



Informatics on High-throughput Sequencing Data

(Summer Course 2020)

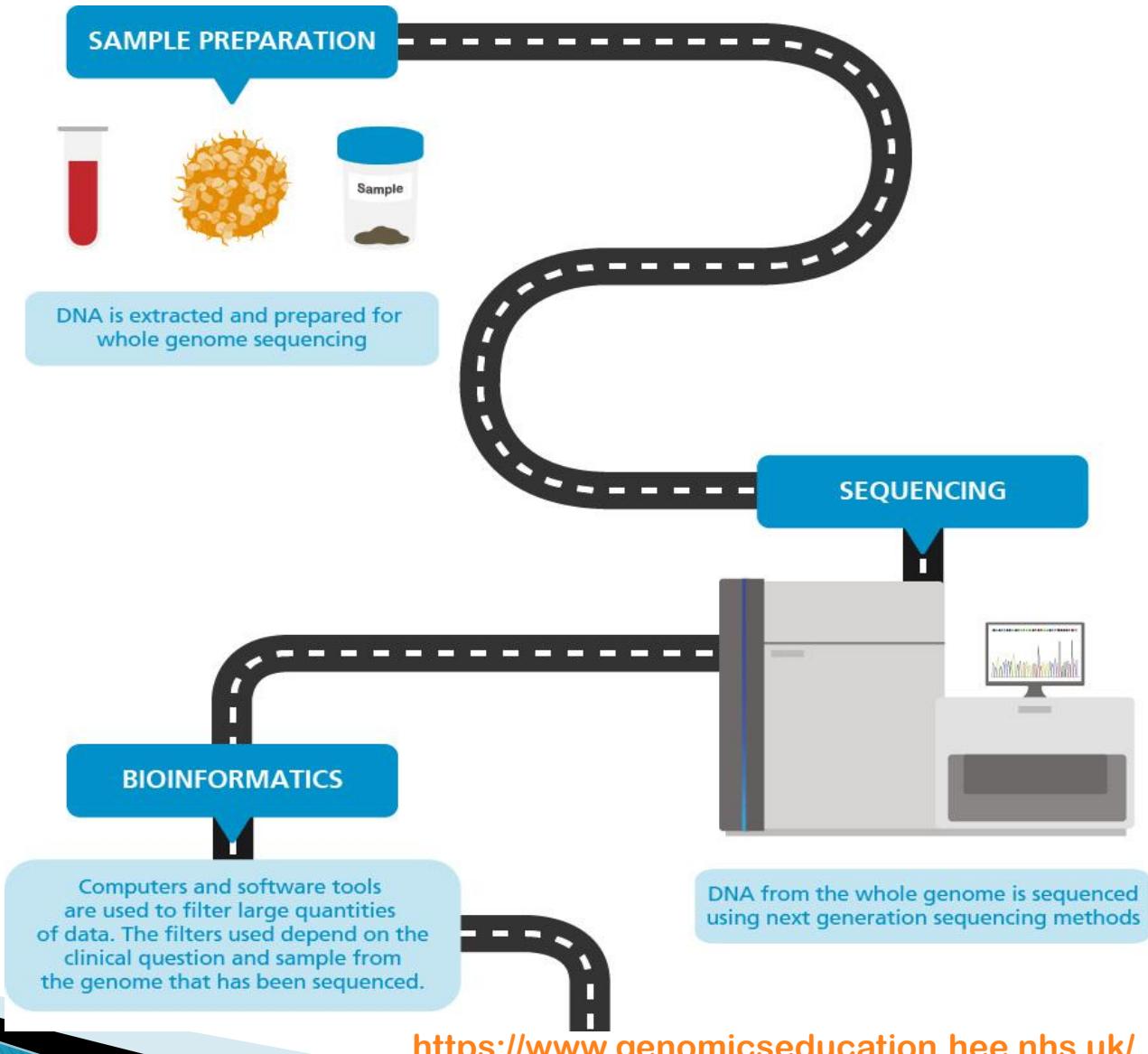
Day 1



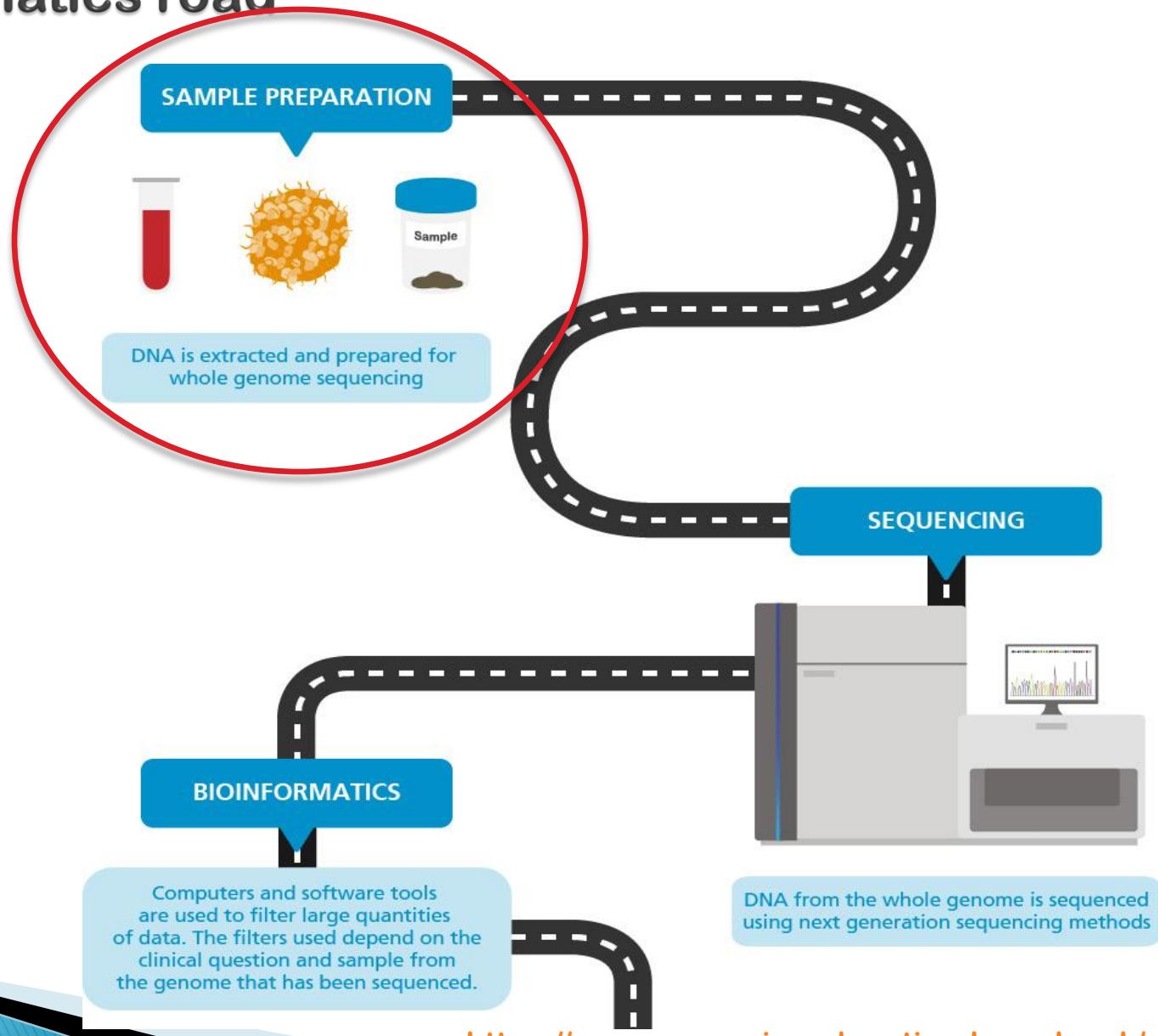
Agenda

- ▶ Introduction to Sequencing technologies.
- ▶ Difference among **Bioinformatics**, **Medical Informatics**, and **Biomedical Informatics**.
- ▶ How to Survive in Bioinformatics Field.
- ▶ Bioinformatics Career in Egypt.
- ▶ Setup our working environment

Bioinformatics road



Bioinformatics road



Prepare a sequencing library

Step 1: Isolate the DNA



Step 2: Break the DNA into small fragments.



We do this because DNA is three billions bases long and the sequencing machines can only sequence short (200-300 bp) fragments.

Prepare a sequencing library

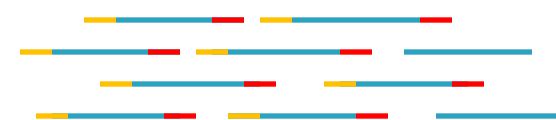
Step 1: Isolate the DNA



Step 2: Break the DNA into small fragments.



Step 3: Add sequencing adapters.



The adapters do two things:

- ✓ Allow the sequencing machine to recognize the fragments.
- ✓ Allow you to sequence different samples at the same time, since different samples have different adapters. (**save time and money**)

Prepare a sequencing library

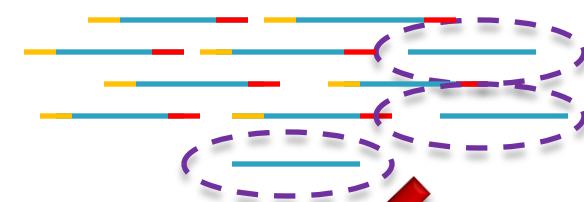
Step 1: Isolate the DNA



Step 2: Break the DNA into small fragments.



Step 3: Add sequencing adapters.



Note:

This step does not work 100% of the time (some fragments are not recognized by machine, so they are not represented in the sample)

Prepare a sequencing library

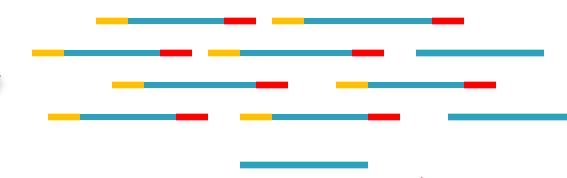
Step 1: Isolate the DNA



Step 2: Break the DNA into small fragments.



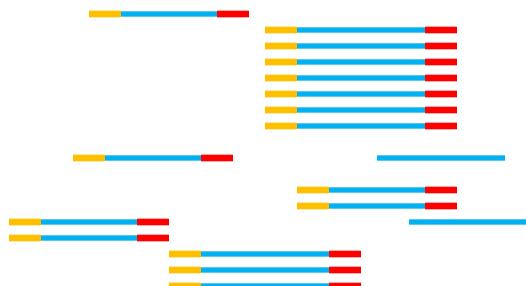
Step 3: Add sequencing adapters.



Step 5: QC

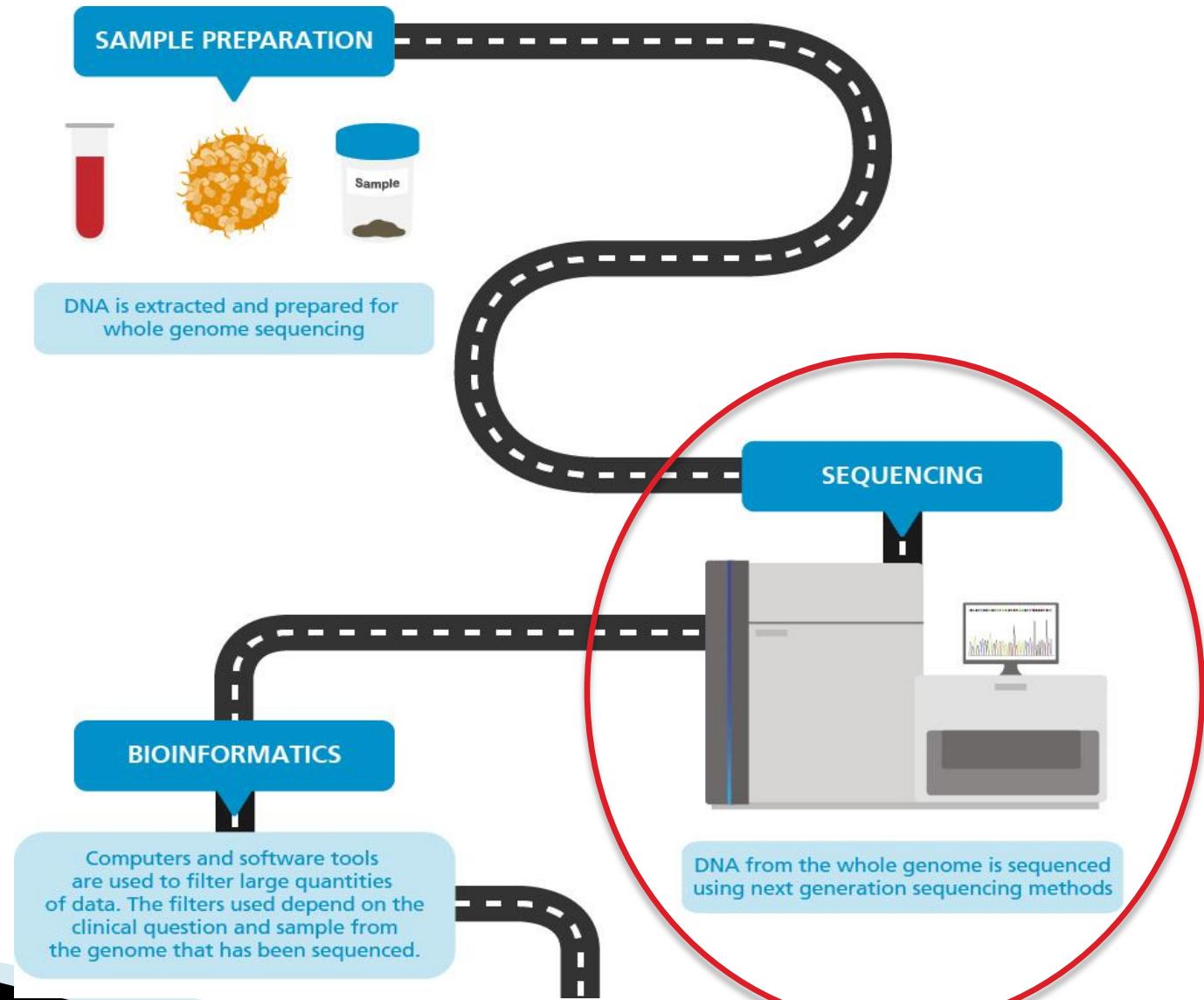
- ✓ Verify Library concentration
- ✓ Verify Library fragment lengths.

Step 4: PCR amplification



Only fragments with sequencing adapters are amplified, they are enriched.

Bioinformatics road



Sequencing methods

- ▶ **Sequencing:** the process of determining the precise order of nucleotides (**A,C,T and G**) or amino acid sequence within a DNA fragment or a protein using chemical and enzymatic reactions.
- ▶ DNA sequencing machines are evolved through three generations.
- ▶ Each generation is characterized by some factors such as the sequencing technology, cost, the quantity and the quality of the sequencing data.

Introduction to Sequencing Technologies

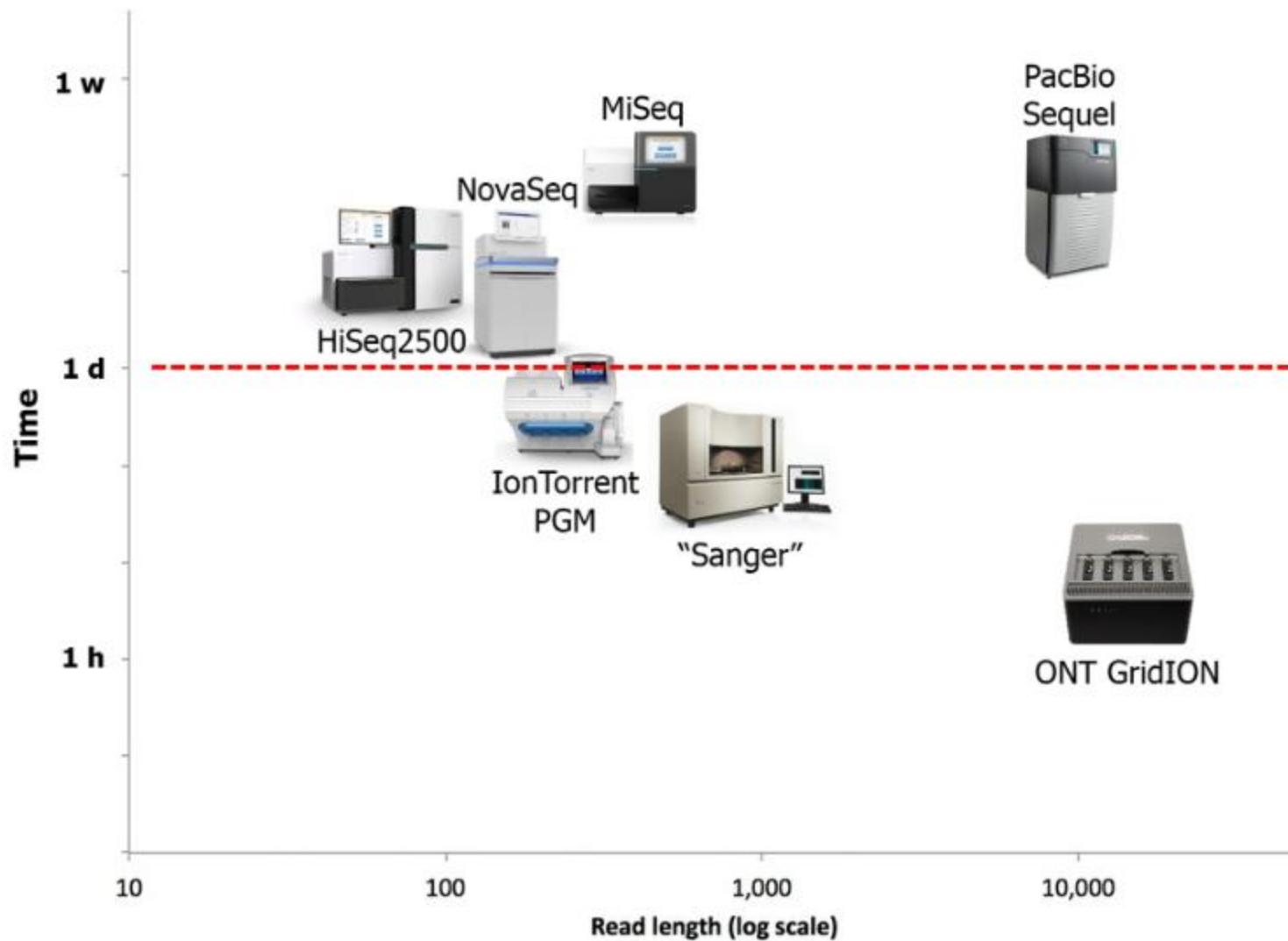


image credits :

<https://academic.oup.com/femsle/article/365/16/fny103/4982775>

Top technologies in the sequencing market.

Table 1. Comparison of the Read Lengths, Error Rates, and Costs of Various DNA Sequencing Technologies

Technology	Method	Read Length	Error Rate (%)	Throughput (GB/run)
Illumina	Synthesis	100–300 bp	0.1	200–600
Pacific Biosciences SMRT	Synthesis	10–100 kb	5–15	10–20
Oxford Nanopore MinION	Nanopore	Variable (up to 1,000 kb)	5–20	5–10

Table credits:

<https://www.sciencedirect.com/science/article/pii/S2589004219302184>

Top technologies in the sequencing market.

Company	Instruments
Illumina	MiniSeq; NextSeq; MiSeq; HiSeq; NovaSeq
Pacific biosciences	RSII; Sequel
Oxford Nanopore Technologies	SmidgION (under dev); MinION; GridION; PromethION (under dev)

Table credits :

<https://academic.oup.com/femsle/article/365/16/fny103/4982775>

Sequencing Power for Every Scale

The broadest portfolio offering available

							
Sequencing System	iSeq™	MiniSeq™	MiSeq®	NextSeq®	HiSeq®	HiSeq® X	NovaSeq®
				4000	Five/Ten	6000	
Output per run	1.2 Gb	7.5 Gb	15 Gb	120 Gb	1.5 Tb	1.8 Tb	1 Tb - 6 Tb ¹
Instrument price	\$19.9K	\$49.5K	\$99K	\$275K	\$900K	\$6M ² /\$10M ²	\$985K
Installed base ³	NA	~600	~6,000	~2,400	~2,300 ⁴		~285

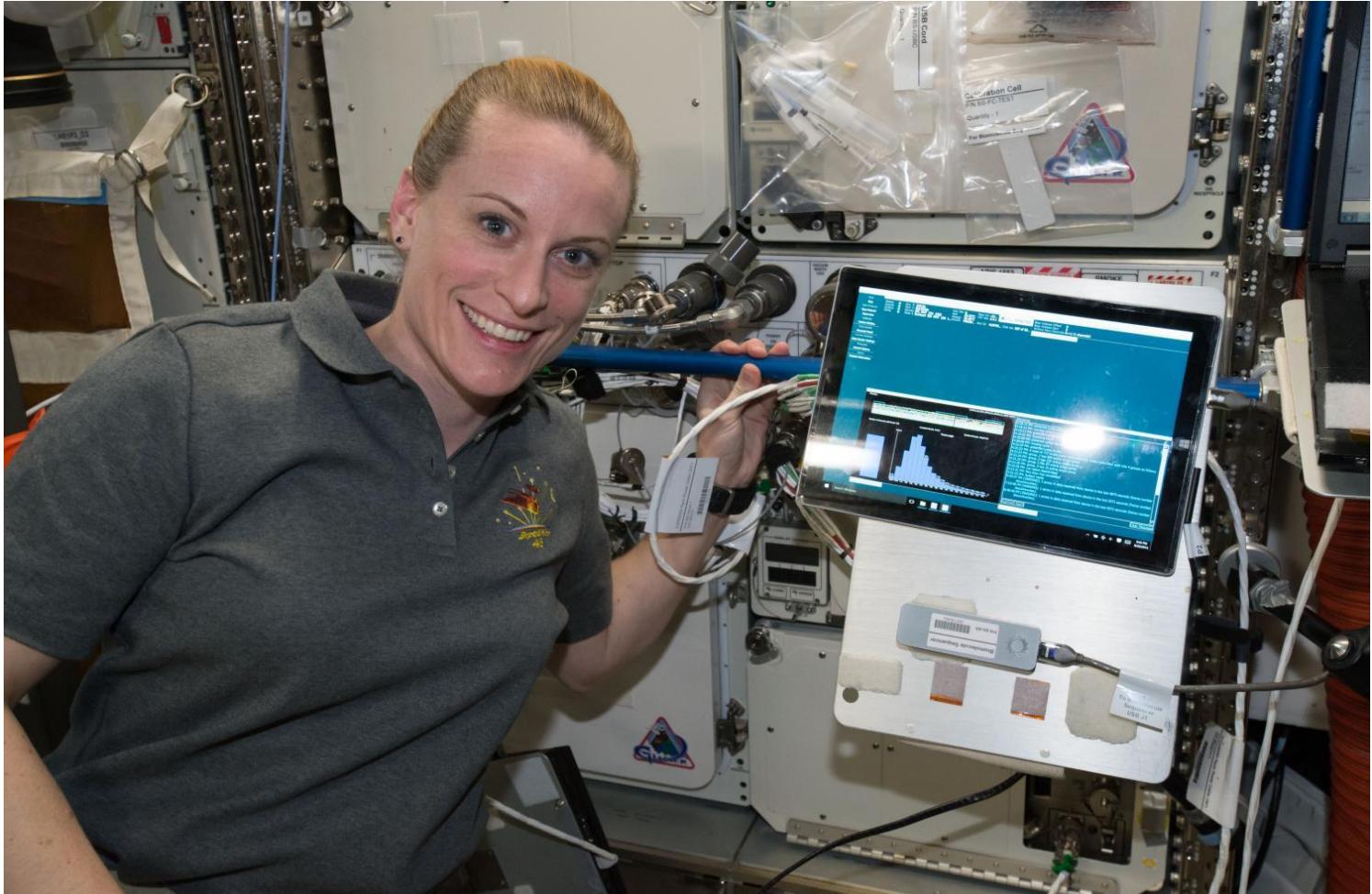
1. Output per run for the S1, S2 and S4 flow cells equal 1 Tb, 2 Tb and 6 Tb, respectively assuming two flow cells per run

2. Based on purchase of 5 and 10 units for HiSeq X Five and HiSeq X Ten, respectively

3. Based on end of fiscal year 2017

4. Combined HiSeq family

Sequencing by Nanopore (**fun!**)



Kate Rubins is pictured aboard ISS with the USB MinION sequencer (lower right) that was used in the first-ever DNA sequencing in space in August 2016.

Sequencing by Nanopore (**fun!**)



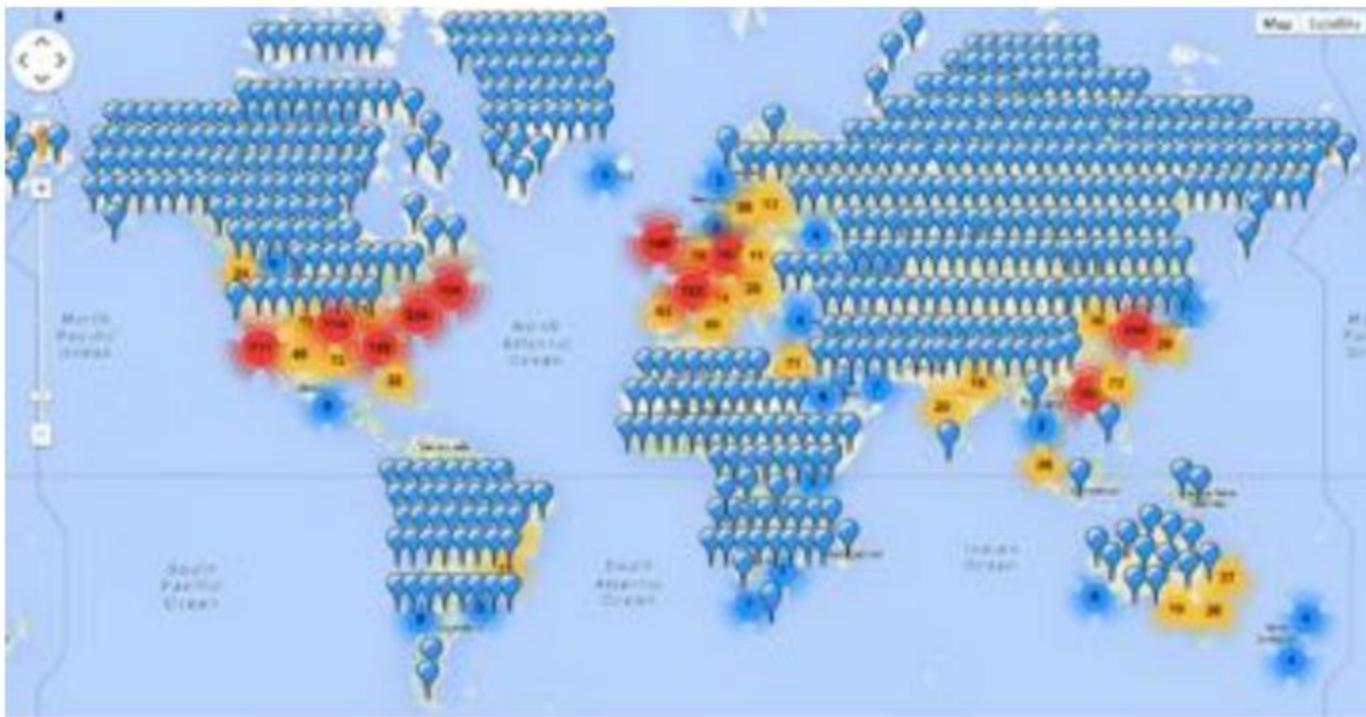
Data Deluge

Sequencing Centers 2018



Data Deluge

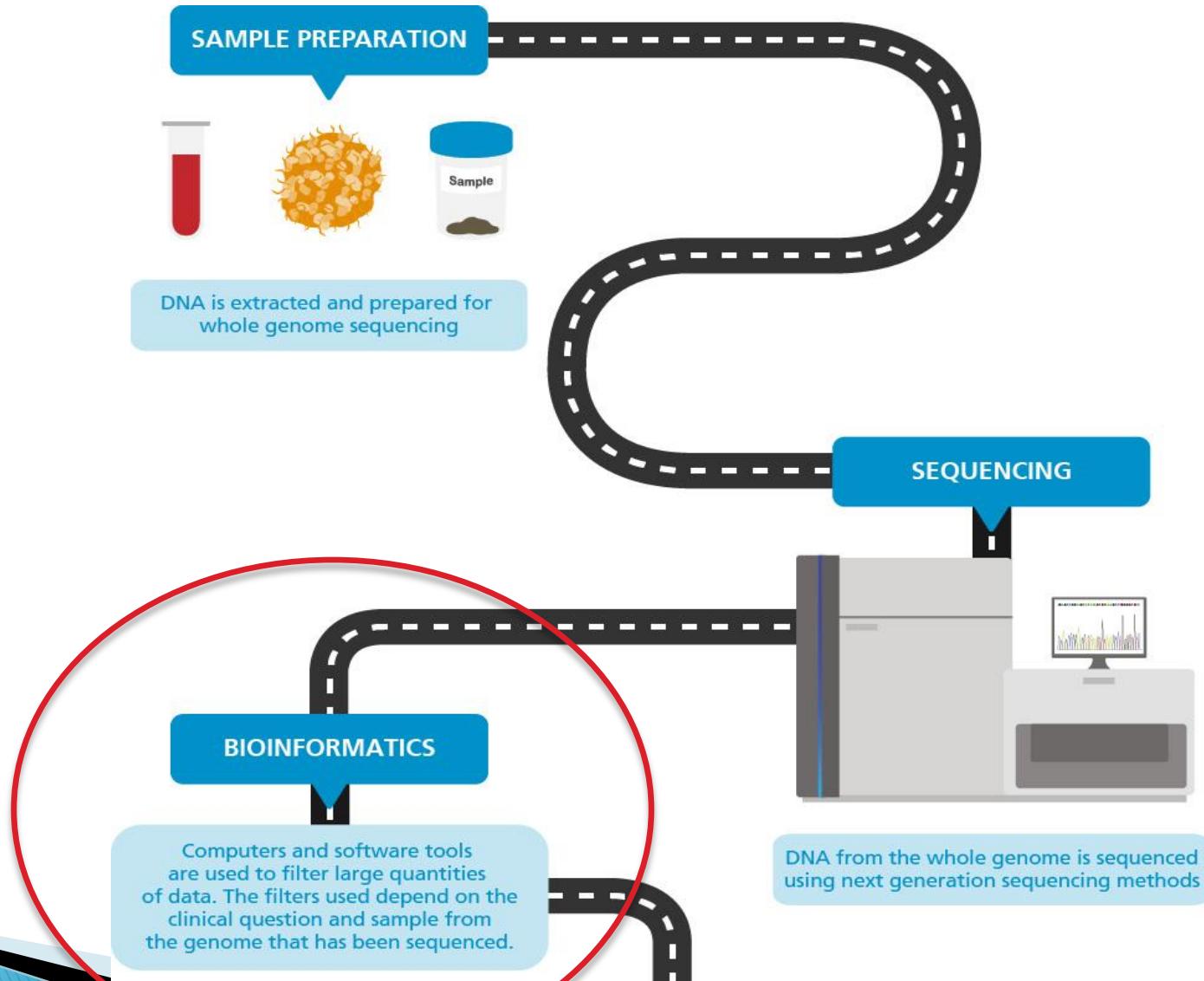
Sequencing Centers 2028



Time to grab some coffee and watch this Videos ☺

- ▶ https://www.youtube.com/watch?v=chnxUJ_0qow
- ▶ <https://www.youtube.com/watch?v=rA8MUR4pqNE>
- ▶ <https://www.youtube.com/watch?v=KfyAwAtyUQE>
- ▶ <https://www.youtube.com/watch?v=gmNw6CWtN5k>
- ▶ https://www.youtube.com/watch?v=tcPgdR9_t64
- ▶ <https://www.youtube.com/watch?v=1PisbDHKXTU>
- ▶ <https://www.youtube.com/watch?v=QYpX94prb0A>
- ▶ <https://www.youtube.com/watch?v=MxDgPFNjkbw>
- ▶ https://www.youtube.com/watch?v=sEjN_fxJN1s
- ▶ <https://www.youtube.com/watch?v=AK8A5OREk34>
- ▶ <https://www.youtube.com/watch?v=bJfed2B2Pzk>
- ▶ <https://www.youtube.com/watch?v=iqAmkNSu3oI>
- ▶ <https://www.youtube.com/watch?v=7ColjBvV274>

Bioinformatics road



Sequencing Services



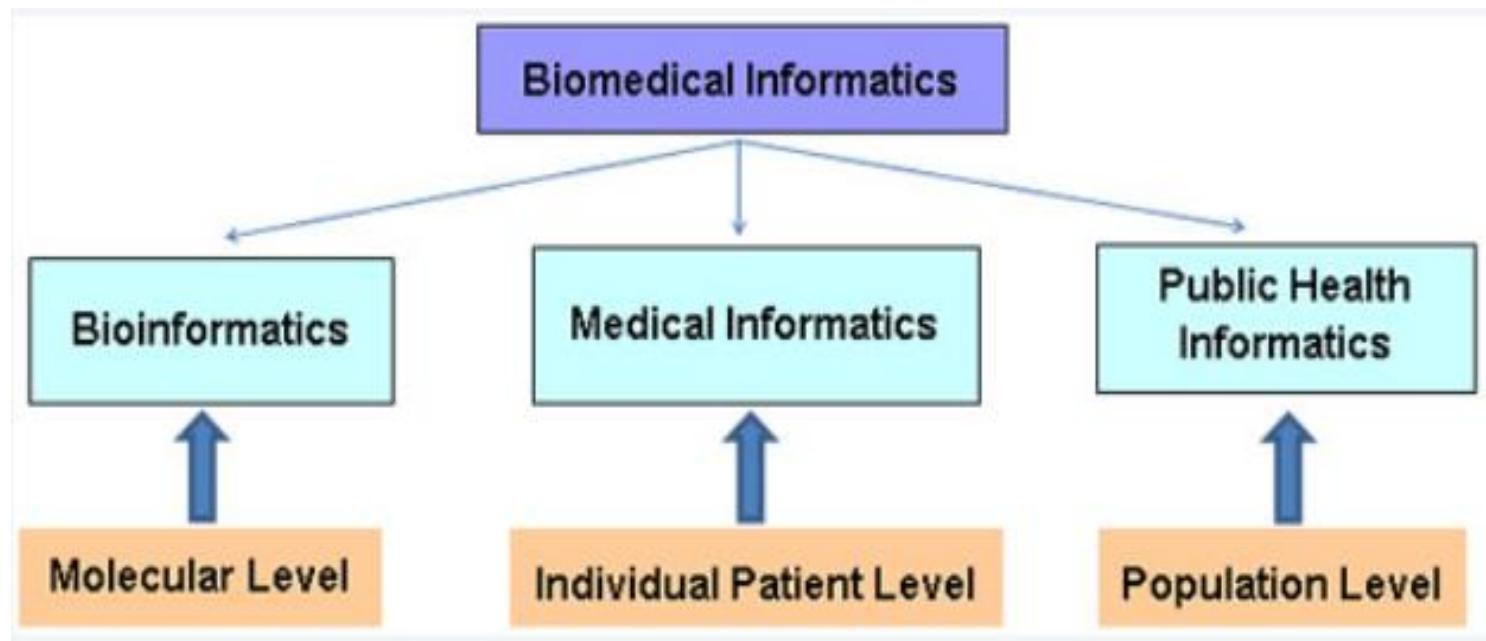
<https://www.abmgood.com/Whole-Genome-Sequencing-Service.html>

For example:

the genes *KRAS* and *TP53* are often targeted across a range of cancer types, as they are commonly found to be mutated with a number of hotspots. *BRAF* and *EGFR* are also screened in many solid tumors, as they contain clinically relevant mutation

Image credits: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6861594/>

Bioinformatics, Medical Informatics & Biomedical Informatics



<https://osteopathic.nova.edu/msbi/evolution.html>

How to survive in the Bioinformatics fields?

Rule 1: Subscribe to the top journals in the field.

Bioinformatics Journals Ranks from Google Scholar

1: Bioinformatics Journals (the most recent Impact Factor :: 5-year Impact Factor)

1. [WIREs Computational Molecular Science](#) (11.885 :: 11.118)
2. [Briefings in Bioinformatics](#) (9.617 :: 7.017)
3. [Bioinformatics](#) (4.981 :: 8.136)
4. [PLOS Computational Biology](#) (4.620 :: 5.279)
5. [Statistical Methods in Medical Research](#) (4.472 :: 3.734)
6. [Database: The Journal of Biological Databases and Curation](#) (3.372 :: 4.510)
7. [BMC Bioinformatics](#) (2.576 :: 3.452)
8. [IEEE Transactions on Information Technology in Biomedicine](#) (2.493 :: 2.873)
9. [BMC Systems Biology](#) (2.435 :: 2.917)
10. [BioData Mining](#) (2.024 :: 2.012)
11. [Journal of Mathematical Biology](#) (1.846 :: 2.344)
12. [Journal of Computational Biology](#) (1.737 :: 1.818)
13. [Medical & Biological Engineering & Computing](#) (1.726 :: 2.005)
14. [Mathematical Medicine and Biology](#) (1.658 :: 2.045)
15. [Molecular Informatics](#) (1.647 :: 1.886)
16. [Evolutionary Bioinformatics](#) (1.452 :: 1.465)
17. [Algorithms for Molecular Biology](#) (1.463 :: 2.155)
18. [IEEE-ACM Transactions on Computational Biology and Bioinformatics](#) (1.436 :: 1.605)

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Rule 1: Subscribe to the top journals in the field.

18. [IEEE-ACM Transactions on Computational Biology and Bioinformatics](#) (1.436 :: 1.605)
19. [Bulletin of Mathematical Biology](#) (1.389 :: 1.553)
20. [Computers in Biology and Biomedicine](#) (1.240 :: 1.459)
21. [IET Systems Biology](#) (1.059 :: 1.467)
22. [Current Bioinformatics](#) (0.921 :: 1.045)
23. [Journal of Bioinformatics and Computational Biology](#) (0.783)
24. [Computational and Mathematical Methods in Medicine](#) (0.766 :: 0.756)
25. [International Journal of Data Mining and Bioinformatics](#) (0.495 :: 0.721)
26. [Journal of Data Mining in Genomics and Proteomics](#) (N/A)

2: Other journals that publish bioinformatics papers

1. [Biochimica et Biophysica Acta-Gene Regulatory Mechanisms](#) (6.332 :: 5.661)
2. [Biology Direct](#) (4.658 :: 3.826)
3. [BioMed Research International](#) (1.579 :: 1.593)
4. [Briefings in Functional Genomics](#) (3.670 :: 3.565)
5. [BMC Biotechnology](#) (2.034 :: 2.511)
6. [BMC Genetics](#) (2.397 :: 2.896)
7. [BMC Genomics](#) (3.986 :: 4.360)

How to survive in the Bioinformatics fields?

Rule 1: Subscribe to the top journals in the field.

7. [BMC Genomics](#) (3.986 :: 4.360)
8. [BMC Plant Biology](#) (3.813 :: 4.714)
9. [Epigenetics](#) (4.780 :: 5.081)
10. [Frontiers in Genetics](#)
11. [G3-Genes Genomes Genetics](#) (3.198 :: 3.508)
12. [Gene](#) (2.138 :: 2.185)
13. [Genes](#) (3.242)
14. [Genetics](#) (5.963 :: 5.241)
15. [Genome](#) (1.424 :: 1.669)
16. [Genome Biology](#) (10.810 :: 13.480)
17. [Genome Research](#) (14.630 :: 15.567)
18. [Genomics](#) (2.284 :: 2.847)
19. [Human Mutatione](#) (5.144 :: 5.119)
20. [International Journal of Genomics](#) (0.953 :: 0.953)
21. [International Journal of Medical Informatics](#) (2.004 :: 2.610)
22. [Nature Biotechnology](#) (41.514 :: 38.276)
23. [Nature Communications](#) (11.470 :: 11.904)
24. [Nature Methods](#) (32.072 :: 31.232)
25. [Nature Protocols](#) (9.673 :: 13.469)

How to survive in the Bioinformatics fields?

Rule 1: Subscribe to the top journals in the field.

26. [Nucleic Acids Research](#) (9.112 :: 8.867)
27. [OMICS-A JOURNAL OF INTEGRATIVE BIOLOGY](#) (2.362 :: 2.698)
28. [Plant and Cell Physiology](#) (4.931 :: 5.156)
29. [Plant Methods](#) (3.102 :: 3.651)
30. [Plant Physiology](#) (6.841 :: 8.030)
31. [Plant Science](#) (3.607 :: 3.904)
32. [PLOS ONE](#) (3.234 :: 3.702)
33. [Proceedings of the National Academy of Sciences](#) (9.674 :: 10.563)
34. [RNA-A PUBLICATION OF THE RNA SOCIETY](#) (4.936 :: 4.900)
35. [RNA Biology](#) (4.974 :: 5.237)
36. [Scientific Reports](#) (5.578 :: 5.597)
37. [Scientific Data](#)
38. [FEBS Journal](#) (4.001 :: 4.068)
39. [Tree Genetics & Genomes](#) (2.451 :: 2.563)

3: Low-cost or no-cost journals

1. [eLIFE](#) (9.32 :: 9.33)
2. [F1000Research](#)
3. [PeerJ](#) (2.1)

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Rule 1: Subscribe to the top journals in the field.



THE PREPRINT SERVER FOR BIOLOGY

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COVID-19 SARS-CoV-2 preprints from medRxiv and bioRxiv

Subject Areas

All Articles

Animal Behavior and Cognition	Ecology	Paleontology
Biochemistry	Epidemiology*	Pathology
Bioengineering	Evolutionary Biology	Pharmacology and Toxicology
Bioinformatics	Genetics	Physiology
Biophysics	Genomics	Plant Biology
Cancer Biology	Immunology	Scientific Communication and Education
Cell Biology	Microbiology	Synthetic Biology
Clinical Trials*	Molecular Biology	Systems Biology
Developmental Biology	Neuroscience	Zoology

<https://www.biorxiv.org/>

How to survive in the Bioinformatics fields?

Rule 2: Attend Bioinformatics meetings, conferences (online/offline/videos).

- A good source for conferences is the website of the International Society for Computational Biology (<https://www.iscb.org/>).

Upcoming Conferences



Conferences Calendar



ISCBacademy Webinar Series Calendar



ISMB 2020

July 13 - 16, 2020

Virtual Event



ECCB 2020

August 31 – Sept 08, 2020

Virtual Conference



ISCB-Latin America
SoiBio BioNetMX 2020

SAVE THE DATE!

October 28 – 29, 2020

Virtual Symposium



RSGDREAM 2020

SAVE THE DATE!

November 16 - 18, 2020

Virtual ISCB Event



GIW/ISCB-Asia 2020

SAVE THE DATE!

December 9 – 11, 2020

Tainan, Taiwan



GLBIO 2021

May 10 - 13, 2019

Twin Cities, Minnesota, USA



Affiliated Conference Application

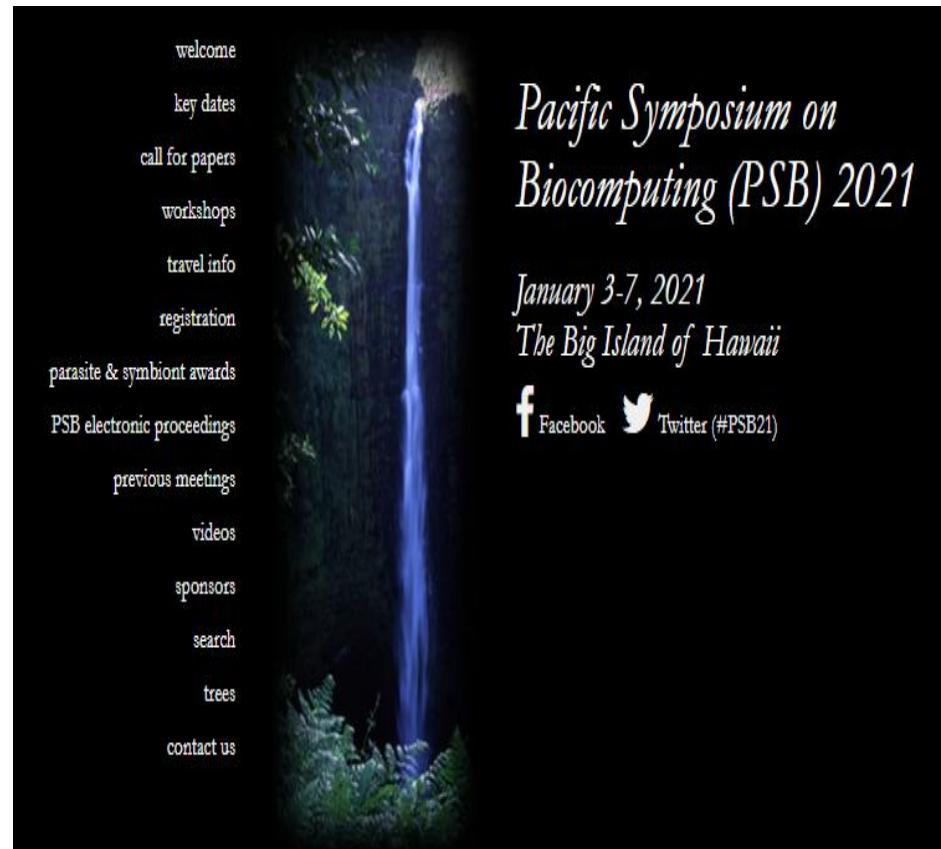
become a ISCB affiliated conference, learn more here

How to survive in the Bioinformatics fields?

**Rule 2: Attend Bioinformatics meetings, conferences
(online/offline/videos).**



<https://www.recomb2020.org/>



<https://psb.stanford.edu/>

How to survive in the Bioinformatics fields?

**Rule 2: Attend Bioinformatics meetings, conferences, courses
(online/offline/videos) .**



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<https://meetings.cshl.edu/meetingshome.aspx>

How to survive in the Bioinformatics fields?

Rule 3: Follow famous scientists on the field on twitter



Steven Salzberg

American computer scientist

Steven Lloyd Salzberg is an American computational biologist and computer scientist who is a Bloomberg Distinguished Professor of Biomedical Engineering, Computer Science, and Biostatistics at Johns Hopkins University. [Wikipedia](#)

h-index: 141

Books: [Learning with Nested Generalized Exemplars](#)

Education: Harvard University, Yale University, John A. Paulson School Of Engineering And Applied Sciences

<https://salzberg-lab.org/>

<https://twitter.com/StevenSalzberg1>

[Steven Salzberg \(@StevenSalzberg1\) · Twitter](#)

Trump administration and ICE back down completely in response to university outcry across the country:
www.cnn.com/2020/07/14/
...

Twitter · 11 hours ago

Add one more scientist to the list of those criticizing the Trump administration's shameless attacks on
[@DrAnthonyF](#)
www.washingtonpost.com/
...

Twitter · 1 day ago

of course Trump does it on a Friday night. Criminal Roger Stone, friend of Trump, won't go to jail after all. One criminal pardons another
www.cnn.com/2020/07/10/
...

Twitter · 4 days ago

How to survive in the Bioinformatics fields?

Rule 3: Follow famous scientists on the field on twitter

<https://salzberg-lab.org/lab-members/>



*Mike Schatz, Ph.D.

Bloomberg Distinguished Associate Professor of Computer Science and Biology, Johns Hopkins University



*Adam Phillippy, Ph.D.

Senior Investigator, National Human Genome Research Institute, NIH



*Cole Trapnell, Ph.D.

Assistant Professor, Genome Sciences, University of Washington



*Ben Langmead, Ph.D.

Associate Professor, JHU Computer Science Dept.



*Daehwan Kim, Ph.D.

Michael L. Rosenberg Assistant Professor, Dept. of Bioinformatics, UT Southwestern Medical Center

How to survive in the Bioinformatics fields?

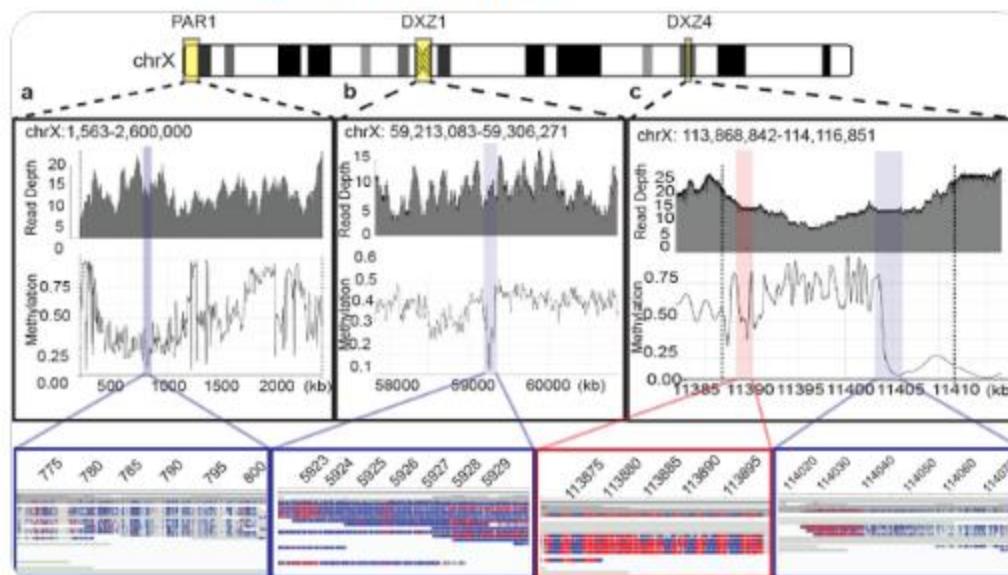
Rule 3: Follow famous scientists on the field on twitter



1 Ewan Birney and 8 others liked

Adam Phillippy @aphillippy · 16h

So proud of @khmiga @sergekoren and our entire #T2T consortium for the first-ever "Telomere-to-telomere assembly of a complete human X chromosome"! Fills all reference gaps and reveals methylation patterns of satellite arrays nature.com/articles/s4158...



How to survive in the Bioinformatics fields?

Rule 3: Follow famous scientists on the field on twitter



Rayan Chikhi @RayanChikhi · 9h

Congrats to @GuillaumeRizk (Minia & DSK co-developer, among other things) & the Enancio team. Their FASTQ compression startup company just got acquired by Illumina.



Illumina ✅ @illumina · 8h

Welcome to the Illumina family, Enancio. Together with this genomic compression software company, we will reduce data storage and transfer costs associated with today's data deluge.

bddy.me/2OrwWRy

enancio
an Illumina® company

How to survive in the Bioinformatics fields?

Rule 3: Follow famous scientists on the field on twitter



Lior Pachter @lpachter ·



Daniel MacArthur @dgmcarthur ·



Michael Hoffman @michaelhoffman ·



Aaron Quinlan @aaronquinlan



Titus Brown @ctitusbrown ·



Ewan Birney @ewanbirney



Nick Loman @pathogenomenick ·



EMBL Events @EMBLEvents



Keith Robison @OmicsOmicsBlog



Oxford Nanopore ✅
@nanopore



Heng Li @lh3lh3 ·

How to survive in the Bioinformatics fields?

Rule 4: Follow famous bloggers in the field

Omics! Omics!

A computational biologist's personal views on new technologies & publications on genomics & proteomics and their impact on drug discovery

<http://omicsomics.blogspot.com/>

Heng Li's blog

Archive Categories Pages Tags

Homepage

Links

My Homepage at SourceForge.net, GitHub, Twitter, Disqus, publications at ResearcherID, Google Scholar and FTP at Broad Institute.

Posts 2

- 27 May 2020 » Base quality scores are essential to short read variant calling
- 25 May 2020 » Format, quality binning and file size
- 17 May 2020 » Fast high-level programming languages
- 08 Apr 2020 » auN: a new metric to measure assembly contiguity
- 12 Jul 2019 » On a reference pan-genome model (Part II)
- 08 Jul 2019 » On a reference pan-genome model
- 18 May 2019 » How much does development time matter?

<https://lh3.github.io/>



Bits of DNA

Reviews and commentary on computational biology by Lior Pachter

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<https://liorpachter.wordpress.com/about/>

Living in an Ivory Basement Stochastic thoughts on science, testing, and programming.

misc personal python research science teaching testing

training

<http://ivory.idyll.org/blog/>

How to survive in the Bioinformatics fields?

Rule 5: Join Ask & Answers Bioinformatics Platforms

LATEST OPEN RNA-SEQ CHIP-SEQ SNP ASSEMBLY TUTORIALS TOOLS JOBS FORUM PLANET ALL »

Welcome to Biostar!

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0 votes 0 answers 1 views **Monster Test :All natural ingredients** written 3 minutes ago by vikoanna • 0

0 votes 1 answer 2.0k views **Which computational tool should I use to remove eukaryotic sequences from my sample (created with RNA-seq and Shotgun Metagenomics and Illumina)?** written 4.9 years ago by BioNtE • 0 • updated 25 minutes ago by csidhu • 0

4 votes 2 answers 68 views **Got an error while Translating a mRNA sequence into a protein** written 19 hours ago by caro-ca • 0

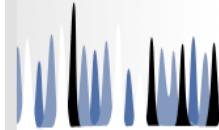
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- C: Hope Biostars can keep text even you click Cancel button
- A: How can I call both somatic and germline variants from bam file?
- A: How to calculate "Tissue specificity score" using JSD
- C: Help improve search paper skill.
- C: Hope Biostars can keep text even you click Cancel button
- C: How to handle 4 fastq file for one paired-end sample?

<https://www.biostars.org/>

How to survive in the Bioinformatics fields?

Rule 5: Join Ask & Answers Bioinformatics Platforms



SEQanswers

the next generation sequencing community



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Ten Simple Rules for Getting Help from Online Scientific Communities! ECO	Today 12:22 AM by icyberops22	22	35,802	Introductions	No Threads to Display.
PhD in Bioinformatic at San Raffaele Institute,Milan,Ital... silviasantoro	Yesterday 12:45 AM by DanoGeorge	1	959	Academic/Non-Profit Jobs	
Demultiplexing IONA® generated data LucasIII	07-13-2020 10:44 PM by LucasIII	1	103	Ion Torrent	
Upcoming online UC Davis Bioinformatics Core workshops najoshi	07-13-2020 04:28 PM by najoshi	0	97	Bioinformatics	
Bismark: paired-end low mapping efficiency. dideco	07-13-2020 09:00 AM by fkrueger	35	33,204	Epigenetics	

<http://seqanswers.com/>

How to survive in the Bioinformatics fields?

Rule 5: Join Ask & Answers Bioinformatics Platforms

Where to ask for bioinformatics help online

November 02, 2015



<http://www.acgt.me/blog/2015/11/1/where-to-ask-for-bioinformatics-help-online>

1. [SEQanswers](#) — the most popular online forum devoted to bioinformatics?
2. [Biostars](#) — another very popular forum.
3. Mailing lists — many useful bioinformatics tools have their own mailing lists where you can ask questions and get help from the developers or from other users, e.g. [SAMtools](#) and [Bioconductor](#). Also note that resources such as [Ensembl](#) have their own [mailing lists for developers](#).
4. [Google Discussion Groups](#) — as well as having very general discussion groups, e.g. [Bioinformatics](#), there are also groups like [Tuxedo Tool Users](#)...the perfect place to ask your TopHat or Cufflinks question.
5. [Stack Overflow](#) — more suited for questions related to programming languages or Unix/Linux.
6. [Google](#) — I'm including this here because I have solved countless bioinformatics problems just by searching Google with an error message.
7. [Reddit](#) — try asking in [r/bioinformatics](#) or [r/genome](#).
8. [Twitter](#) — this may be more useful if you have enough followers who know something about bioinformatics, but it is potentially a good place to ask a question, though not a great forum for long questions (or replies). Try using the hashtag #askabioinformatician (this was [@sjcockell](#)'s idea).
9. [Voat](#) — Voat is like reddit's younger, hipster nephew. However, the [bioinformatics](#) 'subverse' is not very active.
10. [Research Gate](#) — you may know it better as 'that site that sends me email every day', but some people use this site to ask questions about science. Surprisingly, they have [15 different categories relating to bioinformatics](#).
11. [LinkedIn](#) — Another generator of too many emails, but they do have discussion groups for [bioinformatics geeks](#) and [NGS](#).

How to survive in the Bioinformatics fields?

Rule 6: Read & Learn



- ▶ YouTube Video
- ▶ Coursera Courses
- ▶ Github pages

Lù ChiBi

قناة طيور الجنة | toyora... •

PacBio

Ben Langmead

Ben Langmead

Browse channels

Ben Langmead

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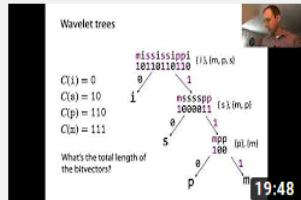
All activities ▾

FEATURED CHANNELS

mathematicalmonk

SUBSCRIBE

Ben Langmead uploaded and added to Indexing



Wavelet trees, part 2

Ben Langmead • 44 views • 1 day ago

We discuss the space required to store wavelet trees and the time required to answer queries. We discuss this both for balanced and for Huffman-shaped trees. Channel: @Ben

$C(1) = 0$
 $C(0) = 10$
 $C(p) = 110$
 $C(s) = 111$

What's the total length of the bitvector?

19:48

How to survive in the Bioinformatics fields?

Rule 6: Read & Learn

- ▶ YouTube Video
- ▶ Coursera Courses
- ▶ Github pages

The screenshot shows the Coursera website interface. At the top, there is a navigation bar with the Coursera logo, an 'Explore' dropdown, a search bar containing 'What do you want to learn?', a magnifying glass icon, and links for 'For Enterprise' and a notification bell.

The main content area displays a course card for 'Genomic Data Science Specialization'. The course is offered by 'JOHNS HOPKINS UNIVERSITY'. The title is 'Genomic Data Science Specialization'. A description below the title reads: 'Be a next generation sequencing data scientist.. Master the tools and techniques at the forefront of the sequencing data revolution.' The course has a rating of '4.2 5,891 ratings' and a 'Share' button. It features a photo of Steven Salzberg, PhD, and '+7 more instructors'. The enrollment status is 'Enroll Starts Jul 15'. Premium access is offered at '\$39/mo' with 'Financial aid available'. The number of enrolled students is '25,900 already enrolled'.

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The screenshot shows a GitHub repository page for 'applied-computational-genomics' owned by 'quinlan-lab'. The repository has 81 watchers, 562 forks, and 120 issues. The 'Code' tab is selected. The repository contains 1 branch and 0 tags. A recent commit by 'arq5x' titled 'Update README.md' is shown, along with other files like 'LICENSE', 'README.md', 'Todo.md', and 'aaron_class_2017.pdf'. The 'About' section describes it as an 'Applied Computational Genomics Course at UU: Spring 2020'. There are sections for 'Readme', 'CC-BY-SA-4.0 License', 'Releases', and 'Contributors'.

github.com/quinlan-lab/applied-computational-genomics

quinlan-lab / applied-computational-genomics

Watch 81 Star 562 Fork 120

Code Issues 4 Pull requests Actions Projects Wiki Security Insights

master 1 branch 0 tags Go to file Add file ▾ Code ▾

arq5x Update README.md 486af4b on Apr 21 120 commits

AaronsClass-3-30-17.pdf Add files via upload 3 years ago

LICENSE add cc-by-sa 4.0 license 3 years ago

README.md Update README.md 3 months ago

Todo.md Create Todo.md 3 years ago

aaron_class_2017.pdf Add files via upload 3 years ago

README.md

About

Applied Computational Genomics
Course at UU: Spring 2020

Readme

CC-BY-SA-4.0 License

Releases

No releases published

Contributors 3

How to survive in the Bioinformatics fields?

Recommended liked pages on Facebook



National Research Centre Com...
Government Organization

Liked ...



Biotechinformatics
Product/Service

Liked ...



National Institutes of Health (N...
Government Organization

Liked ...



ABC_Bioinformatics
Education Website

Liked ...



H3ABioNet
Organization

Liked ...



Genomics Education Program...
Medical & Health

Liked ...



NCBI - National Center for Biot...
Educational Research Center

Liked ...



National Institute of Biomedica...
Government Organization

Liked ...



MERC
Medical Lab

Liked ...



Center for Genomics, Zewail C...
Science, Technology & Engineering

Liked ...

How to survive in the Bioinformatics fields?

Recommended liked pages on Facebook



EMBL Events
Education

Liked ...



Wellcome Sanger Institute
Nonprofit Organization

Liked ...



European Bioinformatics Institut...
Non-Governmental Organization (NGO)

Liked ...

Molecular And Computational Biology
Private group

illumina®

Illumina, Inc.
Biotechnology Company

Liked ...

Bioinformatics Career @ Egypt



Mohamed El Hadidi

May 15 at 4:30 PM ·

...

On behalf of my colleagues at 57357 Hospital:

Searching for a talented candidate to join our team as a Bioinformatics Research Associate in Genomics Unit in Children's Cancer Hospital - Egypt 57357.

Requirements:

- Bachelor's or Master's Degree in Bioinformatics, Computational Biology, Biostatistics, Computer Science, or biology related fields.
- Fluency in a scripting languages (Python, R, and Bash), with good working knowledge of relevant data analysis and visualization packages.
- Good knowledge of commonly used tools and workflows used to analyze NGS data.
- Ability to use development tools, including git, Unix-based shells, and IDEs/editors.

So, if you're interested, please send your CV to me on
usama.abdelatty@57357.org

#Share

#Job_Vacancy

#Bioinformatician

#57357_Hospital

Bioinformatics Career @ Egypt

Opportunity: Two bioinformatics positions in genomics of heart diseases @ Aswan Heart Center -- Aswan, Egypt

BACKGROUND

Two bioinformatics openings to work on genomics of cardiovascular diseases at Aswan Heart Center (aswanheartcentre.com) in Magdi Yacoub Heart Foundation (www.myf-egypt.org).

This is a fabulous opportunity to contribute to a great cause with a positive impact on the society while doing exciting science in a super friendly and dynamic environment in the charming, lovely city of Aswan (www.google.com/maps/place/Aswan).

REQUIREMENTS

Required skills: Unix/Linux, Python and/or Perl, Bash, R (or Matlab), SQL, Web Development

PREFERENCES

Plus skills: NCBI, Ensembl, UCSC Genome Browser

Plus Plus skills: BLAST, MAFFT, MUSCLE, PhyML, RAxML, MrBayes, Velvet, Bowtie

HOW TO APPLY

Send résumé to amoustafa at aucegypt dot edu.

Bioinformatics Career @ Egypt

WUZZUF

Browse Jobs ▾

Browse Learning ▾

Search jobs, companies..



Bioinformatics internship (Remote)

Proteinea - Downtown, Cairo

Posted 5 days ago



Apply to Internship

129 Applicants for
2 open positions

52 Viewed 3 In Consideration 38 Not Selected

Experience Needed:

1 year

Career Level:

Entry Level

Job Type:

Internship

Salary:

Paid

Vacancies:

2 open pos

Experience Needed:

1 year

Career Level:

Entry Level

Job Type:

Internship

Job Roles:

R&D/Science | IT/Software Development

Salary:

Paid

Vacancies:

2 open positions

About the Internship

Job Roles:

R&D/Science | IT/Software Development

About the Internship

- You will be working on something you have probably never done before.
- Proteinea is disrupting the bio-manufacturing market using insects. We are an insect-based bio-manufacturing platform that integrates mass-reared insects with engineering, biology, and molecular sciences to accelerate building with biology. This could mean cheaper and faster **vaccines, pharmaceuticals, bioplastics, bioelectronics**, and much more.

The accepted candidate will be working on:

- Analyzing genomic, transcriptions, and proteomic data to gain relevant insights.
- Developing new methods and maintain bioinformatics pipelines.
- Providing bioinformatics support to R&D by analyzing and interpreting biological data.
- Providing troubleshooting and improvement for bioinformatics pipeline and applications.

Bioinformatics Career @ Egypt

Internship Requirements

- We are not looking for a regular employee but a business partner who believes in the importance of green and circular economy. We love to work with imaginary who can connect the dots and those who love to have an impact:
- Interdisciplinaries are best suited for this position.
- Excellent Research, negotiation and communication skills
- We value fast- and self-learners and people with diverse backgrounds even if they have limited experience.
- Experience with at least one programming language (Python, Perl, R, C/C++, Java) in Linux/Unix environment.
- Experience in working with bioinformatics tools.
- Experience in the use of bioinformatics databases.
- Ability to work within a team, among cross-departments, and as an independent contributor, requiring minimal supervision
- At least basic knowledge of biology and bioinformatics related concepts.

Keywords:

Agriculture | Engineering | Science | Biotechnology | Bioinformatics | Computational Biology

Bioinformatics Career @ Egypt

Bioinformatics Specialist

HITS Technologies - Nasr City, Cairo

Posted 4 months ago



55 Applicants for
1 open position | 3 Viewed

Experience Needed:

More than 1 year

Salary:

Confidential

Job Roles:

R&D/Science | Analyst/Research

Job Roles:

R&D/Science | Analyst/Research

About the Job

Responsibilities will include but not limited to:

- Work on bioinformatics tools and develop tools for targeted gene analysis
- Analyze 3rd generation sequencing data
- Analyze data and write project reports and publications
- Works independently or as a part of a team
- Genome assembly (Whole genome sequencing – Targeted genome sequencing)

Job Requirements

- Bachelor degree or equivalent courses in bioinformatics.
- Master degree in bioinformatics is an asset.
- Prior experience in analyzing next generation sequencing
- Documentation skills required.
- MUST be research Oriented

Keywords:

Bioinformatics | Analysis | Research | Science | Healthcare | Medical

Bioinformatics Career @ Egypt



Find Freelancers & Agencies

HOW IT WORKS

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SIGN UP

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Hire Bioinformatics Specialists in Egypt

Work with the world's best talent on Upwork - the top freelancing website trusted by over 5 million businesses.

Get Started



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Explore some of Upwork's top Bioinformatics Specialists in Egypt

Filters: Any hourly rate



Sort By:

Most Relevant



Bioinformatics Career @ Egypt

Freelancers / EG / Bioinformatics Specialists

Explore some of Upwork's top Bioinformatics Specialists in Egypt

Filters: Any hourly rate 

Sort By: Most Relevant 



Omar A.
python, machine learning and

\$35/hr Egypt

Data Analysis Python
Data Science
Genomic Data Analysis

[See More](#)



Mo A.
Computer Science Research Assistant at
100% SUCCESS (11 jobs)

\$35/hr Egypt

Python Data Science PHP
MySQL Programming HTML
Bioinformatics Microsoft Excel

[See More](#)



Ehab A.
My focus is in Algorithms,

\$100/hr Egypt

Cryptography WordPress
Moodle Ethical Hacking
Bioinformatics LaTeX

[See More](#)



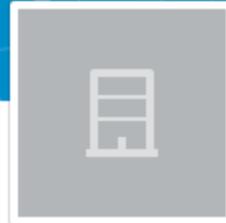
Rehab A.
Microbial ecologist - Bioinformatician

\$15/hr Egypt

Python Bioinformatics
Biology Microbiology R
Genomic Data Analysis

[See More](#)

Bioinformatics Career @ Egypt



Alkhwarizmi for Bioinformatics

Biotechnology · Cairo · 89 followers

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Website <http://khbio.info/>

Industry Biotechnology

Company size 11-50 employees
2 on LinkedIn

Type Sole Proprietorship

Founded 2013

Specialties Bioinformatics, Drug design, Structural bioinformatics, primer design, Genomics, Proteomics, Transcriptomics, Systems biology, Molecular biology, Phylogenetics, and Viral Bioinformatics



Patients Research & Development



Bioinformaticians

The bioinformatics and data mining team at Novo Nordisk supports a broad range of activities across our R&D pipeline. We use both internal and external biomedical data to identify disease targets and markers, and therefore to develop next-generation medicines for severe chronic diseases such as diabetes. We also use data to build a molecular-level understanding of our own medicines and attempt to create a more efficient and better-informed drug discovery process.



MARTIJN VAN DE BUNT, Head of Department
VANESSA IURTZ, STAR PostDoc
Global Research Technologies, R&D
Novo Nordisk Denmark



Bioinformaticians usually have 2+ years experience post-PhD, either in industry or as a post-doc. Some bioinformaticians have a strong computational background and develop tools and apply algorithms to power our research. Others are biological experts: talented analysts who can translate biological questions into data ones.

Setup our working environment (Go to the course Github page)

➤ https://github.com/SaraEl-Metwally/Informatics-on-High-throughput-Sequencing-Data-Course-Summer-2020-/blob/master/Setup_Our_Working_Environment.md

SaraEl-Metwally / Informatics-on-High-throughput-Sequencing-Data-Course-Summer-2020- Watch 0 Star 2 Fork 0

Code Issues Pull requests Actions Projects Wiki Security Insights Settings

master 1 branch 0 tags Go to file Add file Code

 SaraEl-Metwally	Update Setup_Our_Online_Session.md	29e8b7a 2 days ago	51 commits
 OnlineScreens	Add files via upload	2 days ago	
 VM_ScreenShots	Add files via upload	3 days ago	
 README.md	Update README.md	4 days ago	
 Setup_Our_Online_Session.md	Update Setup_Our_Online_Session.md	2 days ago	
 Setup_Our_Working_Environment.md	Update Setup_Our_Working_Environment.md	2 days ago	

About 

This is a summer training course at CCIC (Faculty of Computers and Information), Mansoura University, Egypt.

Readme

Releases

No releases published [Create a new release](#)