

*CIAR Evolutionary Biology Program  
14<sup>th</sup> Annual Meeting -- Program  
October 11-15, 2000  
The Pines, Digby, Nova Scotia*

**Wednesday, October 11**

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**ARRIVALS DAY**

**CHECK-IN**

6:00 PM                      Reception  
7:00 - 8:30 PM              Dinner buffet

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Meeting Room:	Salon A
All Meals:	Annapolis Dining Room
Reception (Wed.):	The Verandah
Reception (Sat.):	Edna Stark Room
Poster Displays:	Digby Hall
Small Groups:	The Pines Boardroom

## Thursday, October 12

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7:00 AM Breakfast

8:30 AM **Session 1. The Web of Life (Chair: Andrew Roger)**

8:30 AM Charles Delwiche  
Congruence, conflict, and organismal phylogeny in chimeric organisms

9:00 AM Peter Gogarten  
Does horizontal gene transfer shape microbial taxonomy?

9:30 AM Thomas Sicheritz-Ponten  
A phylogenomic approach for the analysis of microbial genomes

10:00 AM Jonathan Eisen  
Genome comparisons and the inference of lateral gene transfers: just because everybody's doing it doesn't mean we can detect it

10:30-11:00 **Coffee Break**

11:00 AM Camilla Nesbo/Yan Boucher  
Is there a core of nontransferrable genes?

11:30 AM Mark Ragan  
Surrogate methods for detecting LGT

12:00 PM General discussion: Is there any consensus on what the questions and answers really are?

12:30 PM **Lunch**

2:00-3:00 PM **Set-up your posters in Digby Hall**

**Poster Session: 3:00-5:30 PM**

Refreshments available. Poster presenters should be present at this session, but posters will remain up through Saturday.

5:45-7:30 PM **Dinner**

7:30 PM **Session 2. Coalescents and Molecular Evolution (Chair: Marc Feldman)**

7:30 PM Joe Felsenstein  
Coalescents, microorganisms, and deep divergence (and likelihood, of course)

8:00 PM Bruce Rannala  
Coevolution, cospeciation and gene coalescence

8:30 PM Brian Golding  
Methods to aid the determination of allelic histories

9:00 PM Wayne Maddison  
What is phylogeny?

9:30 PM General discussion

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## Friday the 13th

7:00 AM      **Breakfast**

8:30 AM      **Session 3. General Genomics (Chair: Mike Zuker)**

8:30 AM      Terry Gaasterland  
Comparative Genomics: Annotation of the *Drosophila melanogaster* genome

9:00 AM      Stephen Michnick  
Dynamic visualization of expressed gene networks in living cells

9:30 AM      Tim Littlejohn  
Integrated bioinformatics systems for genome and evolutionary research

10:00 AM      Nadia El-Mabrouk  
Reconstructing ancestral genomes by reversals and multiple gene duplication

10:30-11:00      **Coffee Break**

11:00 AM      David Sankoff  
Gene families and genome phylogeny

11:30 AM      Rob Charlebois  
Genomic phylogenies

12:00 PM      General discussion: Is genomics really rocket science?

12:30 PM      **Lunch**

*AFTERNOON: Small group meetings, informal talks, recreation*

5:45-7:30 PM      **Dinner**

7:30 PM      **Session 4: Big, thought-provoking issues (Chair: Rosie Redfield)**

7:30 PM      Walter Gilbert  
Introns and modules in ancient conserved genes

8:00 PM      Tom Cavalier-Smith  
Serial origins of Eubacteria, Archaeobacteria, and Eukaryotes

8:30 PM      Andrew Roger/Jan Andersson  
Bacterial genes in the eukaryotic nucleus

9:00 PM      Paul Liu  
Intein origins and evolution

9:30 PM      Robert Hirt  
A gene discovery program in *Trichomonas vaginalis*: the usual and the "un"-usual in an eukaryote genome

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## Saturday, October 14

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- 7:00 AM      **Breakfast**
- 8:30 AM      **Session 5. Organellomics (Chair: Patrick Keeling)**  
8:30 AM      Jeff Palmer  
Evolutionary transfer of mitochondrial genes to the nucleus: When, what, how, and why?
- 9:00 AM      Mike Gray  
Evolution of the mitochondrial genome within the green algal/land plant lineage
- 9:30 AM      Franz Lang  
A comparative analysis of jakobid mitochondrial genomes
- 10:00 AM     Gertraud Burger  
Cyanophora paradoxa and its relationship to red and green algae: insights from complete mitochondrial DNA sequences
- 10:30-11:00 **Coffee Break**
- 11:00 AM     Naomi Fast  
Plastid-targeted enzymes and the origin of red-algal secondary endosymbionts
- 11:30 AM     Sue Douglas  
The cryptomonad nucleomorph
- 12:00 PM     General discussion: Haven't we learned enough about organelles by now?
- 12:30 PM     **Lunch**
- 2:00 PM      **Session 6. A short but exciting session on RNA metabolism, followed by a free-for-all discussion on what to do with 10 million (Canadian) dollars (Chair: Ford Doolittle)**
- 2:00 PM      Chuck Daniels  
The evolving transcription system of the Archaea
- 2:30 PM      Skip Fournier  
Effects of nucleotide modification in eukaryotic ribosomal RNA
- 3:00 PM      Ford Doolittle  
If I had ten million dollars. Plans for the new Genome Canada Centre and what it might mean for CIAR. Advice and consent.
- 6:00 PM      Reception (Edna Stark Room)  
Awarding prizes for best student/postdoc talk or poster
- 7:00 PM      **Dinner**
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**Sunday, October 15:**

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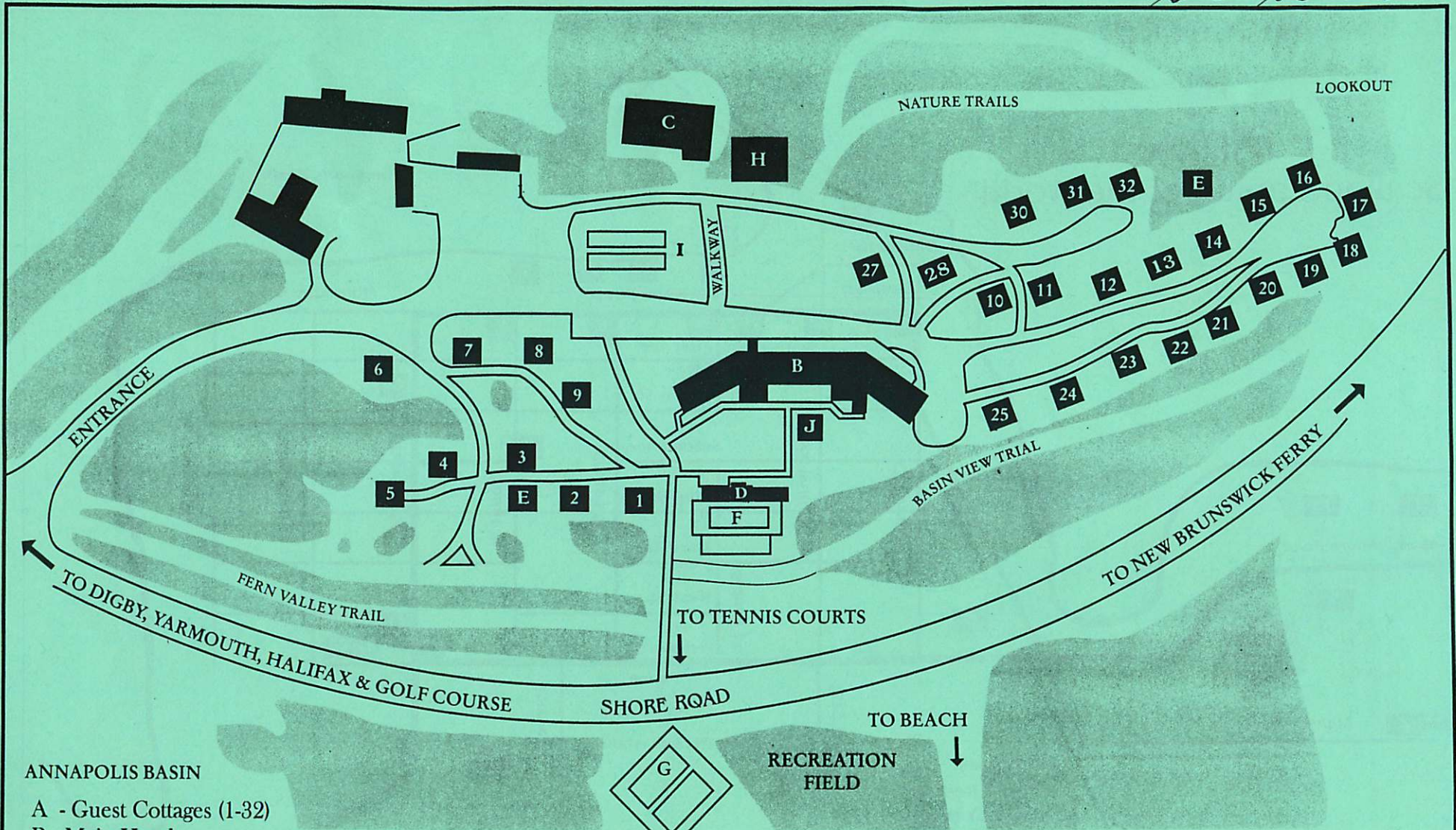
**DEPARTURES**

**-- SCHEDULE OF SHUTTLE PICK-UP TIMES WILL BE POSTED**

7:00 AM      Breakfast buffet, as usual

# The Pines Resort

*see over →*



## ANNAPOLIS BASIN

A - Guest Cottages (1-32)

B - Main Hotel

- Dining Room - Lower Level
- Gift Shop - Lower Level
- Grande Lounge - Main Level
- Garden Room
- / Culinary Studio - Lower Level
- Pines Room - Main Level
- Verandah - Main Level

C - Digby Hall

- Salon A, B, and C - Lower Level

D - Pool Patio Cafe

E - Ice / pop

F - Swimming Pool

G - Tennis Courts

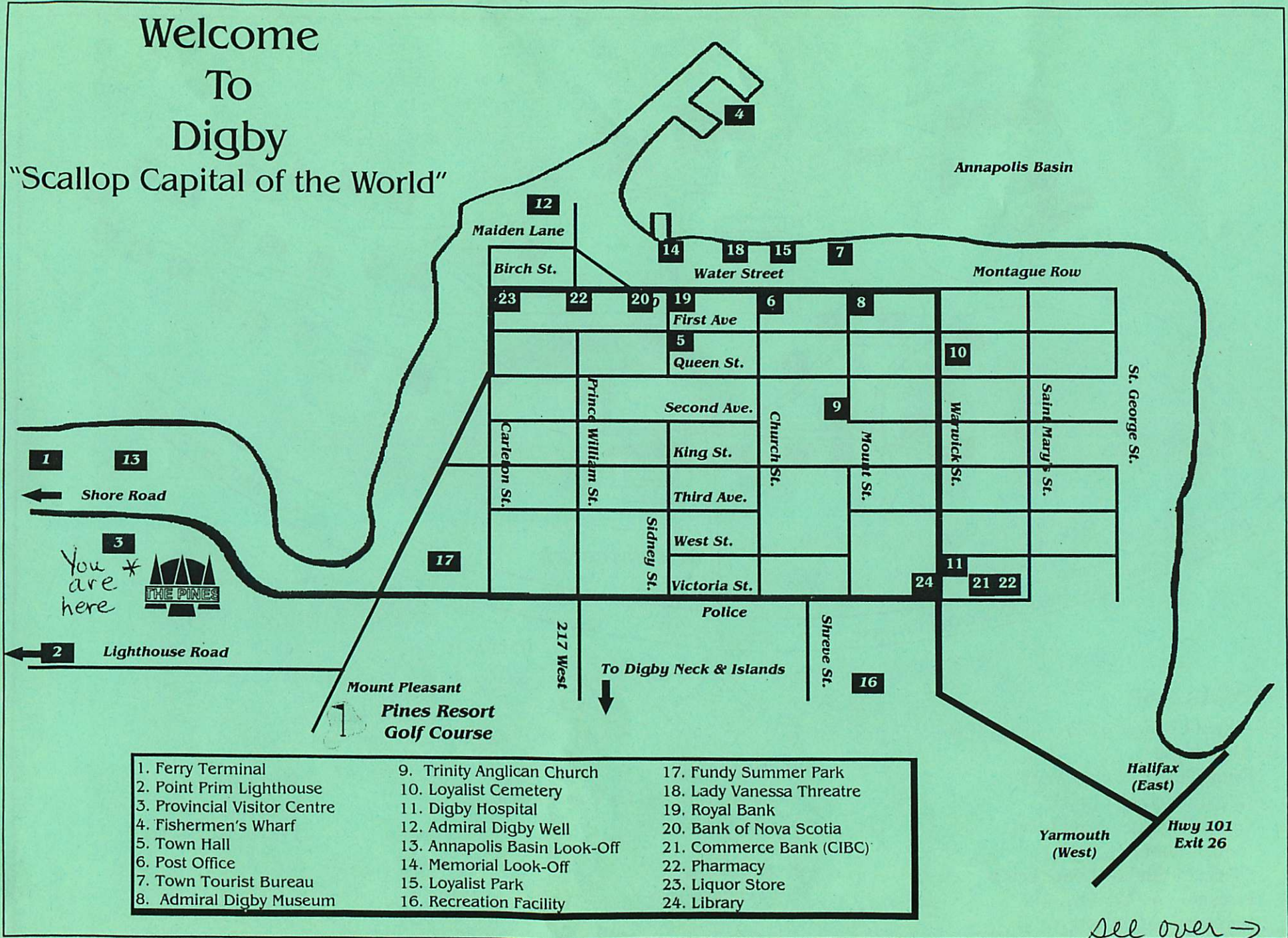
H - Playground

I - Shuffleboard

J - Garden Terrace

# Welcome To Digby

"Scallop Capital of the World"



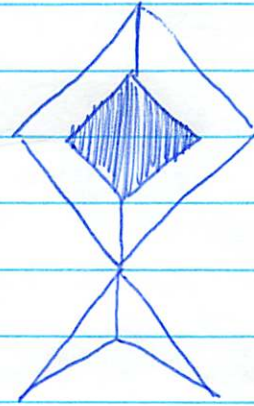
- |                              |                              |                          |
|------------------------------|------------------------------|--------------------------|
| 1. Ferry Terminal            | 9. Trinity Anglican Church   | 17. Fundy Summer Park    |
| 2. Point Prim Lighthouse     | 10. Loyalist Cemetery        | 18. Lady Vanessa Theatre |
| 3. Provincial Visitor Centre | 11. Digby Hospital           | 19. Royal Bank           |
| 4. Fishermen's Wharf         | 12. Admiral Digby Well       | 20. Bank of Nova Scotia  |
| 5. Town Hall                 | 13. Annapolis Basin Look-Off | 21. Commerce Bank (CIBC) |
| 6. Post Office               | 14. Memorial Look-Off        | 22. Pharmacy             |
| 7. Town Tourist Bureau       | 15. Loyalist Park            | 23. Liquor Store         |
| 8. Admiral Digby Museum      | 16. Recreation Facility      | 24. Library              |

See over →

## C. Delwiche

### - primary

- glycoctophytes
- green algae
- red algae



HGT

TI + DR  
close relatives

### - secondary

- dinos
- apico
- ciliates



## P. Bogen

- what is impact on phylogeny



- ~~H~~

- species could be defined by HGT.

- protobacteria are so b/c they exchange genes

- deepest branches should be between species that do not freq. exchange genes (either mechanically or due to environment).

- ~~deep branches should~~



If this is true - then should have  
coalescence

Is there a different MOE of evolution  
for X-changed genes.

Protein genes have less recomb  
betw. distant relatives

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T. Schenck



Get his system

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Is there a core? C. Nesbo

what about a stable core between phyla?

don't have  
enough  
sequences

isoprenoid biosynthesis

DOMAINS  
SLIDING  
WINDOW

Trees  
can agree  
for  
wrong  
reasons

## M. Ragan - Surrogate Methods for detecting HGT.

### Problem

LGT inferred from incongruence:

- need stat support
- tree topology can be misled by
  - lack of signal
  - rate variation
  - paralogy
- unusual selection of LGT genes

### Other methods

subset of ORFs

Method	Authors	Ecoli
GC-base composition	Och + Lan	756
atypical HMM	Hays + Borodovsky	649
out distribution	Ragan + Charlebois	474
phylog. discordant seqs	Charlebois	418

How many ORFs?

- but the HMM methods  
is using same principle as JL

JL finds all genes/ISS?

JL finds recent

- Uli Gogarten

- if trees are due to transfer  
certain patterns should be  
different ages.

450  
503-844-0304

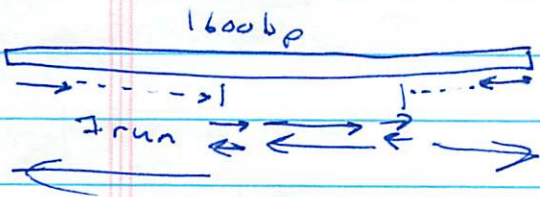
W. Maddison

- what is phylogeny?
  - a robust history
  - an important history

2400 m  
4:20

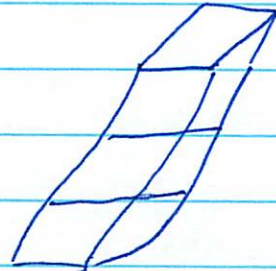
- phylogeny is to biology  
as einstein is to physics

- flat view of history/biology = similarity
- phylogeny adds "curvature" to biological space
- wrapping similarity along branches of phylogeny



- 1 run

- GRUNTS = 6\$
- TEMPLATE = 2\$
- PCR = 2\$



\$10/FRNA = 3,000,000

# Simulate LGT

## Parameters

- # of environments
- # of codon usage groups
- # of GC groups
- # of competency groups
- # tree shape
- # rate variation
- # of genes exchanged

① - starting genome

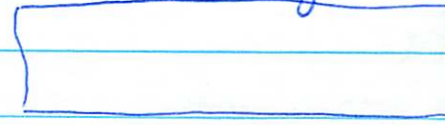
- variation in GC, codons
- protein interactions
- pathway

② vertical inheritance

- divergence of
- GC, codon
  - gene loss
  - duplication
  - selection
  - converging
  - inversions
  - replication origins

③ LGT

- evol. distance
- selection
- environment
- GC / codon
- proximity



## Jeff Palmer

- found epiphagus
- seems to be less transfer in euk., but there are some. For example homing group I introns.

+ transfer  
- evolution of mt genes to nucleus

- most of organelle genes we transferred or lost early in organelle evolution

- continues to be transfer of genes

- largest mt genome contains all genes of smaller ones.

- genetic cote divergence limits transfer in some lineages

- some genes are "easy" to transfer

- DNA mediated events can be bad b/c of lack of RNA editing

- look for mt gene loss, by blotting mt DNA.

- targeting to mitochondria can also affect likelihood of transfer.

→ easier to lose  
→ early gene loss



## ribosomal proteins

- 14 genes in flowering plant ancestor
- many losses in evolution
- MOST have been transferred to nucleus
- could be early transfer and then parallel gene loss
  - ↓
  - favor idea that each loss represents a separate transfer

## EXAMPLE - rps10 transfer in *A. thaliana*

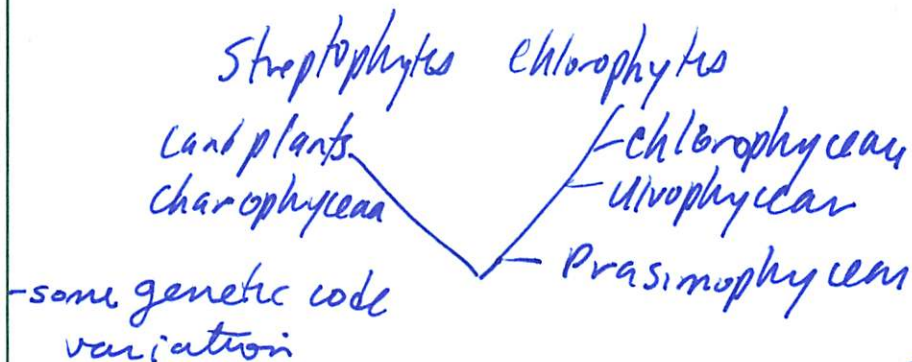
- frequently insert into other genes

How many  
copies of this  
present in both.

Mike Gray - land plants + green algae mt

1st 2 genomes  
reduced deamid Chlamydomonas } very different  
complete Marchantia

expanded  
ancestral



- check A. thaliana for duplications  
in mt or p / asked

pull out syn. best hits



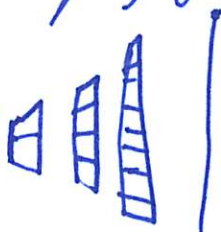
## Nucleomorph Genome

- only in cryptomonads + chloroalveolates
- compact genome

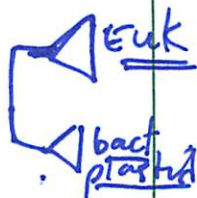
- rad3, rad25

- many overlapping genes
- many introns (mostly in r. proteins)
- mostly housekeeping genes.

## Apicomplexan plastids



- Alveolates
- including dinoflagellates and ciliates
- secondary endosymbiosis
- no nucleomorph left  
but plastid surrounded by four membranes.
- GAP-C - 2 versions in Dinoflagellates  
- these are nuclear genes.
- GAPDHs from many bugs





## Tom Cavalier-Smith

### Model

bacteria v. old

Archaea middle aged

Eukaryotes younger

### why

- ① fossil evidence of eukaryotes not v. old
- ② much of the evidence could be bacterial
- ③ many fossil protist

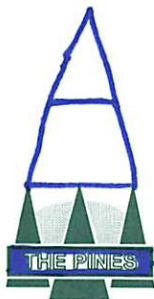
## Ron Pearlman

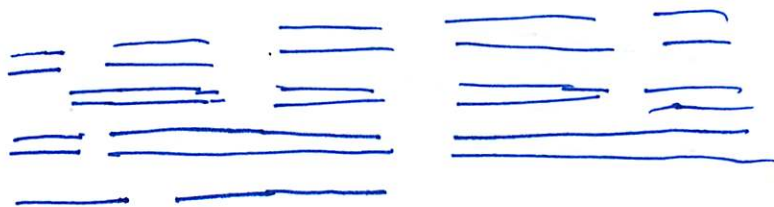
- Paramecium

## Las. S Jermin

Assessment of stationarity in seq. data

- ~~most~~  
- med to assess data



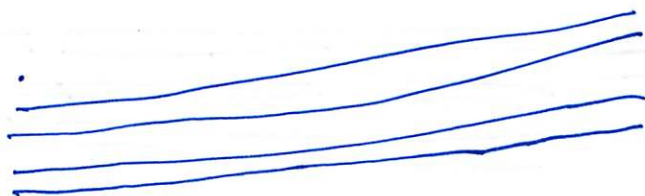
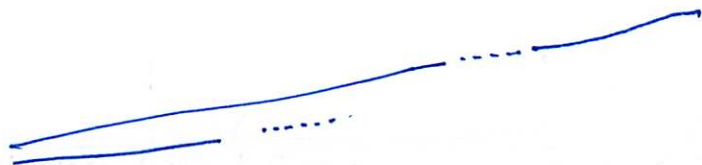


DEMG LGQRQ	EKLYDKDDWKR
DDLAMGKWY	KRRELIV
	DYRS

Hand-drawn musical notation with a table structure. The table has two columns and two rows of text. There are three triangles: one above the top-right cell, one below the bottom-left cell, and one below the bottom-right cell. The table is enclosed in a double-line border.



Are intars in the same place old?  
How determine position?



D. Sankoff

## Genome Analysis

why don't bacteria conserve gene order?  
but conserve clusters.

- f(x) constraints
- transfer
- selfish operons
- ordinary evolution

Genome - circle of circumference 1

Rearrangements - all of length  $f$

Gene cluster - interval of length  $d$

Probability that 2 random  
intervals of length  $d$  and  $f$  intersect.  
 $= \underline{2} \times$  length of shorter interval.

mean size of interval grows exponentially  
for large inversions but linearly for  
small inversions.

when



## R. Charlebois - Genomic Phylogenomics

rRNA tree

why are extreme thermophiles at base of bacterial tree?

NS Proportion Tree (90 of shared ORFs)

pull out phylog. discordant genes  
+ then do the rest.

recA misleading in Bacsu.

guarantee high bootstrap

As per  
Peter.

Plucking out homogenized  
genes.

Don't assume 16S tree  
is right

It's more interesting  
to use  $\neq$  genes.

