

modENCODE Data Coordination Center

www.modencode.org

modENCODE Scope



- Transcriptome
- Regulatory elements
- Chromosome and chromatin associated elements
- Small and microRNAs
- Origins of replication

modENCODE is a Resource



DCC: Delivers data to you, the community

We ask you to tell us what you want

DCC is listening

~ 100 Year History of Community Cooperation



- Resource/ Stock Centres (BDGP, CGC, DGRC...)
- Shared reagent resources
- Genome projects (single, multiple)
- Annotation jamborees
- Online resources
- Drosophilal C. elegans coordination (modENCODE)

modeNCODE in Relation to ENCODE ENCODE

- Both working on functional elements of DNA
- Exchange of technologies with ENCODE (UCSC)
- modENCODE advantages:
 - can do experimental validation
 - identify functional elements in repetitive sequences
 - Comparisons between worm and fly (and human...)
- This community must set an example for ENCODE

Who are the DCC?



- Principal Investigators
 - Lincoln Stein (PI)
 - Suzi Lewis (coPl)
 - Gos Micklem (coPl)
 - Jim Kent (coPl)
- Wiki and Web Site
 - Sergio Contrino
 - François Guillier
- ENCODE Contacts
 - Kate Rosenbloom
 - Galt Barber

- Data Managers
 - E.O. Stinson (fly)
 - Nicole Washington (fly)
 - Sheldon McKay (worm)
 - Zheng Zha (worm)
- Infrastructure
 - Richard Smith
 - Kim Rutherford
 - Chris Mungall

The DCC's Charge

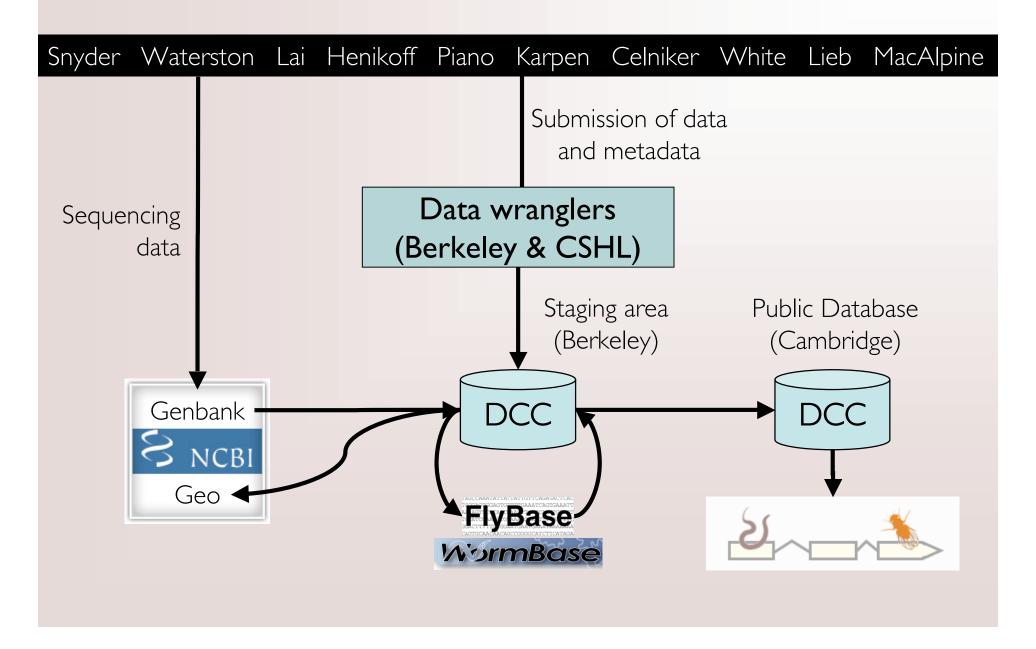


- Provide support for data submission and tracking
- Ensure data integrity and consistency
- Integrate with other information sources
- Make available to the research community

Types of Queries

- Retrieve data by:
 - Protocol type
 - Submitting lab
 - Platform (e.g. Affy Chip set 5.x)
 - Experimental attribute (e.g. Show me the expression array results that use a sliding window > of 30bp)
- Ask useful questions:
 - What antibodies were produced in rabbit that work for ChIP-chip?
 - What is the EST evidence for a particular gene model?
 - What gene models lack cDNA evidence for their TSS?
 - What genomic regions show transfrags that don't have RNA Pol II binding sites within 500bp?

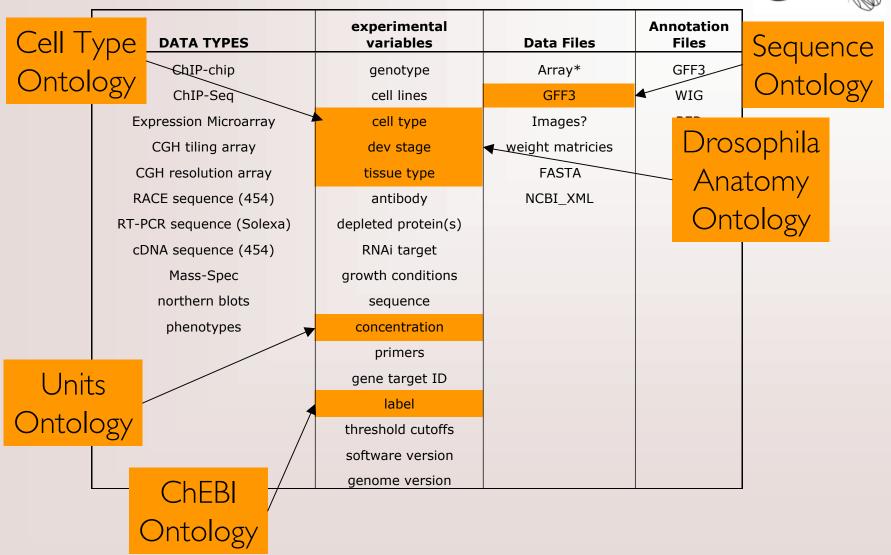
modENCODE & the DCC





DATA TYPES	experimental variables	Data Files	Annotation Files
ChIP-chip	genotype	Array*	GFF3
ChIP-Seq	cell lines	GFF3	WIG
Expression Microarray	cell type	Images?	BED
CGH tiling array	dev stage	weight matricies	
CGH resolution array	tissue type	FASTA	
RACE sequence (454)	antibody	NCBI_XML	
RT-PCR sequence (Solexa)	depleted protein(s)		
cDNA sequence (454)	RNAi target		
Mass-Spec	growth conditions		
northern blots	sequence		
phenotypes	concentration		
	primers		
	gene target ID		
	label		
	threshold cutoffs		
	software version		
	genome version		







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	primers	Prev	Previously provided	
	gene target ID			
	label	des	scriptions	strom
	threshold cutoffs	expe	rimental	project
	software version	3,49		p. 0,000
	genome version	4		

Biological Investigation Report Tabular Format: BIR-TAB



- A superset of microarray submission formats (MAGE-TAB)
- Extensive support for controlled vocabulary
- Supports any protocol that can be abstracted as an operation with inputs and outputs

Steps in Validation



- Syntax checking
- Only terms from specified controlled vocabularies
- External identifiers exist
- Agrees with previously supplied protocol and reagents descriptions
- Check format of data files (currently WIG, GFF3, and BED supported)
- Load into database
- Generate downstream output files

Why Consistency



- Comparison, CompaRison, Comparison
- Without consistency there can be no comparison





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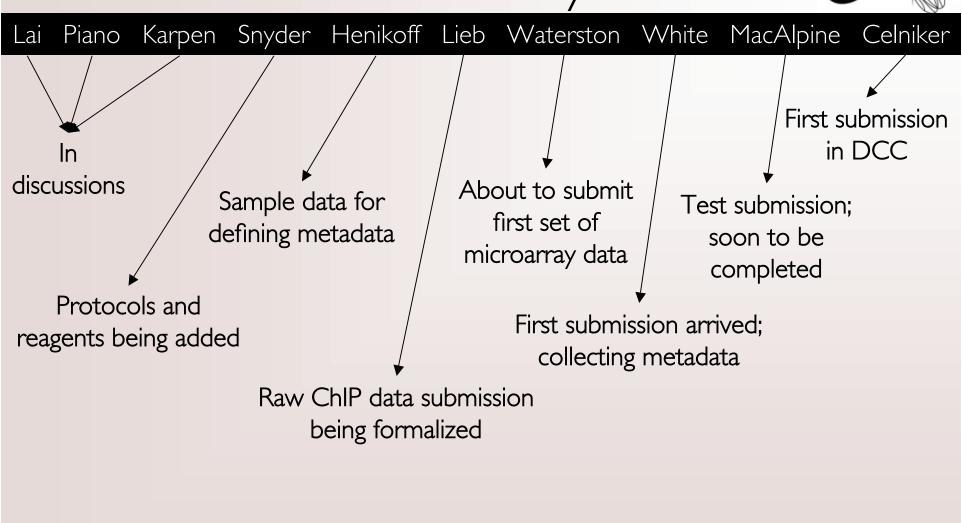
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modENCODE Q & A



- Royal Palm Salon 4
- Personal question and answer sessions
- Ask for Richard, Nicole, Gos or EO









