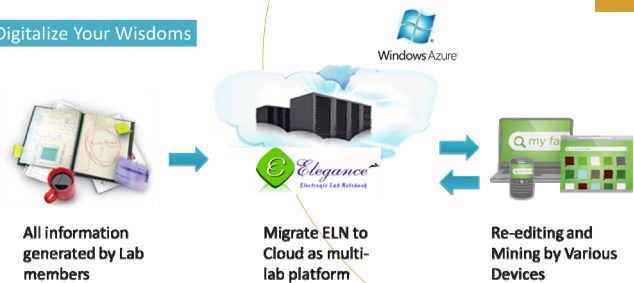


實驗室電子記錄本
ELECTRONIC LABORATORY
NOTEBOOK (ELEGANCY, ELN,
submitted)

<http://eln.iis.sinica.edu.tw>

Digitalize Your Wisdoms



Digitalization of Lab notebook from text, gif, raw data, even animations with functions of **full text search, backup, sharing** and **security** into server, notebook and even USB memory stick, Viewing/Editing them by web browser

將實驗室中所產生的各種紀錄，以電子化方式儲存於網路伺服器/筆記型電腦/USB 隨身碟，並經由網路瀏覽器方便管理、分享、搜尋、備份、列印，及與研究伙伴線上討論相關問題

Three kinds of version will be provided in the future:

1. For group use: Linux-based version
2. For small group/personal use: USB-ELN, windows/ Mac-based version
3. Cloud version, Supported by World Research on Cloud, MS Azure (2013)

將提供三種 ELN 版本:

1. 大型實驗室群組版本: 相容於 Linux 平台環境
2. 中小型實驗室與個人單機版本: USB-ELN, 可相容於微軟視窗/麥金塔作業環境
3. 微軟 Azure 雲端平台(微軟公司全球雲端研究贊助 · 2013)

Access ELN in Various Devices



更多線上研究成果(More Achievements available on Web) :

- PDA** Primer design Assistant (PDA), for PCR primer design, *NAR* 2003, <http://dbb.nhri.org.tw/primer>, 聚合酶反應核酸引子線上設計平台
- hp-DPI** Database of Protein Interactome of *Helicobacter pylori*, *Bioinformatics*, 2005, <http://dpi.nhri.org.tw/hp> 幽門桿菌蛋白質交互作用資料庫
- flyDPI** *Fly-DPI*, Database of Protein Interactome of *Drosophila melanogaster*, *BMC bioinformatics*, 2006,
- POWER** POWER, phylogenetics web repeater, *NAR*, 2005, <http://power.nhri.org.tw> 線上生物巨分子親緣關係分析平台
- MyBLAST** *myBLAST (web version)*, a BLAST platform with customized databases and results management, submitted, 客製化BLAST高速序列比對平行化平台 · 可自行建立資料庫並以條列式方式解析大量結果 · 並能透過網路分享
Web version: <http://mybioweb.nhri.org.tw/myblast>, Windows/ MAC version:<http://eln.iis.sinica.edu.tw>,
- AfterGen-Bank** An updated, value-added data gateway of gene information derived from GenBank database, submitted, <http://aftergenbank.nhri.org.tw>, 以圖像化方式擷取特定基因特徵或物種之核酸或蛋白質序列 · 並提供下載與序列比對
- HUNTER** A hub-attachment based method to detect functional modules from confidence-scored protein interactions and expression profiles, *BMC Bioinformatics*, 2010, <http://hub.iis.sinica.edu.tw/Hunter>, 以基因表現資料與蛋白質交互網路來找出具生理功能的蛋白質複合體
- Spotlight** Assembly of Protein Complexes by Integrating Graph Clusters, *Gene*, 2012, <http://hub.iis.sinica.edu.tw/spotlight> 複雜網路中蛋白質複合體鑑別平台
- PAGE** *Penaeus* Genome Database, *Marine Biotechnology*, 2011 <http://sysbio.iis.sinica.edu.tw/page>, 對蝦類基因體資料庫



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Institute of Information Science, Academia Sinica

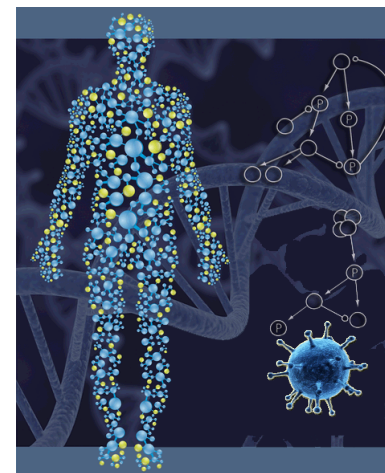
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INSTITUTE OF INFORMATION
SCIENCE, ACADEMIA SINICA, TAIWAN

以創新資訊技術來增進人類的生命品質

IT Innovations for Better Life

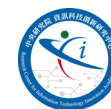


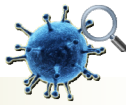
LAB OF System Biology & Network Biology

中央研究院資訊科學研究所 @iis, Academia Sinica, TAIWAN

系統生物學與網路生物學實驗室

合作單位(Collaborators) :





快速病原檢測開發平台

病原檢測晶片與基因晶片線上設計系統
Unique Probe Selector (UPS), BMC Bioinformatics (2008), BMC Genomic (2010)

<http://array.iis.sinica.edu.tw/ups>

UPS is a probe design tool for hybridization in low and high throughput experiments. UPS selects unique probes for submitted sequences and evaluates probe-to-target hybridization under a user-defined condition *in silico* to ensure the high performance of hybridization as well as low possibility of non-specific reaction.

UPS 為高專一度探針線上設計工具，所設計的探針可用於小規模核酸雜交實驗，如南方墨點法，或微陣列晶片般的大規模核酸雜交實驗，並可應用於環境基因體學、非模式生物基因體之基因表現，與病原體檢測等的小型晶片設計。



Web form for Unique Probe Selector (UPS) 2.0. Fields include: Probe Uniqueness (radio buttons for unique probe based on specific organism), Sequence (paste or file upload), Probe Length (30), Probe # for each sequence (1-10), Job note, E-mail, and Advanced Options (Salt, Degenerate probe allowed).

Generate Best Probes for each submitted sequences with

對每一條送入的序列設計單一最佳的基因探針，並經由BLAST比對驗證

```
>ABL_1
agtccccatcaaatggaactgacccgagagcctggcctacaacaaagtctccatcaagtccgagctctg
>ARG_1
ccctattcaagtggacagaccagagagctcttgcctacaatccctctcaatcaaatctgagctcggct
>EGFR_1
aagtgcctacaagtggatggatggatcaatcttacaagaatctataccacagagatgctctg
>TNF1_1
actctgggcttggcggcctctgggggctggccggggcgctcagctcctggggggcccccctatccc
>TXK_1
atgacaggtacgtcttggatgagatgctcctcttggagccaaagtcccaatcaagctccc
>TYK2_1
gtactaccggctggcggagagatggggacagcccgctgctcgtatgcccagagctgctgaaggatct
```

Send to factory for array production

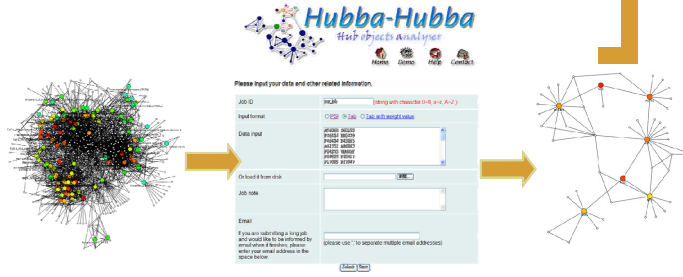
委由廠商生產高密度基因晶片



新一代藥物標的鑑定系統

複雜生物巨分子交互網路分析平台
Hub Object Analyzer, (HUBBA), Nucleic Acids Res(2008)

<http://hub.iis.sinica.edu.tw/hubba>



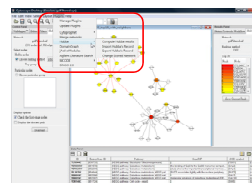
Hubba is a powerful prediction tool for hub/essential proteins with a user-friendly interface. Hubba can decipher the critical keys inside biochemical pathways and complex network, there will be significant clues to provide candidates for gene knockout and potential drug-targets for developing novel treatment in cancer cells and emerging pathogens. Here we also converted Hubba into cytoHubba, a Cytoscape Plug-in for Hub Object Analysis in Network Biology

Hubba 線上分析平台，可用以分析生物複雜網路交互作用系統中的重要樞紐分子，以圖像化手法呈現重要性來對樞紐蛋白質排名，並顯示這些重要結點之間的關連性，協助辨識疾病細胞內與感染過程中的重要網路次模組，及特定基因群所關連的小網路，提供網路醫學研究與新的治療方法的開發。為了利用 Cytoscape 的輔助與其軟體能見度，與 cytoscape 平台其他 plug-in 的協助，我們將 hubba 變成 cytoscape 的一個分析模組，稱為 cytoHubba 得以提供更多生物學家對龐大的基因網路，採取更精闢、便利的分析，進而提升生物網路分析的準確度。

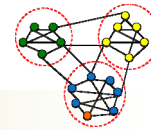


YouTube cytohubba
<http://hub.iis.sinica.edu.tw/cytohubba>

or Find it in Cytoscape



Compute the Hubba Score
綜合網路指數計算



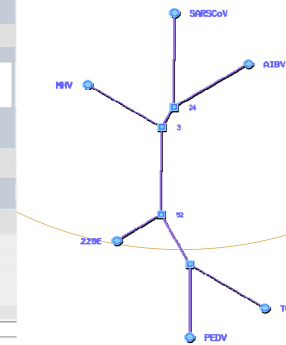
最佳化分子親緣關係高速分析平台

Phylogenetic Reconstruction by Automatic Likelihood Model Selector (PALM), (PLoS One, 2009)

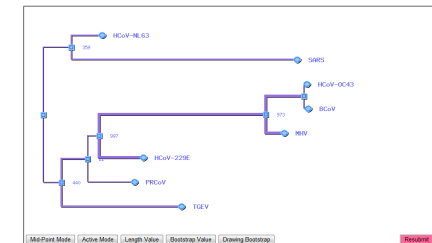
<http://palm.iis.sinica.edu.tw>



Web form for PALM. Fields include: Input Sequences (FASTA or PHYLIP format), Sequences (paste or file upload), Number of bootstrap data sets, Job Note, Enter your email, and Advanced Options (Starting Tree, Model Selection Criterion, Optimize tree topology).



Best Model Selected	Blosum62
Model Selection Criterion	AIC
AIC	4516.39
-lnL	-2249.19



Automatic phylogenetic analysis with model chosen -free approach according to the ranked score maximum likelihood in various criterion (AIC, AICc, BIC and LnL) and Interactive Tree visualization, 56 substitution models for DNA (JC69, GTR, etc.) and 112 substitution models (JTT, Blosum62, HIVb, etc.) for protein with paralleled mechanism

自動選擇最佳演化模型化之生物分子親緣關係分析平台，共有56種DNA演化模型及112種蛋白質演化模型，可供本系統同時評估，並提供互動式親緣樹檢視介面及平行化運算機制