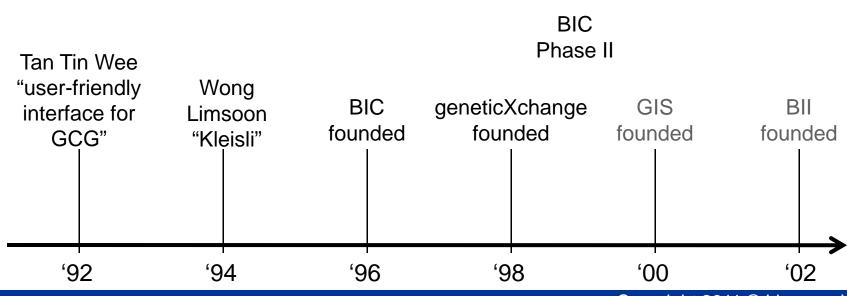
# Singapore Bioinformatics in the Early Days

Limsoon Wong
17 March 2011





### Significant Milestones





### 1<sup>st</sup> Bioinformatics Paper from S'pore



Tan Tin Wee

### **CABIOS**

Vol.9. no.5. 1993 Pages 581 – 586

### A general UNIX interface for biocomputing and network information retrieval software

B.K.Kiong and T.W.Tan<sup>1,2</sup>

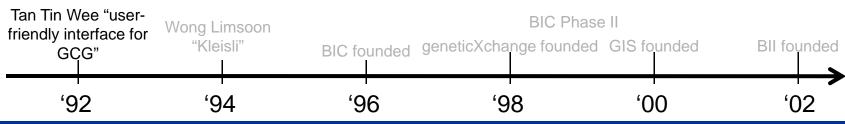
#### Abstract

We describe a UNIX program, HYBROW, which can integrate without modification a wide range of UNIX biocomputing and network information retrieval software. HYBROW works in conjunction with a separate set of ASCII files containing embedded hypertext-like links. The program operates like a

network access to remote databases. This has been hitherto difficult to achieve.

One strategy that is frequently adopted for proprietary packages in the design of unified interfaces is by writing new software or rewriting existing programs. However, the pace at which new software is being generated is faster than what a commercial package can reasonably incorporate and distribute.

### TTW is now Deputy Head of Biochem Dept in NUS



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# Kleisli --- the 1<sup>st</sup> Major Bioinformatics Solution from S'pore





Wong Limsoon

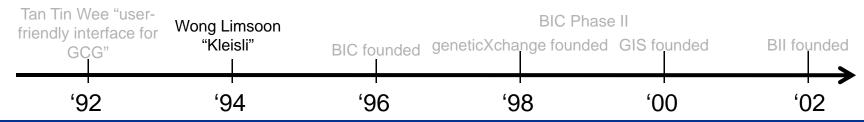


G. Christian Overton

**Applications** User query **APIs** The Kleisli Query Engine Metadata **Query language Ontologies** Complex object data model Vocabularies **Query optimizer** Wrapper Wrapper Wrapper Wrapper **₩** DB1 DB<sub>2</sub> Flat File Oracle Sybase Copyright © 2005 by Limsoon Wong

Buneman, Davidson, Hart, Overton, Wong, VLDB '95

WLS is now Head of CS Dept in NUS GCO passed away in 2000



## Integration: What are the problems?



A US DOE "impossible query", circa 1993:

For each gene on a given cytogenetic band, find its non-human homologs.

Source	type	location	remarks
GDB	Sybase	Baltimore	Flat tables SQL joins Location info
Entrez	ASN.1	Bethesda	Nested tables Keywords Homolog info

location



### Data Integration Results

### Using Kleisli:

- Clear
- Succinct
- Efficient

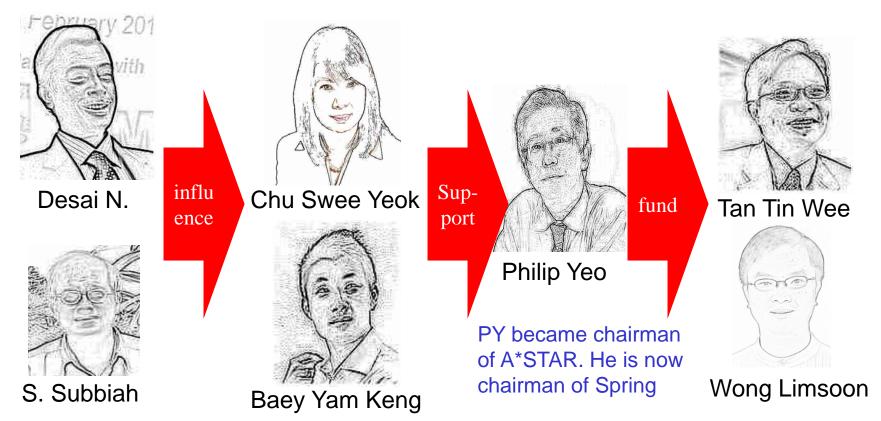
### Handles

- heterogeneity
- complexity

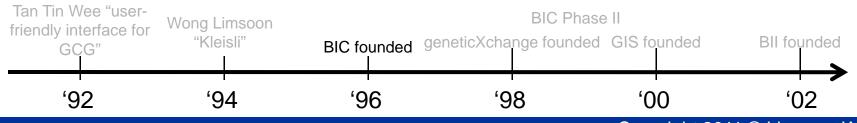
```
sybase-add (#name:"GDB", ...);
create view L from locus cyto location using GDB;
create view E from object genbank eref using GDB;
select
  #accn: g.#genbank ref, #nonhuman-homologs: H
from
  Lasc, Easg,
  {select u
   from g.#genbank ref.na-get-homolog-summary as u
   where not(u.#title string-islike "%Human%") &
         not(u.#title string-islike "%H.sapien%")} as H
where
  c.#chrom num = "22" &
   q.#object id = c.#locus id &
   not (H = { });
```



### **NUS BioInformatics Centre**



BYK is now a Member of Parliament





### Some BIC Stories

- Provided bioinfo resources for NUS
- Developed Kleisli
- Made first steps into comp bio
  - 1st structure solved in S'pore
  - WebPHYLIP

- Recruited talent
  - 1st "algorithmic" comp biologist
  - 1st "structural" comp biologist



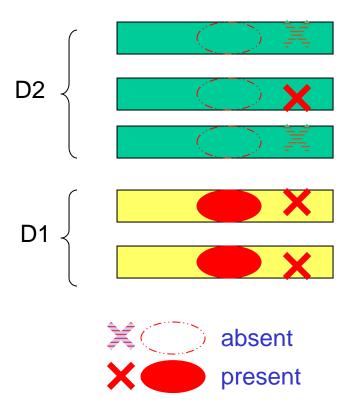
Prasanna Kolatkar



Zhang Louxin

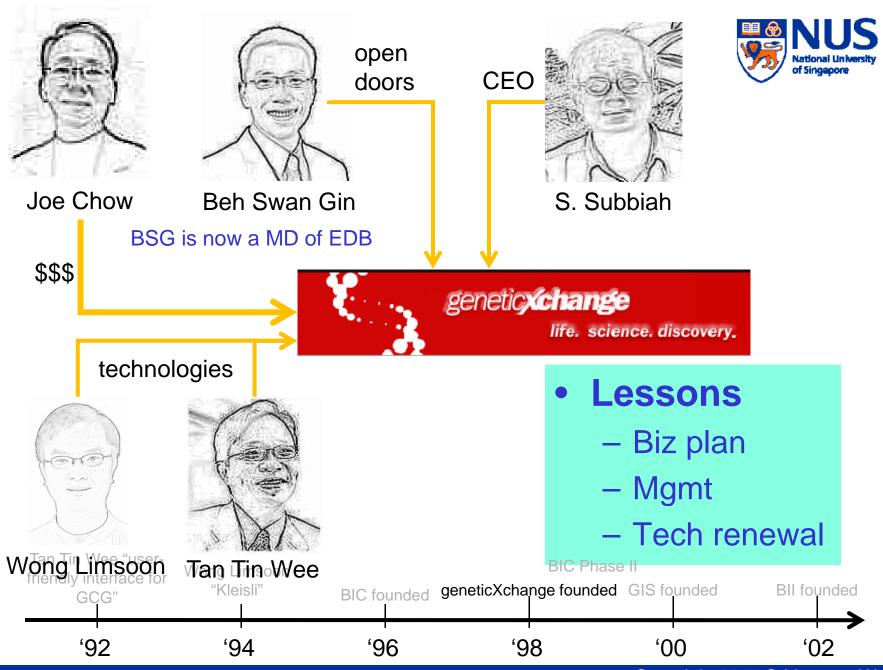
Key Mutation Sites of PTP D2

K.L.Lim et al., *JBC*, 273:28986--28993, 1998 pTyr



gi|00000|P D2 gi|126467| gi|2499753 gi|462550| gi|2499751 gi|1709906 D1 gi|126471| gi|548626| gi|131570| gi|2144715 QFHFHGWPEVGIPSDGK(
QFHFTSWPDFGVPFTPI(
QFHFTGWPDHGVPYHAT(
QYHYTQWPDMGVPEYAL)
QFHFTSWPDHGVPEHPTI
QLHFTSWPDFGVPFTPI(
QFHFTGWPDHGVPYHAT(
QFHFTGWPDHGVPYHAT(
QFHFTSWPDHGVPYHAT(
AFHFTSWPDHGVPTTD)

\* . . \*\* . \* . \*





### **BIC Phase II**





Wong Limsoon

**Peter Saunders** 

PS was Deputy Director S'pore Health Services when he passed away in mid 2000s

- Pioneer a new area in comp bio → immunoinformatics
- Pioneer a new area in bioinfo → bioNLP
- Leap frog in an established topic
- Compete in an emerging topic



# National University of Singapore

## Pioneering Immunoinformatics

### Predict epitopes, Find vaccine targets

- Vaccines are often the only solution for viral diseases
- Finding & developing effective vaccine targets (epitopes) is slow and expensive process



EVCNDQVDLYLLMDCS&SIKKHNWVNHAVPLAMKLIQQLI LNDNAIHLY**VNVFSNNAK**EIIRLHSDASKNKEKALIIIR: LLSTNLPYGRTNLTDALLQVRKHLNDRINRENANQLVVII TDGIPDSIQDSLKESRKLSDRGVKIAVFGIGQGINVAFNI



 Develop systems to recognize protein peptides that bind MHC molecules

 Develop systems to recognize hot spots in viral antigens ADSAWENVKNVIGPFMKAVCVEVEK ICGKGTRSRKREILHEGCTSEIQEQ PDEPEDDQPRPRGDNSSVQKPEENI KDENPNGFDLDENPENPPNPDIPEQ VPKNPEDDREENFDIPKKPENKHDN SPLPPKVLDNERKQSDPQSQDNNGN RNNENRSYNRKYNDTPKHPEREEHE KIAGGIAGGLALLACAGLAYKFVVP ILGEEDKDLDEPEQFRLPEENEWN





Vladimir Brusic

VB is now
Director of
Bioinfo at Dana
Farber Cancer
Vaccine Center

Victor Tong who took over from VB won a 2009 SYA for immunoinfo

# Pioneering BioNLP, Starting Molecular Connections

# Understand proteins, Fight diseases Understanding function and

 Understanding function and role of protein needs organised info on interaction pathways

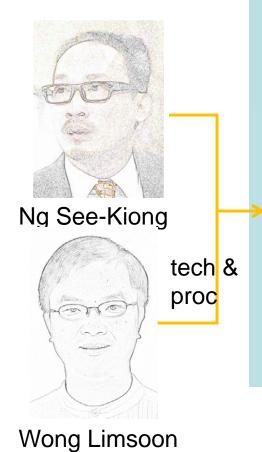
 Such info are often reported in scientific paper but are seldom found in structured databases



 Knowledge extraction system to process free text

- extract protein names
- extract interactions

MC has grown profitably to ~700 curators and engineers



Jignesh Bhate

CEO

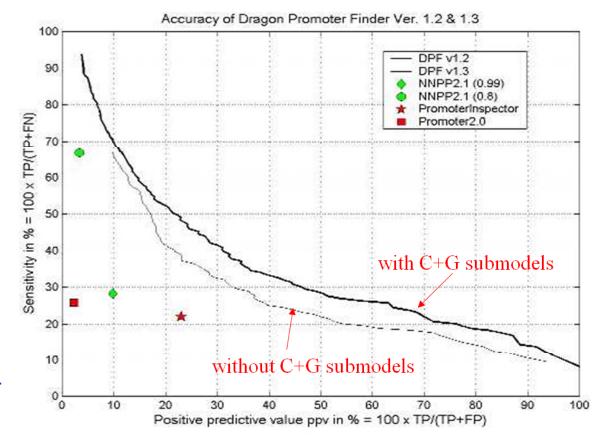


# Leapfrog in Promoter Finding



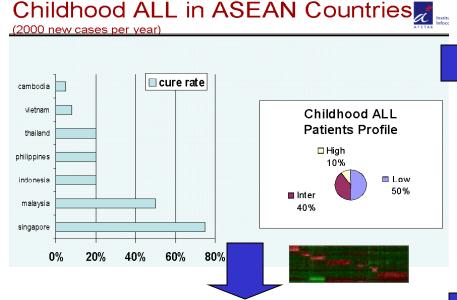
Vladimir Bajic

VBB became Director of SANBI. He is now Director of Comput Bio Science Center at KAUST



# Compete in an Emerging Topic – Gene Expression Analysis





### **Bioinformatics-optimized Tx:**

- high intensity to 10%
- intermediate intensity to 40%
- low intensity to 50%
- costs US\$100m/yr

### **Conventional Tx:**

- intermediate intensity to all
- ⇒ 10% suffers relapse
- ⇒ 50% suffers side effects
- ⇒ costs US\$150m/yr

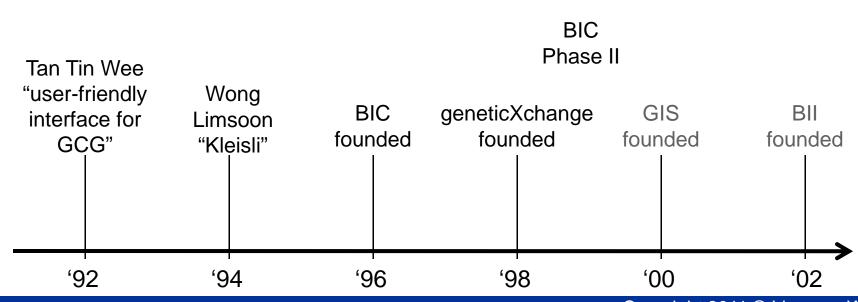
High cure rate of >80%

- Less relapse
- Less side effects
- Save US\$51.6m/yr

Yeoh et al, CANCER CELL, 2002



# The first 10 years were an exciting fruitful experience...



## Today, there are $\sim 100$ bioinfo & comp bio RSEs in Singapore. Their activities in 2008/09...



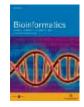
Journals edited:



**TCBB** 



**JBCB** 



**Bioinformatics** 



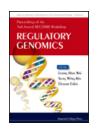
**DDT** 





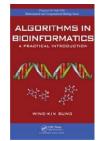
JOURNAL OF BIOMEDICAL SEMANTICS

**Books/Proceedings edited:** 



3<sup>rd</sup> Regulatory RECOMB'08 **Genomics** 





Algo in Bioinfo

- Involved in ~20 bioinformatics conf prog & org committees
  - RECOMB08, ISMB08/09, CSB08/09, GIW08/09, APBC08/09, ...
- Published ~70 papers
  - Bioinformatics, JCB, BMC, JBCB, DDT, PLoS CB, EMBO, Cell Stem Cell, NAR, Cell, JBC, TKDE, VLDBJ, SIAM J Comput, Clin Cancer Res, ...
  - ~30 keynotes & invited talks in conferences



## A photo from my first meeting with ...



# BGRS 1998, Siberia

