

# BioPivot: Applying Microsoft Live Labs' Pivot to Problems in Bioinformatics

Stephen Taylor, CBRG

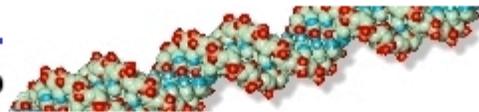
GMOD Europe 2010

# Introduction

- Visualization of large numbers of genome regions
- Querying and filtering properties of genome regions
- Pivot and BioPivot tools
- Open discussion of other applications of technology

# CBRG

Computational **B**iology  
Research **G**roup



## Introduction

You are here: CBRG home

### CBRG Home

- CBRG personnel
- computing support
- contact details
- search CBRG web site

### CBRG Accounts (molbiol)

### Analysis tools

### Training courses

### Tutorials

### Unix help

### Examples

### Papers

### Collaborative data

### Presentations

### Oxford-only section

### FAQ: CBRG + UNIX

### FAQ: Bioinformatics

### Links

## Welcome to the CBRG

The Computational Biology Research Group (CBRG) provides [computing support](#) for bioinformatics analysis at the University of Oxford. We have expertise in many aspects of bioinformatics (sequence analysis, microarrays, proteomics and integration). We especially encourage collaborations that require writing custom software, bioinformatics tools and databases.



An account with the CBRG has many [benefits](#) and gives automatic access to a large number of molecular biology computing packages and to numerous biological databases.

We are based at the [Sir William Dunn School of Pathology](#) and at the [Weatherall Institute of Molecular Medicine](#). Full details can be found on the [contact details](#) page.

## Bioinformatics analysis tools online:

A wide range of bioinformatics programs are available online via [EMBOSS Explorer](#). You will need a molbiol username and password to use these tools.

Other web tools available include: [BLAST](#), [MASCOT](#) and [BASE](#) (see [full list](#)).

# Over 50 different GBrowse databases

- Many labs started wanting GBrowse
- Human
- Mouse
- Bacterial
  
- Time series
- Arrays
- ChIP-Seq
- RNA-Seq

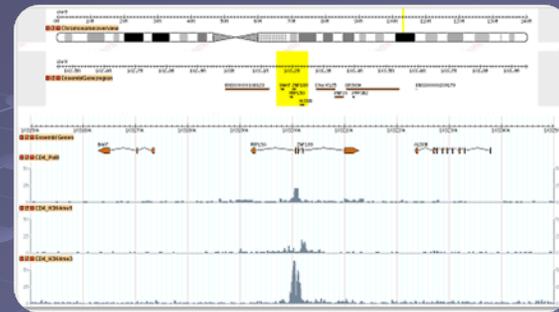
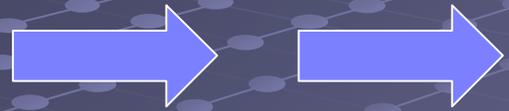
# Next Generation Sequencing

- Histone modification Data
- ChIP-Seq
- Interaction cis/trans data
- PCR amplified regions
- RNA-Seq
- Exome Sequencing/SNP detection

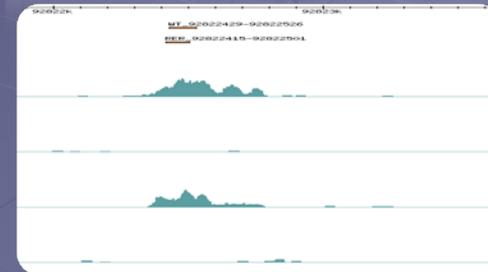
# ChIP-Seq example

NGS reads

Map



Peak pick

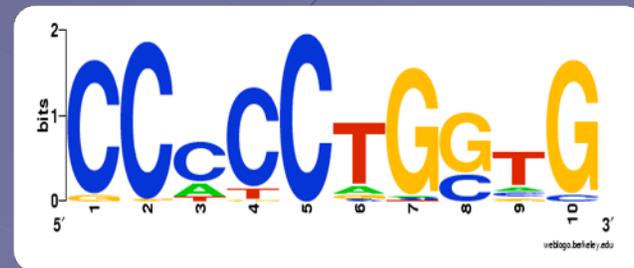


Extract sequences from features

Motif extract



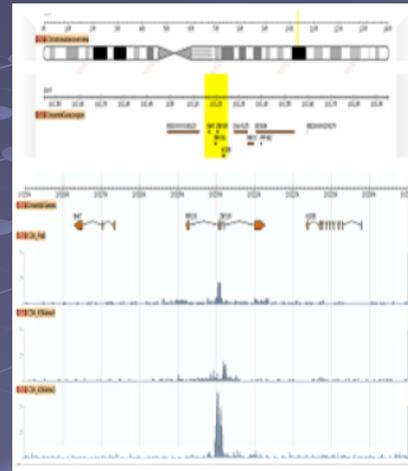
Weblogo



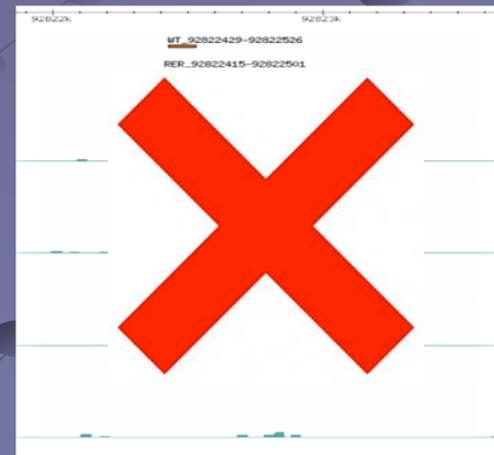
# ChIP-Seq

NGS reads

Map



Peakfind



# Problems

- Experimental conditions
- Antibody
- Peak finders give false positives
  - Lots of parameters
  - Must choose a suitable cut-off
  - Eyeballing lots of peaks

# Further Analysis

- Which of my peaks overlap with:
- Genes
- Exons
- Promoters
- CpG Islands
- Areas of conservation
- etc

# Traditionally

- Make spreadsheet of data with links to Gbrowse/UCSC regions of interest
- Click/Filter various parameters
- Add data to spreadsheet each new analysis

**SLOW!**  
**BORING!**

# Deep Zoom Tech

## ● Blaise Aguera y Arcas (TED 2007)



## ● Seadragon/Photosynth

- <http://www.seadragon.com/showcase/>

## ● Microsoft Live Labs' Pivot

- <http://www.getpivot.com/>

# Wouldn't it be cool...

- To use this in bioinformatics...?
- Take thousands of regions of interest of genome
- View and Filter seamlessly on metadata

# BioPivot Tools

- GFF3 of ROI
- Ninth column contains 'facets'
- Choose your GBrowse or UCSC Browser View
- Run the command:

```
gff32pivot my.gff3 -dzi -generateimages -conf mytypes.cfg  
-o my.cxml -browser gbrowse2
```

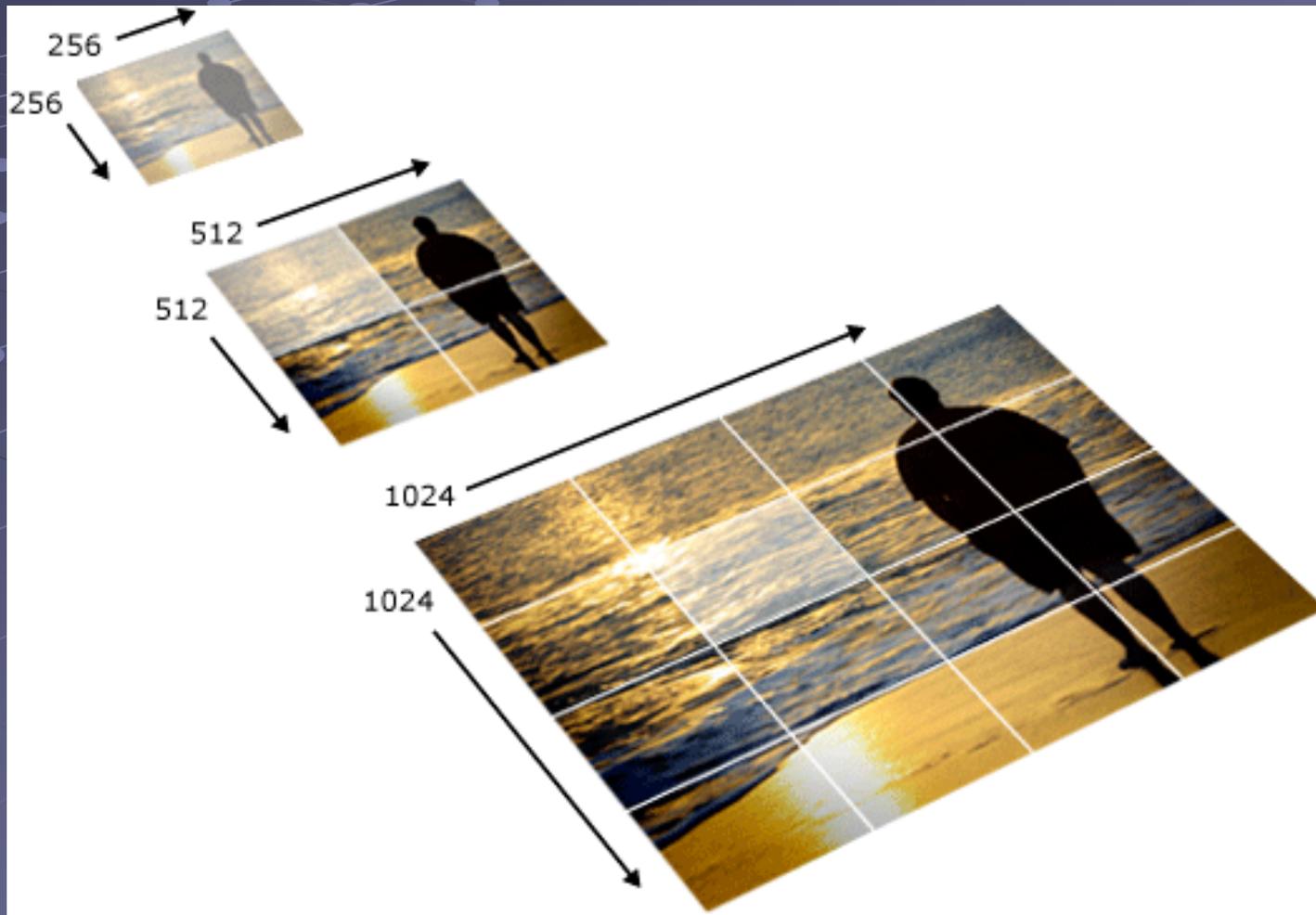
# BioPivot Tools

- Parsers for peakfinders
- Annotate a GFF3 file
  - nearest gene
  - exons, introns, intergenic, intragenic
  - TSS/TES up and down stream regions
- Overlaps of GFF3/BED features

# Open Source

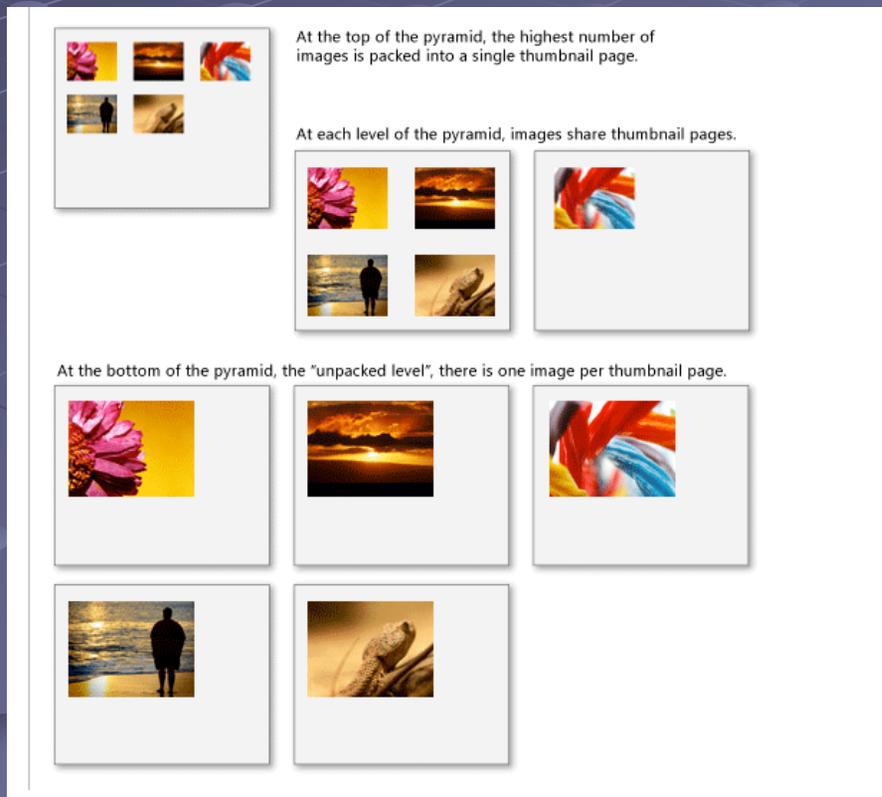
- Zoomable User Interfaces (ZUIs)
- OpenZoom
  - <http://openzoom.org/>
- SDK for Flash, Flex & AIR
- APIs

# Deep Zoom Image



# Deep Zoom Collection

## Groups of tiled images



# CXML File

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```

# To Do

- Installation scripts
- Deploy in a web browser using Silverlight
- RNA-Seq parsers e.g. cufflinks, DESeq
- Get feedback from the community
- What else can we do with this tech?
- <http://www.cbrg.ox.ac.uk/data/biopivot>

# Acknowledgements - Code

## ● OpenZoom

- <http://openzoom.org/>

## ● Cisgenome

- <http://www.biostat.jhsph.edu/~hji/cisgenome/>

## ● BEDtools

- <http://code.google.com/p/bedtools/>

# Acknowledgements - People

- Jim Hughes
- CBRG Team
- GMOD Team