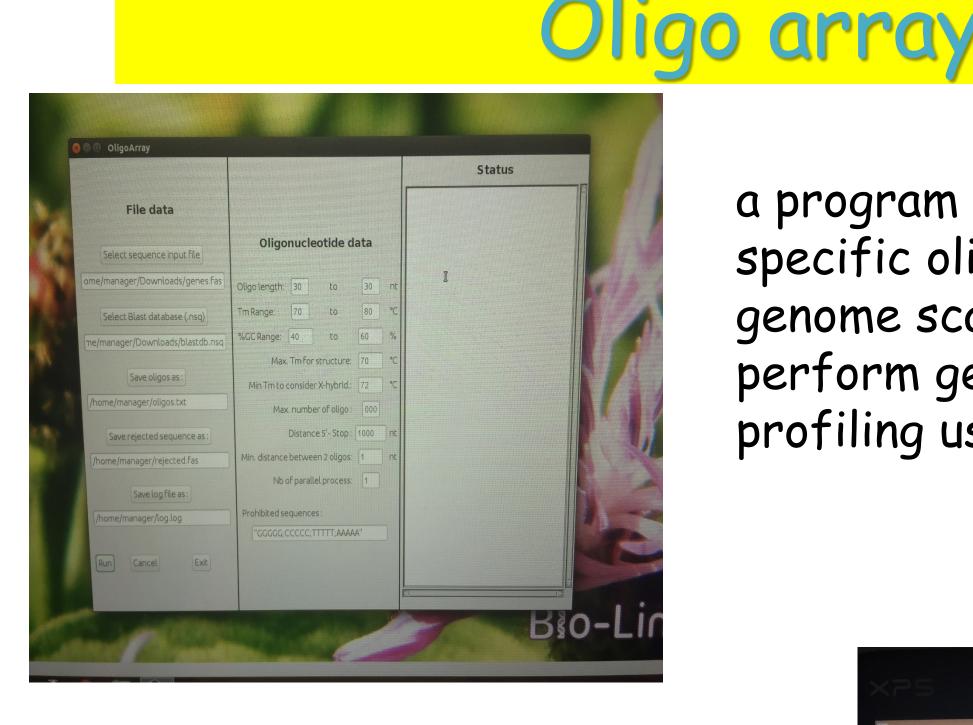
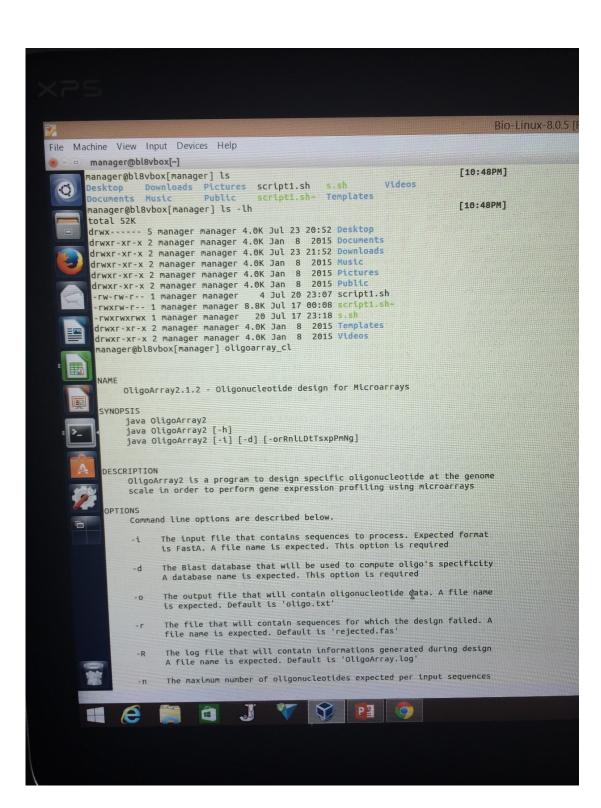


The Department of Chemistry & Biochemistry, University of California San Diego, 9500 Gilman drive, La Jolla, California



specific oligonucleotide at the genome scale in order to perform gene expression profiling using microarrays

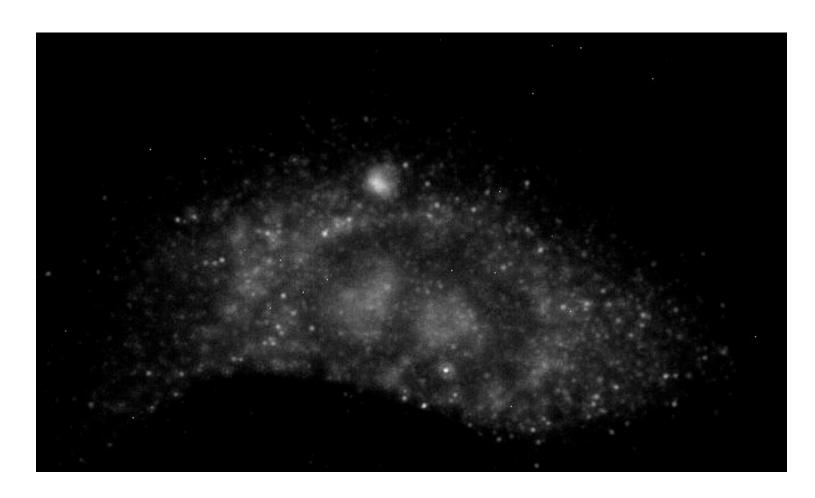
A command-line interface or command language interpreter (CLI), also known as command-line user interface, console user interface, and character user interface (CUI), is a means of interacting with a computer program where the user (or client) issues commands to the program in the form of successive lines of text





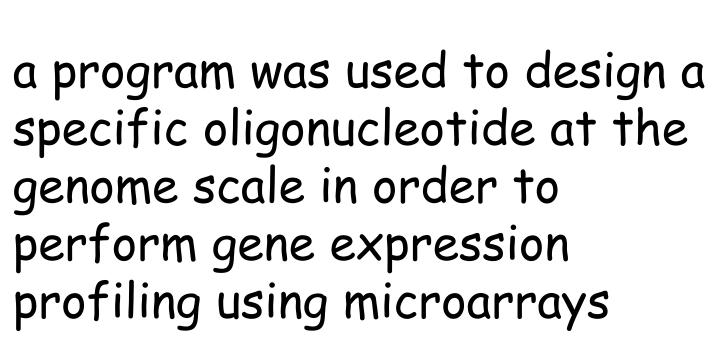
F.I.S.H. probe spots under epifluorescence microscope

The majority of fluorescence microscopes, especially those used in the life sciences, are of the epifluorescence design shown in the diagram. Light of the excitation wavelength is focused on the specimen through the objective lens



Fluorescence In Situ Hybridization (F.I.S.H.)

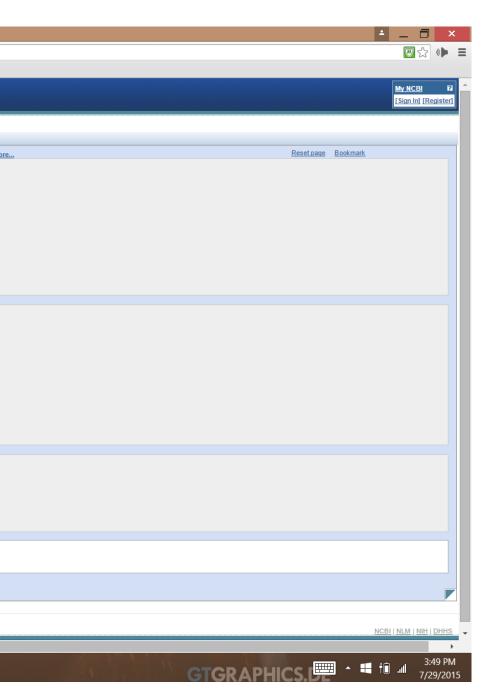
Estevan Negrete, Robert Foreman, Dr. Anna Pilko, Dr. Roy Wollman



| | Blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome Learn LabVIEW i Sixclear LabVIE I High School Co J Tools Orbital E |
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| BLAST® | Basic Local Alignment Search Tool ent Results Saved Strategies Help |
| CBI/ BLAST/ blastr | tn suite Standard Nucleotide BLAST |
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| Enter Query S | Sequence BLASTN programs search nucleotide databases using a nucleotide |
| Enter accession r | number(s), gi(s), or FASTA sequence(s) 😡 Clear Query subrange 😡 |
| | From |
| Or, upload file | Choose File No file chosen |
| Job Title | Enter a descriptive title for your BLAST search 😡 |
| Align two or m | more sequences 🛞 |
| Choose Sear | rch Set |
| Database | O Human genomic + transcript O Mouse genomic + transcript O Others (nr etc.): Nucleotide collection (nr/nt) ▼ |
| Organism Optional | human (taxid:9606) Exclude + Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown @ |
| Exclude Optional | □ Models (XM/XP) □ Uncultured/environmental sample sequences |
| Limit to | Sequences from type material |
| Optional Entrez Query Optional | You Tube Create custom database |
| Program Sele | lection |
| Optimize for | Highly similar sequences (megablast) More dissimilar sequences (discontiguous megablast) Somewhat similar sequences (blastn) Choose a BLAST algorithm @ |
| BLAST | Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences) |
| Algorithm param | Show results in a new window meters |
| | |
| /right Disclaimer P | BLAST is a registered trademark of the National Library of Medicine. |
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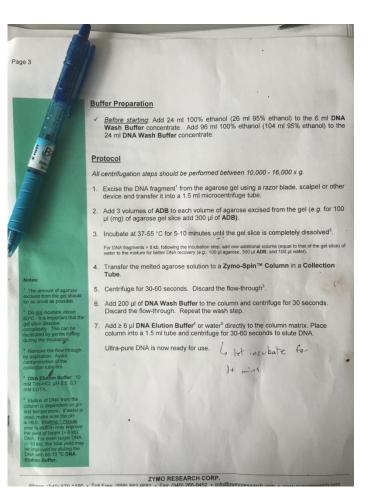
The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

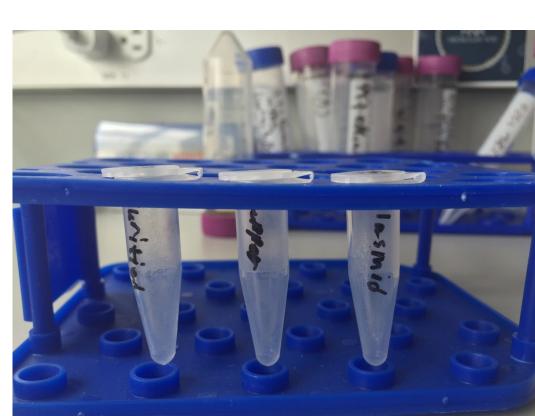




In situ assembled reporter construct

(6313) BstZ17I (6272) BsiW 5070) Fragment 2.RE 5914 .. 5933) Neo-(5894) RsrII (5575...5592) Neo-R (5496) PflFI - Tth1111 5158 .. 5169) SV40-promote



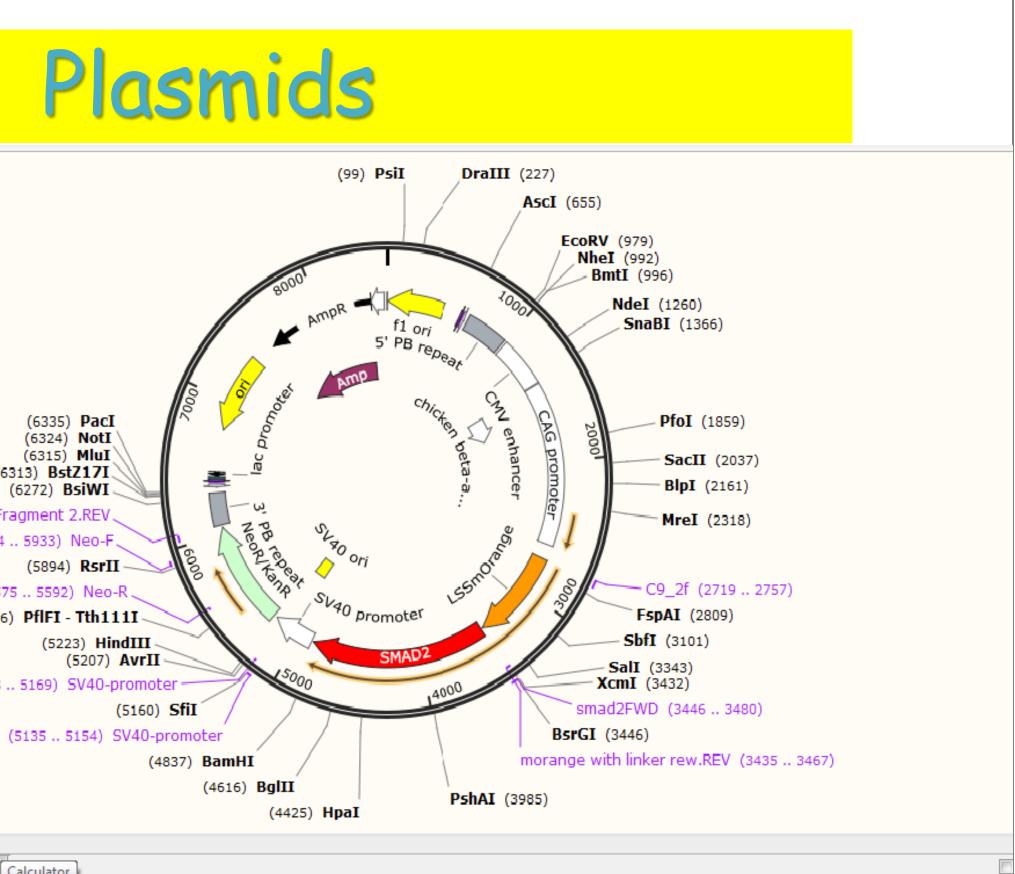


Gel electrophoresis is a method for separation and analysis of macromolecules (DNA, RNA and proteins) and their fragments, based on their size and charge









Following protocol to purify DNA



Polymerase chain reaction, or PCR, is a laboratory technique used to make multiple copies of a segment of DNA. PCR is very precise and can be used to amplify, or copy, a specific DNA target from a mixture of DNA molecules