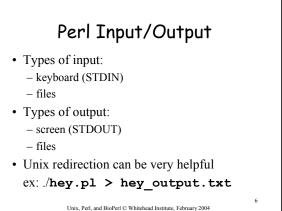
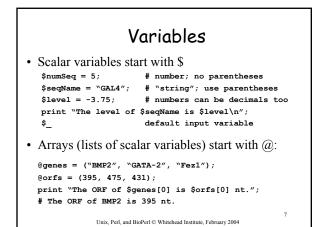




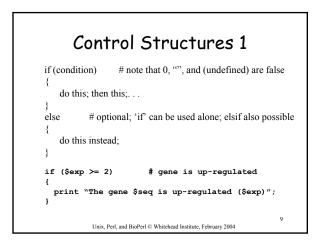
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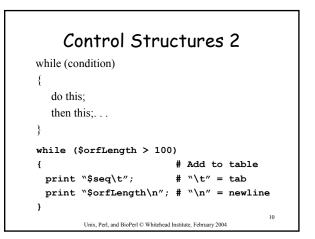
welcome to the urse.\n"; 1 or ey.pl •

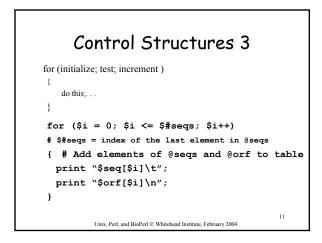


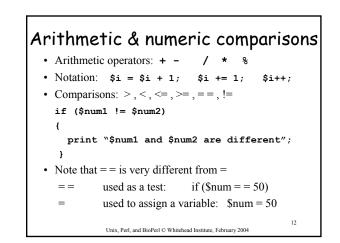


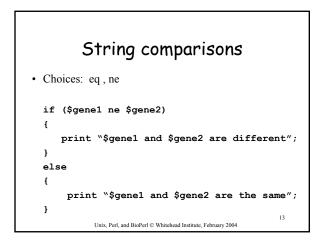
Perl functions - a sample					
print	tr///	closedir	open	m//	
chomp	mkdir	split	close	die	
length	chdir	join	chmod	rename	
substr	opendir	pop	uc	use	
s///	readdir	push	lc	sort	
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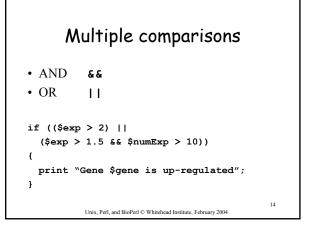


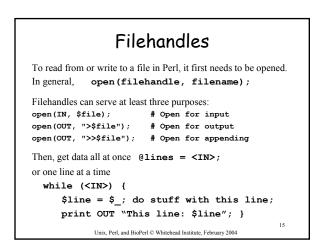


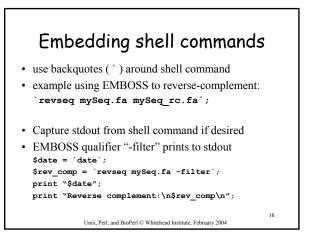


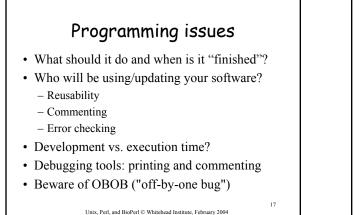


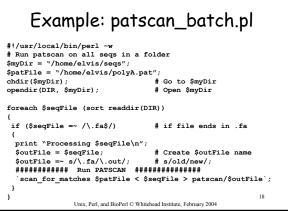








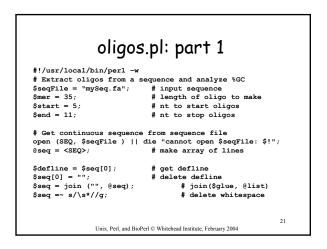


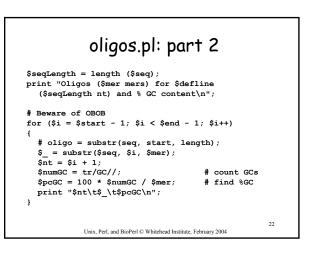


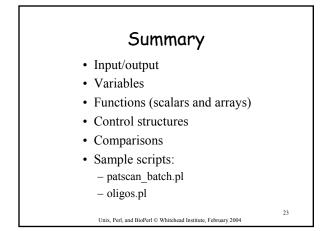
### 

## Basic steps for oligos.pl Open fasta sequence Get raw sequence Extract oligos Analyze oligos Print out results (Modify script to analyze multiple seqs)

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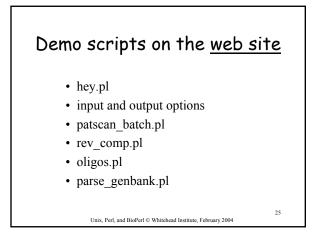




# For more information, books:Learning Perl (Schwartz et al.) - O'Reilly

- The Perl CD Bookshelf O'Reilly
- Beginning Perl for Bioinformatics Tisdall
- Using Perl to Facilitate Biological Analysis (Stein) in *Bioinformatics* (Baxevanis & Ouellette)

#### AND several good web sites (see course page)



### Exercises

- Retrieving and aligning a list of humanmouse orthologs
- Retrieving a set of genes encoding growth factors, extracting their proximal promoters, and analyzing them.

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