

Applications of Bioinformatics in Cancer Treatment

Steve Martinez, Victor Olivares 13356 Eldridge Ave, Sylmar, CA 91342



Data Collection

The first step is to collect the data. Data can be gathered yourself or taken from an existing source. One source of data that is useful for cancer treatment is the National Cancer Institute's Genomic Data Commons Data Portal, which has a repository of genomes taken from cancer tumors.

-> C @	https://www.ensembl.org/nor	n upins/inh/i	rdex	··· 🐨 🕸	IN ED 3
Human (GRCh38.p10) +					
Search Human (Homo saplens)			What's New In Human release	e 91	
Search all + cotogories + Search Alaman			Monarray Probe Mapping Lipdaw Celerral database references update COUMIC data update		Mars news
Hudi + g. BRCA2 or 17.63892002-64036237 or m1	333049 or osteoarthritis				
Genome assembly: GRCh38.p10 (bCA,00001465.25) More internation and attalation Directional EPAA asspanses (FASTR)			Gene annotation What can I find? Provin coding and non- cOVA and patient sequences, non-coding Uses about this penetulal	ooding germe, aplice saviants, 1954a.	Paste III Blickie DMD soft
Convert your data is GRCHOE exercitiaate			Download genes, cDNAs, rcRNA ;	eterni (FASTA)	N
		erne Hall you are ha	nggy to receive all cookies. Further details allow	t nor póvany and cookie policy i	oer be hoed here. X
In the cooline to entrieves the analolity of our \bullet Repeatery \times \bullet \rightarrow \bigcirc \bigcirc \bigcirc \bigcirc \bullet	ebole: Pyra contrae, we'l een https://portal.gdi: Genere gov/	repository		tour phracy and cookie policy o	W. 60 I
n une coolies la metarica Re assolity of our = Pepository X +	idade. E più confisia, well ann Inges//portal.gdr. detem goe' fions leatures available - See	repository			
Repeatery x + 	idade. E più confisia, well ann Inges//portal.gdr. detem goe' fions leatures available - See	repositariy Analysis tab on t			W. D I
the set evolution is a weaklown the availably of our a- proposition y x + weak sector (concessition) and set operate them sector (concessition) and sector (concessition)	Holde II pro continue, evel anno hosper//yours.gale cancer.gon/ Mora Instances available - Sees sone information. Projects Files (310 statement	epository Analysis tab on t & Exploration	the GDC Data Portal	Ο Ω Q. Marage Sets	IN (D) I Dianica X Dianica X
Argunatory	Name//ports our care port Name//ports our care port Name //ports our care port Name //ports our care port Name // Projects Files (310 Name Name Name // Projects Name	epository Analysis tab on I & Depinvation 1.859) Case	the GOC Cash Portal & Analysia es (12:553)	Ο Ω Q. Marage Sets	IN © 3 Denks× Denks×
An extensive to endows the exactling of our of the exactling to endows the exactling of th	Alabite Types contribute, and search International Alabite Types contribute and thermations and thermatio	epository Analysis tab on I & Depinvation 1.859) Case	the GOC Cash Portal & Analysia es (12:553)	← ♥ ☆ Q. Uterage Sets	IN © 3 Denks× Denks×
Argunatory	Adata Proceedina, with see https://portul.gol: cancer.gov/ https://portul.gol: cancer.gov/ https://portul.gol: cancer.gov/ https://portul.gol: cancer.gov/ minutession/ files	epository Analysis tab on I & Depinvation 1.859) Case	In GOC Data Portal (* Anaryan es (22.509) Protect	← ♥ ☆ Q. Uterage Sets	N CO E Dennes # Dannes # no Cangoy
Reporting to extende to the scale for t	Adata Proceedina, with see https://portul.gol: cancer.gov/ https://portul.gol: cancer.gov/ https://portul.gol: cancer.gov/ https://portul.gol: cancer.gov/ minutession/ files	repeatury Analysis tab on 6 Experience Primary Ste 20 of 316,858 (se Piete Name n TCGA, AB	the GOC Date Purel. e Anarysa es (32,559) Presc Presc Tess	C. Manga Bas G. Manga Bas Bas S	N C I Duning M Particular I No Cangony Pros Mars

Data Input

Mutations, or variant bases, are identified by workflow software. Workflow software generates a Variant Call Format file(VCF). VCF is used in bioinformatics for storing gene sequence variations.

Human hg18	•	chr12	•	:hr12:17,3	31,833-1	7,374,52	9 Go	# •	+ 4		< 🖵			- 11			ш	+	
		_	-	_		_			-			-	_	_		_	_	_	
		p13.32	p13.2 p1	2.3 p12.1	p11.21	q12	q13.12	q13.3 q14	12 q15	q21.2	q21	32 q22	e q23	2 q2	411 9242	2 0	2432		
		-						42 kb											
	NUME CATA FILE CATA TYPE		1	17,340	kb	- 1	17,350 kb			ĩ	17,360 kb			17,370 kb					
R.UMICH.201ohpes.vol.gz			1 11											1111				Π	
6984																			
00986				1.1			1.10			1 H H	1.1								
00989									1.1									11	
6994		1.00	1 1		11 1		i 11		1 1								1		
7000							1		11										
07037		1.01	1 1		11.1		1 1			1111	1 I I	11 1	11 111			1 11		11	
07048			1		11 I I				11							1		11	
07051				11	T I I I		1 1 1 1 1		1 1		111	11 I				1		11	
07056					1111				1 1										
7346			I I		11 1	1											11.1	111	
07347			1 1	11	11 1		1 11					1 1						11	
7357																	11.	111	
10847			1 11						1 1									11	
10851			1.11		2														
1829			1.11		•		11111												
11830			1																
11831																			
11832											111								
11840					11.11		()II.												
11843							1 1 1												
11881																			
11892					1111						÷н.		u 10						
11893 11894																			
11894																			
11918					1.1														
11919		1.00	i i		11 I.		i 11		11				1			•	100		
11920					1.1.1.1		1 1				111								
11931			1 1		11.11	1			11	1.11	1.1								
11932							1		11								11	11	
11933			1 1		II I	1	i 11									1	1		
11992			1				1	1.1		1		1					11		
11993			1.511		1.0	1	1 1		1 1	1.11	111	111		111		1.10	11	1	
Seq genes																			
		-																	

Data Output & Communication

iCAGES is a software that identifies cancer driver genes/variants and optimal drug treatments. It inputs VCF files specific to patient's tumor mutations. Then, it outputs the best candidate drug to treat the patient.

