



國家實驗研究院

國家高速網路與計算中心

National Center for High-performance Computing

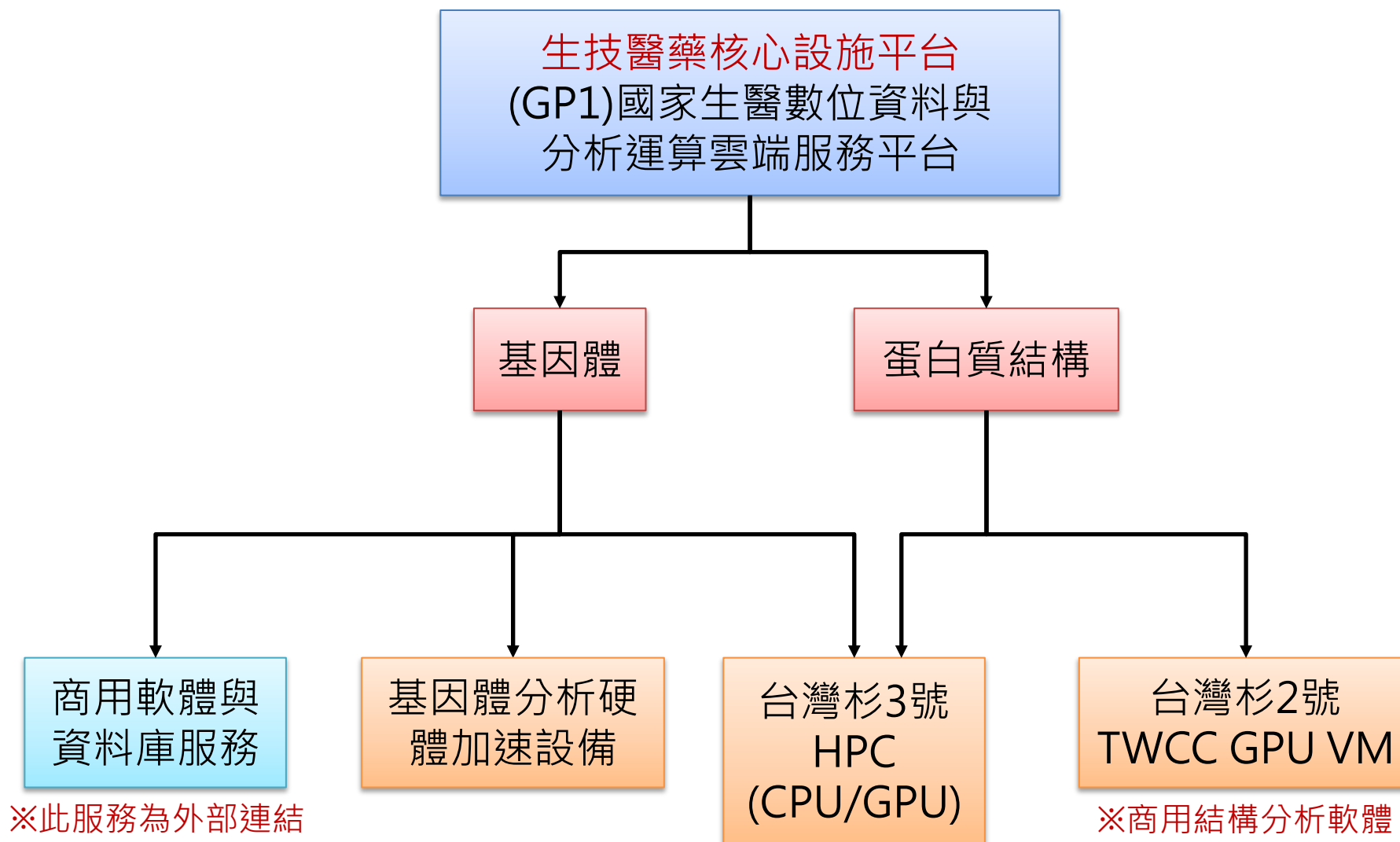
輕鬆上手超級電腦: NGS數據分析

2025/11/4

陳昶瑞 PhD
專案助理研究員
raycc@nlar.org.tw

Topics

- All about \$
- NGS data files
- 如何登入T3主機
- 如何在T3主機跑程式
- 測試job: heatmap
- 如何在T3主機安裝程式
- 真實job: 為什麼橘貓是橘色的?



What can *GP1* 核心設施 do for you?

Cancer Cell


 OPEN ACCESS

Article

Integrative analysis of lung adenocarcinoma across diverse ethnicities and exposures

Shankha Satpathy,^{1,24,25,26,*} Natalie M. Clark,^{1,25} Yi-Ju Chen,^{3,25} Noshad Hosseini,^{3,25} Ya-Hsuan Chang,^{4,25} Yi Hsiao,^{3,25} Jonathan T. Lei,^{5,25} Francesca Petralia,^{6,25} Jin-Shing Chen,^{7,25} Yifat Geffen,^{1,21} David I. Heiman,¹ Indranil Paul,¹ Hanbyul Cho,³ Michelle Hollenberg,⁸ Giacomo B. Marino,⁸ Kuen-Tyng Lin,² Rahul Mannan,³ C. Jackson White,¹ Joe Allen,¹ Shayan C. Avanessian,¹ M. Harry Kane,¹ Ashley Wolfe,³ Miloni Kinarivala,³ Wenke Liu,⁸ Shankara Anand,¹ Mong-Wei Lin,⁷ Moe Haines,¹ Erik J. Bergstrom,¹ Grant Hussey,⁸ Ginny Xiaohu Li,³ Deepak C. Mami,¹ Hao Fang,²

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SCIENCE ADVANCES | RESEARCH ARTICLE

PUBLIC HEALTH

Diversity and longitudinal records: Genetic architecture of disease associations and polygenic risk in the Taiwanese Han population

Ting-Yuan Liu^{1,2}, Hsing-Fang Lu^{1,2}, Yu-Chia Chen^{1,2}, Chi-Chou Liao³, Ying-Ju Lin^{3,4,5}, Jai-Sing Yang^{3,4}, Wen-Ling Liao^{4,7,8}, Wei-De Lin^{3,4,5}, Shih-Yin Chen^{3,4,6}, Yu-Chuen Huang^{3,4,6}, Wei-Yong Lin^{3,7}, Yu-Huei Liu^{4,7,9}, Kai-Cheng Hsu^{10,11,12}, Shih-Sheng Chang¹⁰, Hong-Da Chen¹³, Yu-Pao Chou¹⁴, Jan-Gowth Chang^{14,15}†, Chung-Hsing Wang¹⁶, Chwen-Tzuei Chang¹⁷, Chung-Ming Huang¹⁸, Kai-Jieh Ye¹⁸, Tzu-Yuan Wang¹⁹, Chin-Chung Yeh²⁰, Jiunn-Horng Chen¹⁸, Chi-Ping Huang²⁰, Hsueh-Chou Lai²¹, Rong-Hsing Chen¹⁹, Hui-Ju Lin²², Po-Yuan Wu²³, Jiu-Yao Wang^{24,25}, Chin-Chi Kuo^{3,26,27}, Der-Yang Cho^{28,29}, Chang-Hai Tsai³⁰, Fuu-Jen Tsai^{3,36,31,32,*}

Nucleic Acids Research, 2025, **53**, gkaf597
<https://doi.org/10.1093/nar/gkaf597>
 Genomics


 20TH
 OPEN ACCESS
 ANNIVERSARY
 OXFORD

Telomeric repeat-containing RNA increases in aged human cells

Yu-Hung Hsieh^{1,†}, Chin-Hua Tai^{1,†}, Meng-Ting Yeh^{1,†}, Yu-Chen Chen¹, Po-Cheng Yang¹, Chien-Ping Yen¹, Hong-Jhih Shen¹, Chan-Hsien Yeh^{2,3}, Hung-Chih Kuo^{2,3}, Der-Sheng Han^{4,5,*}, Hsueh-Ping Catherine Chu^{1,*}

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†The first three authors should be regarded as Joint First Authors.

Bioinformatics, 2025, **41**(4), btaf110
<https://doi.org/10.1093/bioinformatics/btaf110>
 Advance Access Publication Date: 13 March 2025

Original Paper

OXFORD

Data and text mining

LipidFun: a database of lipid functions

Wen-Jen Lin^{1,2,†}, Chia-Hsin Liu^{3,†}, Ming-Siang Huang⁴, Pei-Chun Shen³, Hsiu-Cheng Liu³, Meng-Hsin Tsai³, Yo-Liang Lai⁵, Yu-De Wang^{2,6}, Mien-Chie Hung^{3,7,8,9}, Nai-Wen Chang^{10,*}, Wei-Chung Cheng^{2,3,11,*}

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¹⁰Department of Medical Research, National Taiwan University Hospital, Taipei 100229, Taiwan

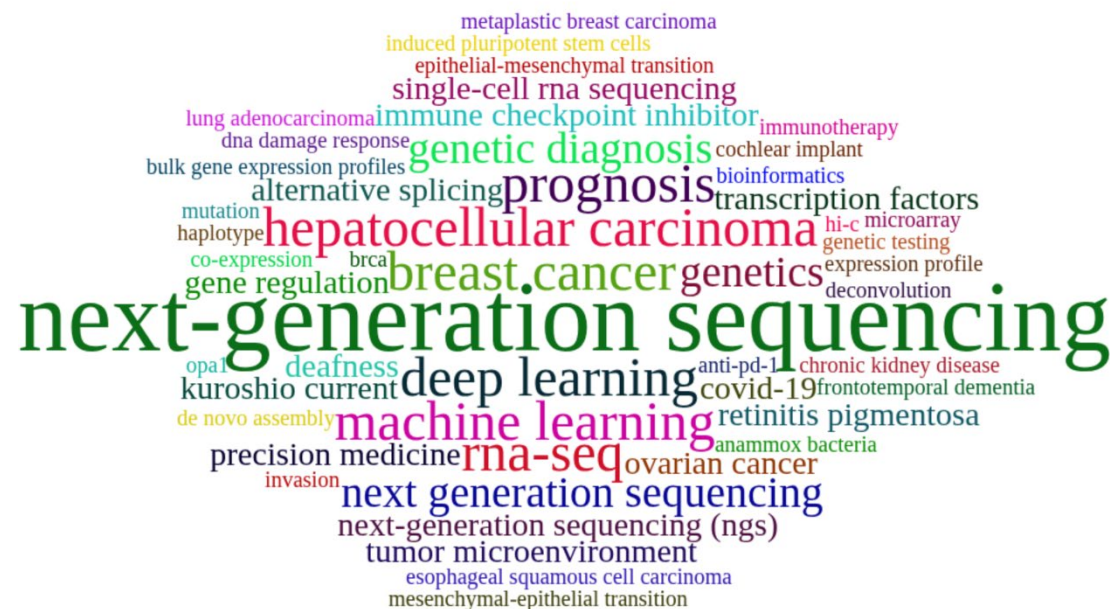
¹¹The Ph.D. Program for Cancer Biology and Drug Discovery, China Medical University and Academia Sinica, Taichung 404328, Taiwan

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† = equal contribution.

Associate Editor: Zhiyong Lu

GP1用戶發表成果



GP1核心設施運算資源

服務代號	服務項目	國科會計畫收費	一般學術界收費	產業界收費	服務用途及獨特性
GP1-1	CPU計算節點	0.08/核心小時	0.24/核心小時	0.48/核心小時	基因體註解、蛋白質結構與電腦模擬
GP1-2	CPU大記憶體節點	0.56/核心小時	1.68/核心小時	3.36/核心小時	基因體組裝分析、大資料統計分析
GP1-3	GPU計算節點	10/GPU小時	25/GPU小時	暫不提供	基因體鹼基判定與蛋白質結構計算
GP1-4	巨量資料儲存 (VirtualStor Scaler /Aspera)	900/TB/year	3,600/TB/year	5,400/TB/year	物件儲存與高速上傳服務
GP1-5	高速計算儲存(GPFS)	250/TB/month 2,500/TB/year	500/TB/month 5,000/TB/year	750/TB/month 7,500/TB/year	提供搭配高速計算節點使用之高速計算空間
GP1-7	IPA資料庫	350/小時	500/小時	暫不提供	IPA生物資訊資料庫及分析工具
GP1-9	基因體分析硬體加速服務	5.2/1Gbases	5.2/1Gbases	7.8/1Gbases	提供DRAGEN基因體分析硬體加速服務

GP1-10 客製化服務 依服務內容議價 客製化分析流程設計與開發

- SU : 1 Service Unit (SU)的定義為1 核心小時

GP1-1,
GP1-2,
GP1-3
服務費用可流用

國網生科雲



國網中心現役主力HPC: T3

900 nodes / 50400 cores



台灣杉三號
TAIWAN A3

台灣杉三號
(TAIWANIA 3)

- 2020/11
- 計算力 2.7 PFLOPS
- Top500 # 181
- Green500 # 69

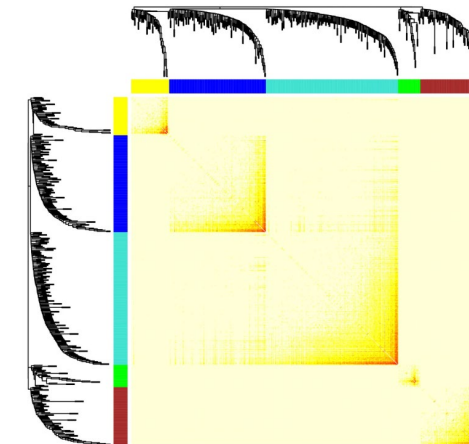
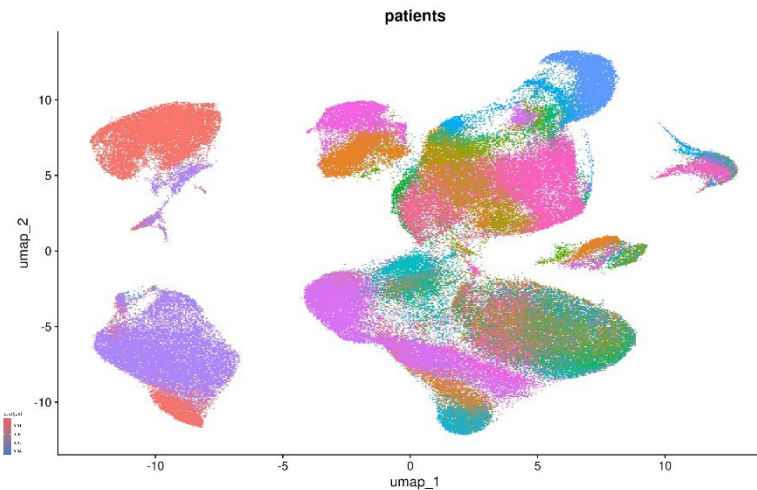
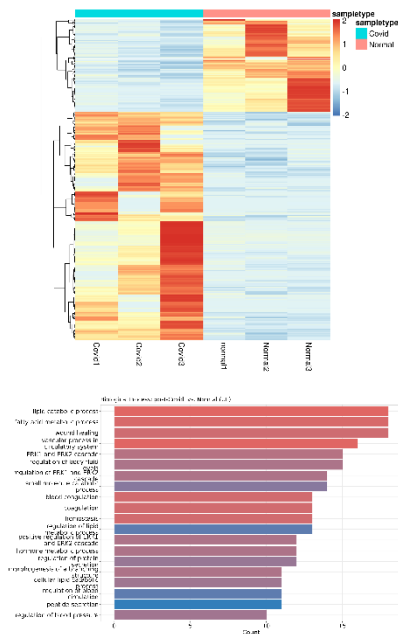
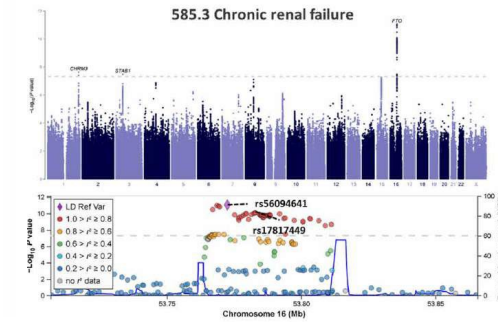
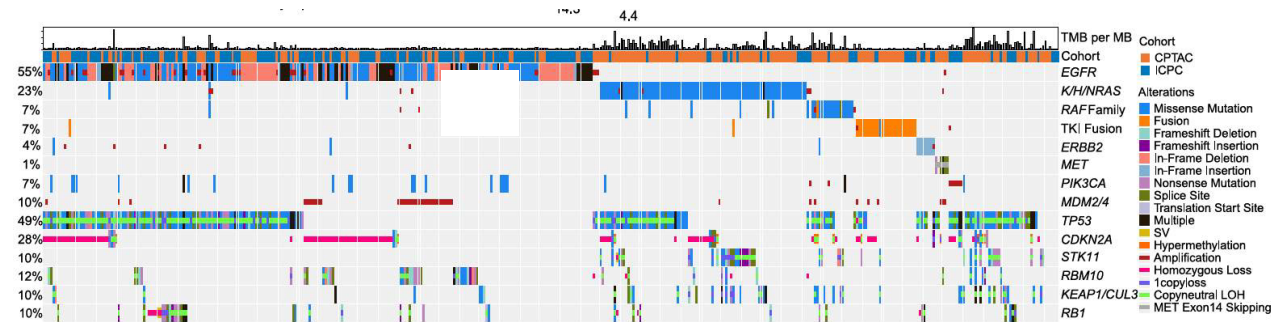
GP1核心設施: ~6% T3包廂專用算力

- 登入節點 : t3-c4.nchc.org.tw
- 計算節點 : 51

	核心數	記憶體	數量
登入節點	56	384G	1
CPU節點	56	384G	45
GPU節點	56(8GPU)	768G	2
超大記憶體節點	36,72,112	2T,4T,6T	1,1,2

- 高速計算用空間
 - /home/userid : 100 GB/user
 - /work/userid : 1.5TB/user(核心設施或另有科技部計劃用戶), 100GB/user(教育訓練用戶)
 - /staging/biology/userid : 5T 提供核心設施用戶
 - /staging/reserve/PI_folder : 付費空間 (GP 1-5)

GP1-1~GP1-3: 400+ open source apps

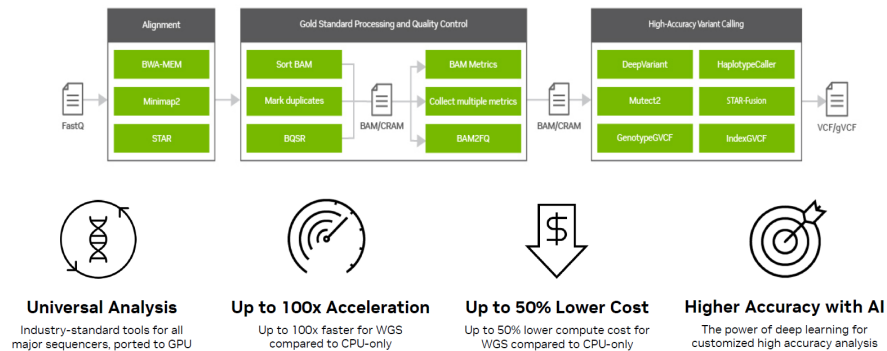


GP1-3: GPU (V100) for NVIDIA apps

Parabricks

NVIDIA Parabricks for Alignment & Variant Calling

Speed, Scale, Accuracy

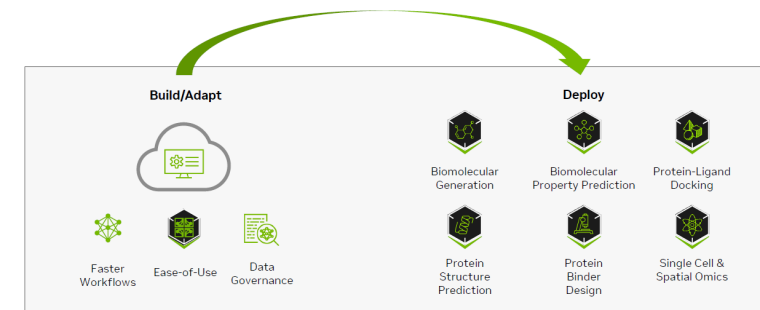


NVIDIA

BioNeMo

What is NVIDIA BioNeMo?

Build, Adapt and Deploy AI Models for Computer-Aided Drug Discovery



BioNeMo Framework
Open-Source (GitHub) | NVIDIA AI Enterprise

BioNeMo NIMs
Developer Program | NVIDIA AI Enterprise



NVIDIA

GP1-7: Ingenuity Pathway Analysis

讓你的discussion讀起來更有料



GP1-9: 基因體分析硬體加速服務

花8X錢 省60X時間



	台灣杉1號 GATK	台灣杉3號 GATK	DRAGEN Server
NA12878(35xWGS) 113.8 GBases	20h:04m:34s	17h:26m:20s	00h:17m:16s
國科會計畫收費	56.2元	78.1元	591元
一般學界收費	562元	234元	591元

nf-core/Nextflow

The screenshot shows the 'Pipelines' page of the nf-core website. The header includes navigation links: Home, Pipelines, Resources, Docs, Community, and About. A search bar is present with the text '10x'. Below the header, a green banner displays the title 'Pipelines' and the text 'Browse the 140 pipelines that are currently available as part of nf-core.' Below the banner, there is a search input field and several filter buttons: 'Released' (84), 'Under development' (44), and 'Archived' (12). There are also buttons for 'Stars' and a menu icon. The main content area displays two pipeline cards. The first card is for 'rnaseq' with a green checkmark and 1121 stars. Its description is 'RNA sequencing analysis pipeline using STAR, RSEM, HISAT2 or Salmon with gene/isoform counts and extensive quality control.' It has tags for 'rna' and 'rna-seq' and shows version '3.21.0' released 'about 1 month ago'. The second card is for 'sarek' with a green checkmark and 496 stars. Its description is 'Analysis pipeline to detect germline or somatic variants (pre-processing, variant calling and annotation) from WGS / targeted sequencing'. It has tags for 'annotation', 'cancer', 'gatk4', 'genomics', 'germline', 'pre-processing', 'somatic', 'target-panels', 'variant-calling', 'whole-exome-sequencing', and 'whole-genome-sequencing'. It shows version '3.6.1' released '5 days ago'.

Home Pipelines Resources Docs Community About

Search 10x 4/8

Pipelines

Browse the 140 pipelines that are currently available as part of nf-core.

Search

Released 84 Under development 44 Archived 12 Stars

rnaseq ✓ ☆ 1121

RNA sequencing analysis pipeline using STAR, RSEM, HISAT2 or Salmon with gene/isoform counts and extensive quality control.

rna rna-seq

3.21.0 released about 1 month ago

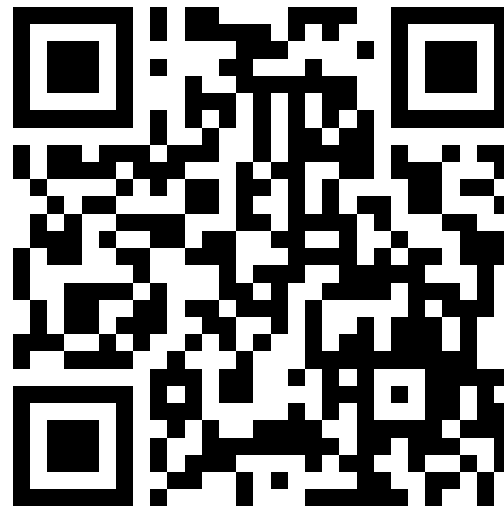
sarek ✓ ☆ 496

Analysis pipeline to detect germline or somatic variants (pre-processing, variant calling and annotation) from WGS / targeted sequencing

annotation cancer gatk4 genomics germline pre-processing
somatic target-panels variant-calling whole-exome-sequencing
whole-genome-sequencing

3.6.1 released 5 days ago

更多資訊



<https://lions.nchc.org.tw/ngsApplyDoc.jsp>

訂閱GP1



國網中心GP1生醫核心設施

@NCHC-GP1 · 9 subscribers · 14 videos

本核心設施提供以生醫專用之計算與儲存設施及分析平台為主的資訊服務，除了涵蓋生醫...more

lions.nchc.org.tw and 2 more links

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Videos Playlists

Latest Popular Oldest



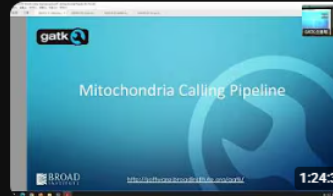
2025 數位生物學AI實作工作坊: NVIDIA Parabricks super-charged genome analysis

119 views · 2 weeks ago



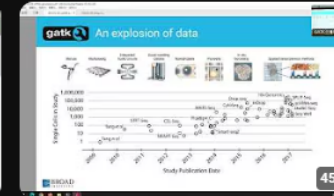
2025 數位生物學AI實作工作坊: NVIDIA BioNeMo Protein Design

91 views · 2 weeks ago



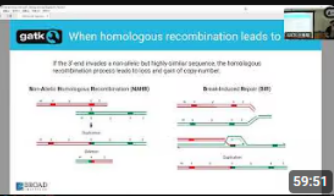
2023 GATK國際教育訓練 Day4 Part1 ([Guided Demo] Mitochondria Data/Intro to...

15 views · 2 months ago



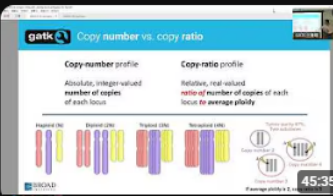
2023 GATK國際教育訓練 Day4 Part2 (Intro to single-cell RNA-seq analysis)

6 views · 2 months ago



2023 GATK國際教育訓練 Day3 Part3 (Germline Copy Number Variation)

6 views · 2 months ago



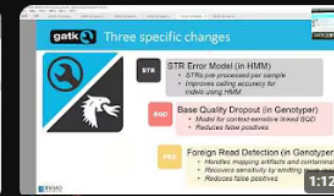
2023 GATK國際教育訓練 Day3 Part2 (Intro to Somatic CNAs)

3 views · 2 months ago



2023 GATK國際教育訓練 Day3 Part1 (Intro to Somatic Variant Discovery/Somatic SNVs...

2 views · 2 months ago



2023 GATK國際教育訓練 Day2 Part3 (Intro to DRAGEN-GATK/Processing Long Reads)

5 views · 2 months ago

吃米要知米價



Illumina Library Prep Services

Fees of sample QC test would be additionally charged depending on services.

Whole Genome Sequencing		Academy	Industry
(S-Ca)	Shotgun Paired-End DNA Lib Prep, Gel-free	4,200	5,250
(S-Cb)	Shotgun Paired-End DNA Lib Prep, Gel-plus	7,500	9,380
(S-D)	Shotgun Long Insert Paired-End DNA Lib Prep, Gel-plus	7,800	9,750
(S-R)	Nextera Paired-End DNA Lib Prep	3,900	4,880
3D Genome Sequencing		Academy	Industry
(S-Ha)	Hi-C DNA Lib Prep (ARIMA)	21,500	26,880
(S-Hc)	Hi-C DNA Lib Prep (Phase Genomics)	22,200	27,750
(S-Hd)	Micro-C DNA Lib Prep (Dovetail)	27,500	34,380
(S-He)	HiChIP DNA Lib Prep (Dovetail)	29,000	36,250
(S-Hf)	Omni-C DNA Lib Prep (Dovetail)	27,500	34,380
Whole Exome Sequencing Target Enrichment		Academy	Industry
(S-X)	Human Whole Exome Capture	12,000	15,000
(S-Y)	Target Panel Capture (Customized Prep)	Inquiry	Inquiry

Illumina 促銷優惠

Special Promotions

Promotions (Detailed kit specifications)		Academy	Industry
(NX2100-LTO)	NextSeq P2 v3, 100 cycles (limited-time offer; 1 FC)	57,000	71,250
(NX2100-LTO2)	NextSeq P2 v3, 100 cycles (limited-time offer; >2 FC)	54,000	67,500
(NX3300-LTO1)	NextSeq P3, 300 cycles (limited-time offer; 1 FC)	212,000	265,000
(NX3300-LTO2)	NextSeq P3, 300 cycles (limited-time offer; 2-3 add-on)	181,700	227,130
(NX3300-LTO4)	NextSeq P3, 300 cycles (limited-time offer; above 4 add-on)	166,600	208,250
(Detailed kit specifications)			
(MS50) [2]	MiSeq 50 cycles v2, SR50	35,400	44,250
(MS300) [3]	MiSeq 300 cycles v2, PE150 or SR300	45,900	57,380
(MS500) [2]	MiSeq 500 cycles v2, PE250	51,700	64,630
(MS150) [2]	MiSeq 150 cycles v3, PE75 or SR150	39,500	49,380

 Find Genomics Services
 Resources Log In

The Most Reliable Way to Order NGS Services from Top Providers.

1. Find and select matching services (optional):

Sequencing & library prep
Sequencing only
Library prep only

Project type: DNA (whole genome)

Number of samples: 1

Match by coverage
Match by number of reads
Help me

Targeted genome size: 3,200,000,000

Minimum coverage per sample: 30

2. Submit your request:

We typically respond within 2 business hours (US Central Time)

Email: Your email

First name: First name

Last name: Last name

I need library preparation and sequencing for 1 samples with a minimum coverage of 30X on genome size of 3,200,000,000 bases for a DNA (whole genome) project

If you're interested in any of the options below, click "Add to Request".
0 options selected.

Total: **\$6,414.68**

Add to Request

Close details

Instrument: **Illumina NextSeq 1000/2000 P2**
Allocation: **2 lanes**
Number of samples: **1**
Location: **Oklahoma, USA**
Turnaround: **~28 days**
Estimated price per Gb: **\$40.09/Gb**

Coverage per sample: **~50X**
Output per sample: **~160Gb**
Reads per sample: **~1,600M**
Read length: **2 x 100bp (Paired End)**
Library type: **Illumina - DNA (whole genome)**
Kit: **Illumina Nextera DNA**

Details:

Description	Qty x Unit Price	Subtotal
Next-Generation Sequencing	2 x \$3,161.62	\$6,323.24
- Instrument: Illumina NextSeq 1000/2000 P2 - PE 100 Cycle - Read length: 2 x 100bp (Paired End) - Pricing unit: per flow cell - Number of samples: 1 - Estimated number of pass filter PE reads/sample: Up to 1,600.0M (800.0M in each direction)* - Estimated output/sample: Up to 160.0 Gb* - Estimated coverage/sample: Up to ~50X (on genome size of 3.2Gb) - Guaranteed number of pass filter PE reads/sample: TBD (to be confirmed by the provider) - Deliverables: FastQ files uploaded to Genohub project bucket		
up to 400 million clusters and 80 Gb (2 X 100 cycles or 1 X 200 cycles)*		
The base price for sequencing does not include library QC costs. The QC costs are charged separately. We require a minimum of 20 microliters at 5 ng/ul (fluorescence method). More is better.		
* Estimates based on manufacturer specs. The guaranteed estimate is 90% of		

Platform/application

Illumina Library Prep Services

Fees of sample QC test would be additionally charged depending on services.

Whole Genome Sequencing		Academy	Industry
(S-Ca)	Shotgun Paired-End DNA Lib Prep, Gel-free	4,200	5,250
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(S-Hc)	Hi-C DNA Lib Prep (Phase Genomics)	22,200	27,750
(S-Hd)	Micro-C DNA Lib Prep (Dovetail)	27,500	34,380
(S-He)	HiChIP DNA Lib Prep (Dovetail)	29,000	36,250
(S-Hf)	Omni-C DNA Lib Prep (Dovetail)	27,500	34,380
Whole Exome Sequencing Target Enrichment		Academy	Industry
(S-X)	Human Whole Exome Capture	12,000	15,000
(S-Y)	Target Panel Capture (Customized Prep)	Inquiry	Inquiry
Metagenome Sequencing		Academy	Industry
(S-P)	Nextera Indexing PCR (2nd Step PCR)	1,000	1,250
(S-Q)	16S Amplicon-seq (V3-V4) Lib Prep	1,300	1,630
Epigenome Sequencing		Academy	Industry
(S-B)	(Bisulfite Seq) DNA Methylation Lib Prep	6,300	7,880
(S-I)	(ChIP-Seq) ChIP DNA Lib Prep	5,800	7,250
(S-Ja)	(DAP-Seq) Genomic DNA Lib Prep for TF Binding	3,500	4,380
(S-Jb)	(DAP-Seq) Indexing PCR	2,000	2,500
Whole Transcriptome Sequencing		Academy	Industry
(S-Sa)	Stranded RNA Lib Prep, Poly-A	4,900	6,130
(S-Ta)	Stranded RNA Lib Prep, Ribo-zero Plus	7,100	8,880
(S-Tb)	Low-input Stranded RNA Lib Prep, Ribo-zero (Mammalian Only)	6,800	8,500
(S-Tz)	Stranded RNA Lib Prep, Ribo-zero (Customized Prep)	Inquiry	Inquiry
(S-U)	Ultra Low-Input RNA Lib Prep, Poly-A (Non-stranded)	6,200	7,750
(S-Sz)	Stranded RNA Lib Prep, Poly-A (Customized Prep)	Inquiry	Inquiry
Small RNA Sequencing		Academy	Industry
(S-E)	Small RNA Lib Prep (miRNA)	9,400	11,750
(S-G)	Degradome Lib Prep (PARE)	16,000	20,000

PacBio Sequel Library Prep Services

Fees of sample QC test would be additionally charged depending on services.

Service Items (SPK3.0)		Academy	Industry
(P-BEL)	SMRTbell Prep	8,100	10,130
(P-MAS)	MAS Prep	23,800	29,750
Amplicon Sequencing		Academy	Industry
(P-A)	Full-length 16S Amplicon Prep (1-step PCR)	1,200	1,500
(P-Bx)	Barcoded Amplicon Prep (2nd PCR)	1,400	1,750
(P-By)	Barcoded Amplicon Prep (2-steps PCR)	2,000	2,500
(P-C)	Plasmid/Amplicon DNA SMRTbell Lib Prep (Barcoded Adapter Ligation)	8,100	10,130
Whole Genome Sequencing		Academy	Industry
(P-D)	Ultra Low-input DNA HiFi SMRTbell Lib Prep (Gel-plus 8-15KB)	26,600	33,250
(P-G)	Genomic DNA SMRTbell Prep, CLR (10-100KB)	12,900	16,130
(P-H)	Genomic DNA SMRTbell Prep, HiFi (5-50KB)	12,500	15,630

*申請(P-H)同一張定序單內大於4個樣品，可享有9折優惠

RNA Iso-Seq		Academy	Industry
(P-I)	RNA Iso-Seq SMRTbell Prep	10,000	12,500
(P-Ix)	Multiplexed RNA Iso-Seq Prep	5,000	6,250
(P-Jx)	Multiplexed RNA FLEP-Seq Prep	8,300	10,380

MAS-seq		Academy	Industry
(P-M)	MAS-Seq SMRTbell Prep for FL16S	1,200	1,500
(P-Nh)	MAS-Seq SMRTbell Prep for Bulk Iso-Seq (homebrew)	22,200	27,750
(P-Nk)	MAS-Seq SMRTbell Prep for Bulk Iso-Seq (Kinnex)	10,800	13,500

ONT Library Prep Services

Fees of sample QC test would be additionally charged depending on services.

ONT Library Prep Services		Academy	Industry
(N-D109)	ONT Genomic DNA Lib Prep (for GridION)	6,600	8,250
(N-D114)	ONT Genomic DNA Lib Prep (for PromethION)	6,600	8,250

GridION Sequencing Services

GridION Sequencing Services		Academy	Industry
(GridION094)	GridION (MiniON R9.4)	39,700	49,630
(GridION104)	GridION (MiniON R10.4)	39,700	49,630
(GridION-P)	PromethION P2 Solo (PromethION R10.4)	55,400	69,250

10x Genomics – Spatial Transcriptome

Fees of sample QC test would be additionally charged depending on services.

10x Visium		Academy	Industry
(X-VTO)	10x Visium Tissue Optimization	44,800	56,000
(X-VGE)	10x Visium Gene Expression	67,500	84,380
(X-VFP)	10x Visium Gene Expression for FFPE	84,100	105,130
(X-VFP-Cyt)	10x Visium CytAssist Gene Expression for FFPE	182,700	228,380
(X-VHD)	10x Visium HD (CytAssist) (human, mouse)	Inquiry	Inquiry
(X-HD3)	10x Visium HD 3-polyA (CytAssist)	Inquiry	Inquiry

10x Xenium		Academy	Industry
(Xe-h5k), (X-h500)	10x Xenium human panel	Inquiry	Inquiry
(Xe-m5k), (X-m500)	10x Xenium mouse panel	Inquiry	Inquiry
(Xe-cust)	10x Xenium custom panel	Inquiry	Inquiry

10x Genomics – Single Cell

Fees of sample QC test would be additionally charged depending on services.

10x Single Cell Chromium X		Academy	Industry
(X-CSC)	10x Chromium X Single Cell 3' GEX	90,700	113,375
(X-CHP1)	Single Cell GEM Chip G (CSC)	12,000	15,000
(X-CIM)	10x Chromium X Single Cell 5' GEX/VD	94,300	117,880
(X-CHP2)	Single Cell GEM Chip K (CIM)	13,000	16,250
(X-BCRh)	VDI-human BCR	9,400	11,750
(X-TCRh)	VDI-human TCR	9,400	11,750
(X-CMM)	10x Chromium X Single Cell Multiome	159,000	198,750
(X-CHP3)	Single Cell GEM Chip J (CMM)	12,250	15,320
(X-CTC)	10x Chromium X Single Cell ATAC	82,400	103,000
(X-CHP4)	Single Cell GEM Chip H (CTC)	14,000	17,500
(X-CITE)	CITE-seq	Inquiry	Inquiry

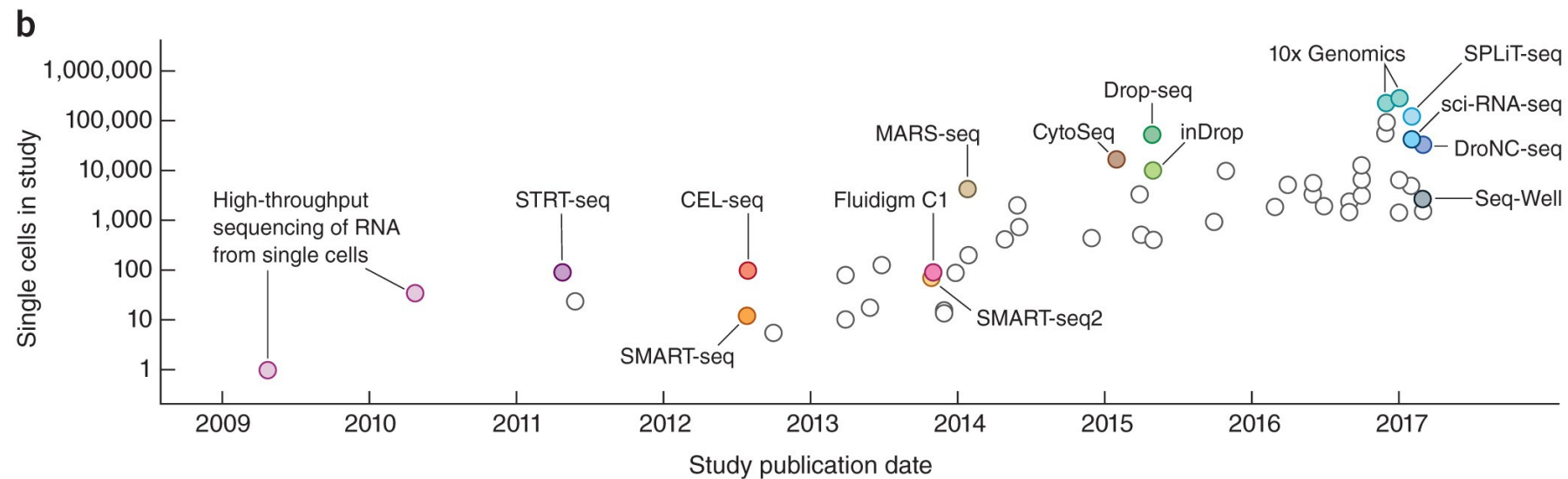
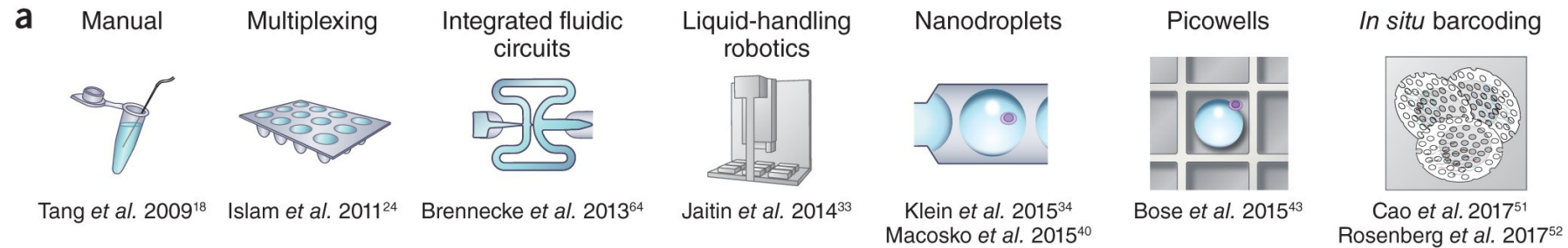


Teton-CytoProfiling

- Elembio CloudBreak FreeStyle
- Avi24 (Biosciences)
- Sequencing Specs
- Optimization and Culture Techniques
- Teton™ CytoProfiling User Guide
- Teton – CytoProfiling

Teton Panels Kit (Detailed kit specifications)	Academy (Chip / FlowCell)	Industry (Chip / FlowCell)
Human MAPK-Cell Cycle Panel Kit	Inquiry	Inquiry
Human MAPK-Apoptosis Panel Kit	Inquiry	Inquiry
Human Neuro Panel Kit	Inquiry	Inquiry
Human Immuno Panel Kit	Inquiry	Inquiry

Evolution of RNA-seq

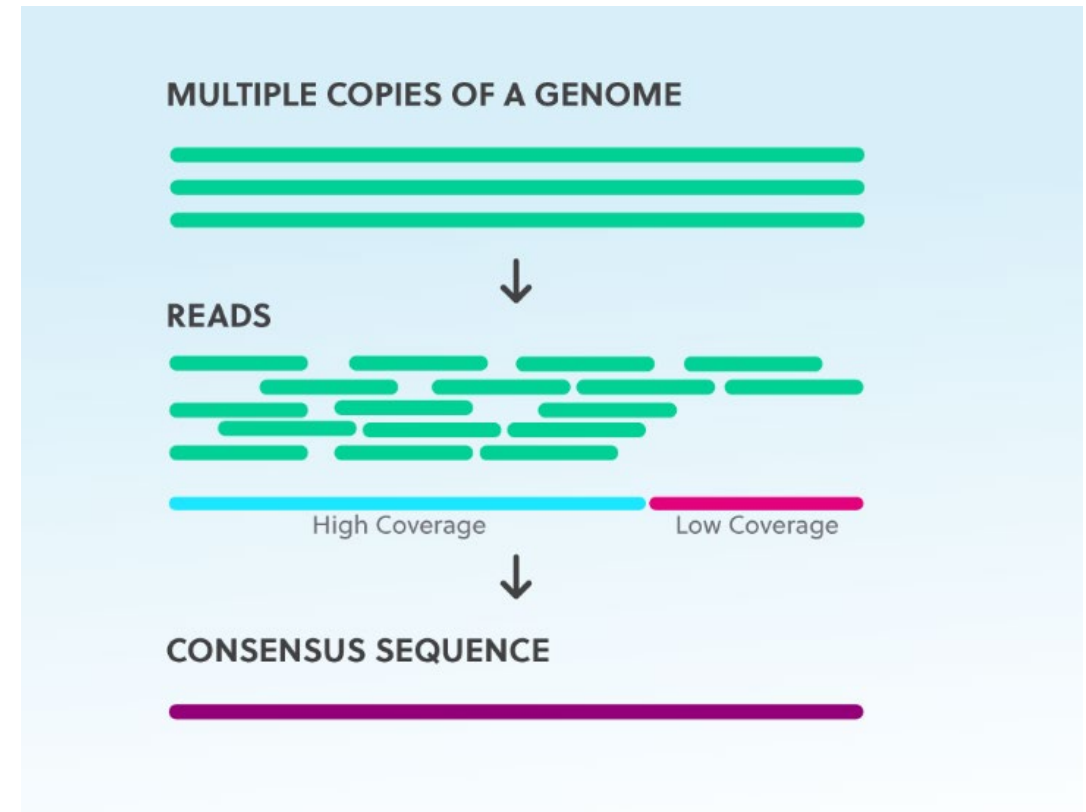
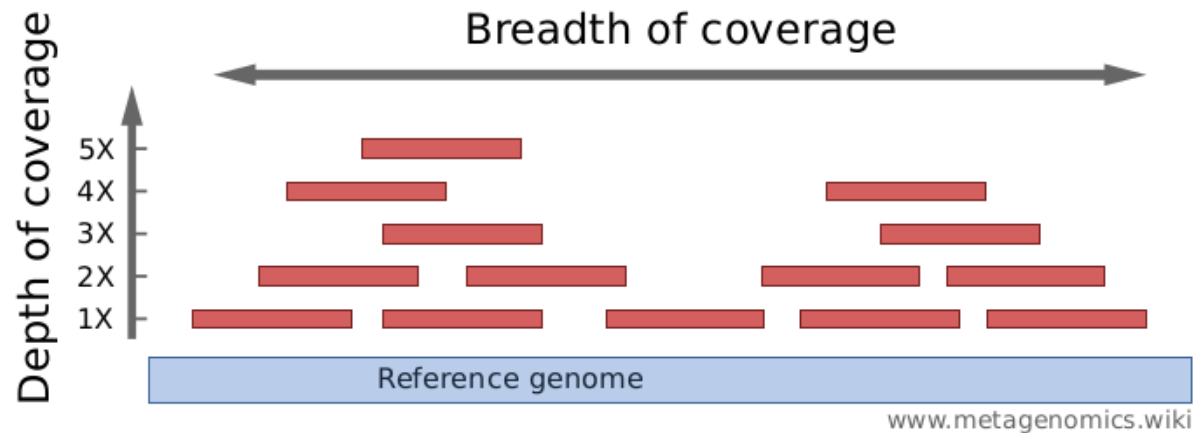


NGS三本柱

Budget-dependent experimental design 玩自己的+別人的data

	Detection or Application	Recommended Coverage (x) / Reads (millions)
Whole genome sequencing	Homozygous SNVs	15x
	Heterozygous SNVs	33x
	INDELs	60x
	Genotype calls	35x
	CNV	1-8x
Whole exome sequencing	Homozygous SNVs	100x (3x local depth)
	Heterozygous SNVs	100x (13x local depth)
	INDELs	not recommended
Transcriptome Sequencing	Differential expression profiling	10-25M
	Alternative splicing	50-100M
	Allele specific expression	50-100M
	De novo assembly	>100M

Depth of coverage



WGS

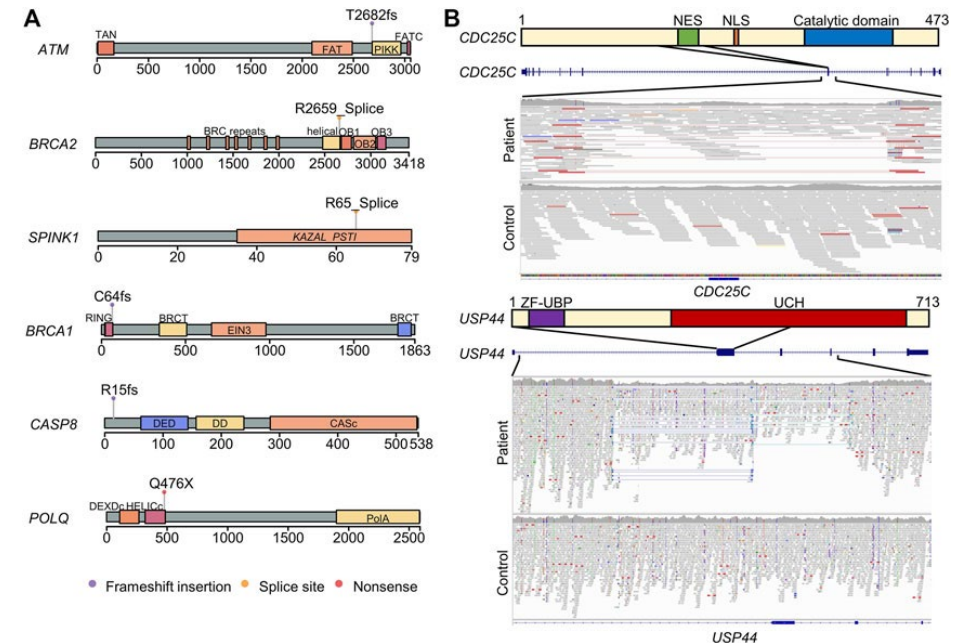
> *Front Genet.* 2023 May 10;14:1172365. doi: 10.3389/fgene.2023.1172365. eCollection 2023.

Diagnostic rate of germline pathogenic variants in pancreatic ductal adenocarcinoma patients using whole genome sequencing

An-Ko Chung ^{1 2}, Ro-Ting Lin ³, Chun-Chieh Yeh ^{4 5}, Chi-Ying Yang ⁶, Chang-Jiun Wu ⁷,
 Pei-Lung Chen ^{1 8}, Jaw-Town Lin ⁹

Affiliations + expand

PMID: 37234870 PMCID: PMC10205989 DOI: 10.3389/fgene.2023.1172365



WES

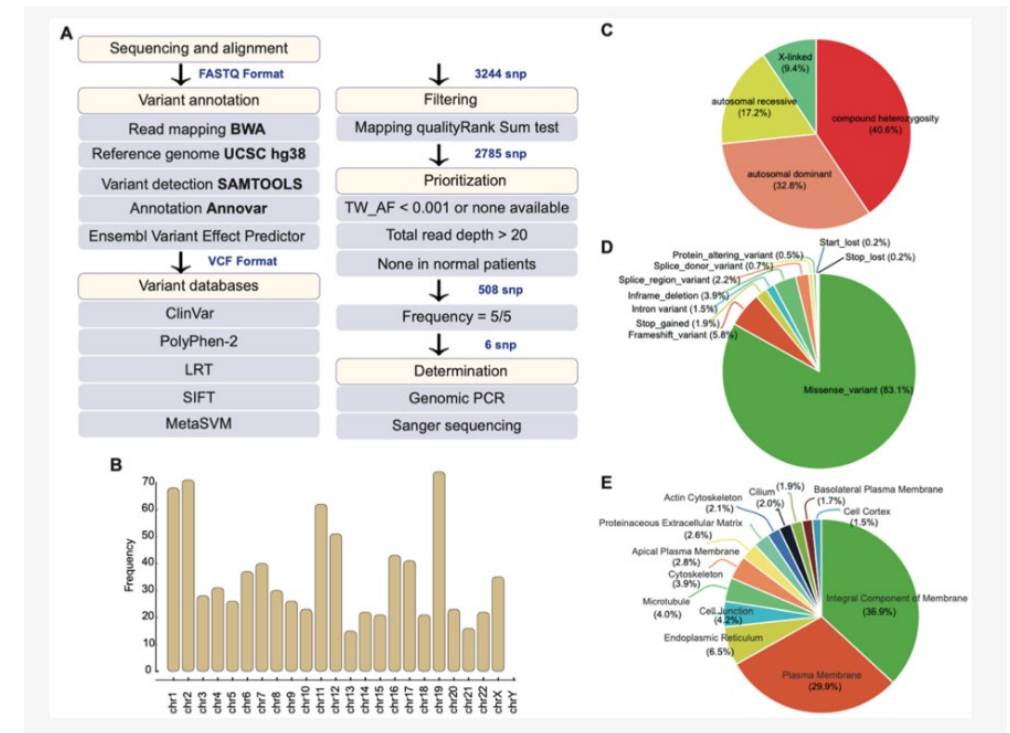
Case Reports > Int J Mol Sci. 2021 May 25;22(11):5594. doi: 10.3390/ijms22115594.

Identification of Novel Genomic-Variant Patterns of OR56A5, OR52L1, and CTSD in Retinitis Pigmentosa Patients by Whole-Exome Sequencing

Ting-Yi Lin ¹, Yun-Chia Chang ², Yu-Jer Hsiao ³, Yueh Chien ^{4 5}, Ying-Chun Jheng ^{4 6 7},
 Jing-Rong Wu ⁴, Lo-Jei Ching ⁴, De-Kuang Hwang ^{2 4 6 8}, Chih-Chien Hsu ², Tai-Chi Lin ^{2 4 6 8},
 Yu-Bai Chou ², Yi-Ming Huang ², Shih-Jen Chen ^{2 6}, Yi-Ping Yang ^{4 6 9 10}, Ping-Hsing Tsai ^{4 5}

Affiliations + expand

PMID: 34070492 PMCID: PMC8198027 DOI: 10.3390/ijms22115594



Bulk RNA-seq

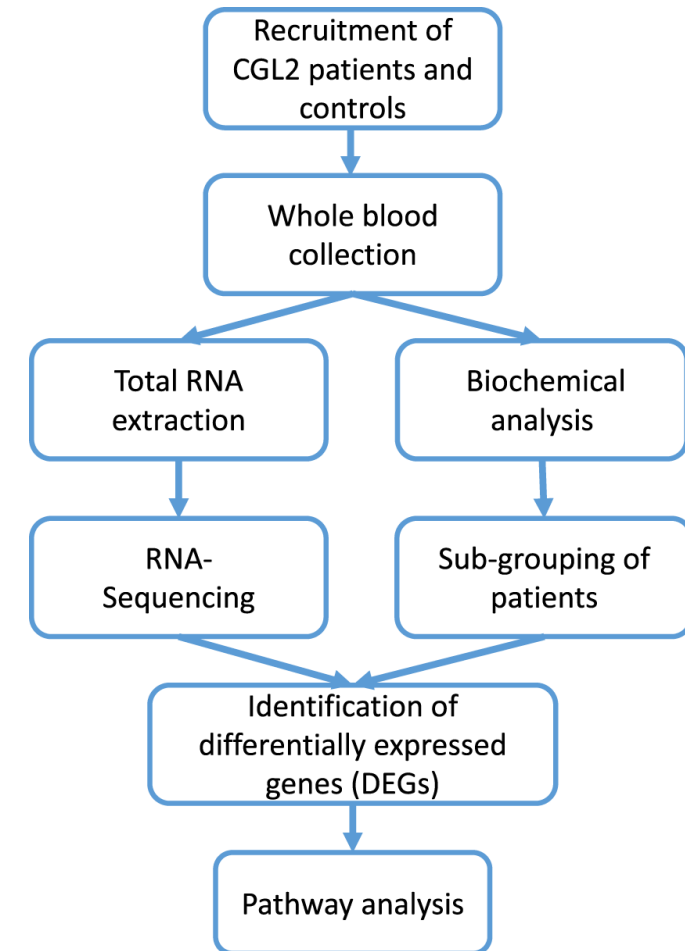
> [Sci Data](#). 2021 Oct 13;8(1):265. doi: 10.1038/s41597-021-01040-4.

RNA-seq of peripheral blood mononuclear cells of congenital generalized lipodystrophy type 2 patients

Yen-Hua Huang^{1 2}, Tzu-Chien Su¹, Chung-Hsing Wang^{3 4}, Siew-Lee Wong⁵, Yin-Hsiu Chien⁶, Yu-Tai Wang⁷, Wuh-Liang Hwu⁶, Ni-Chung Lee⁸

Affiliations + expand

PMID: 34645804 PMCID: PMC8514467 DOI: 10.1038/s41597-021-01040-4



Single-cell RNA-seq

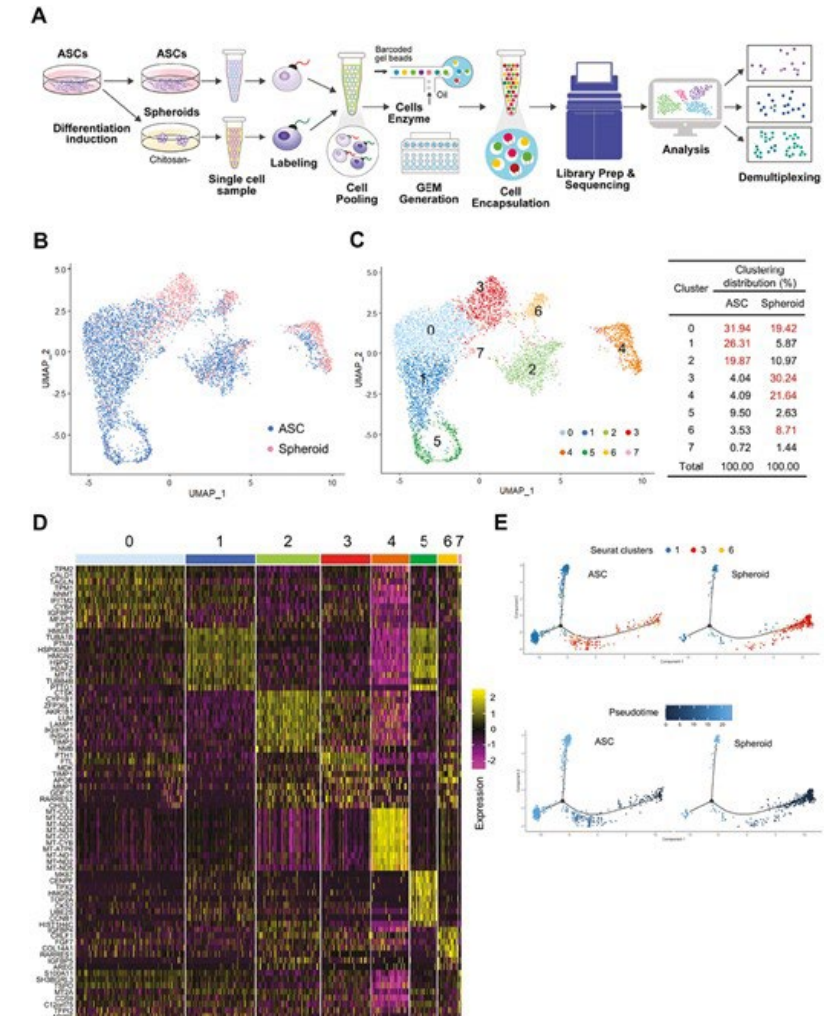
> *Stem Cells Transl Med.* 2024 Mar 15;13(3):293-308. doi: 10.1093/stcltm/szad090.

Histone Trimethylations and HDAC5 Regulate Spheroid Subpopulation and Differentiation Signaling of Human Adipose-Derived Stem Cells

Ming-Min Chang^{1 2}, Yi-Kai Hong^{3 4}, Chao-Kai Hsu^{3 4}, Hans I-Chen Harn⁵, Bu-Miin Huang¹,
 Ya-Hsin Liu⁶, Fu-I Lu⁷, Yuan-Yu Hsueh^{4 8 9}, Shau-Ping Lin¹⁰, Chia-Ching Wu^{1 4 11 12}

Affiliations + expand

PMID: 38173411 PMCID: PMC10940829 DOI: 10.1093/stcltm/szad090



WGS + RNA-seq

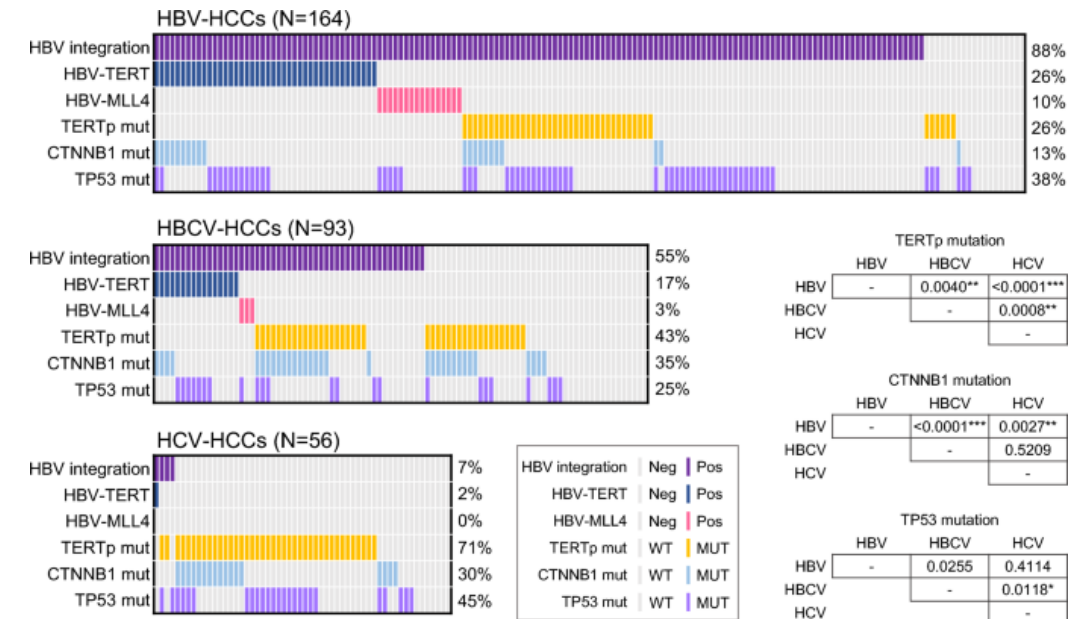
> J Biomed Sci. 2025 Jan 2;32(1):2. doi: 10.1186/s12929-024-01094-7.

HBV DNA integration and somatic mutations in HCC patients with HBV-HCV dual infection reveals profiles intermediate between HBV- and HCV-related HCC

Chiao-Ling Li¹, Chia-Lang Hsu^{2 3 4}, You-Yu Lin^{5 6}, Ming-Chih Ho^{7 8}, Rey-Heng Hu^{7 9},
 Sheng-Tai Tzeng¹⁰, Ya-Chun Wang¹⁰, Yasuhito Tanaka^{11 12}, Pei-Jer Chen^{13 14 15},
 Shiou-Hwei Yeh^{16 17 18}

Affiliations + expand

PMID: 39743539 PMCID: PMC11694426 DOI: 10.1186/s12929-024-01094-7



WES + published RNA-seq

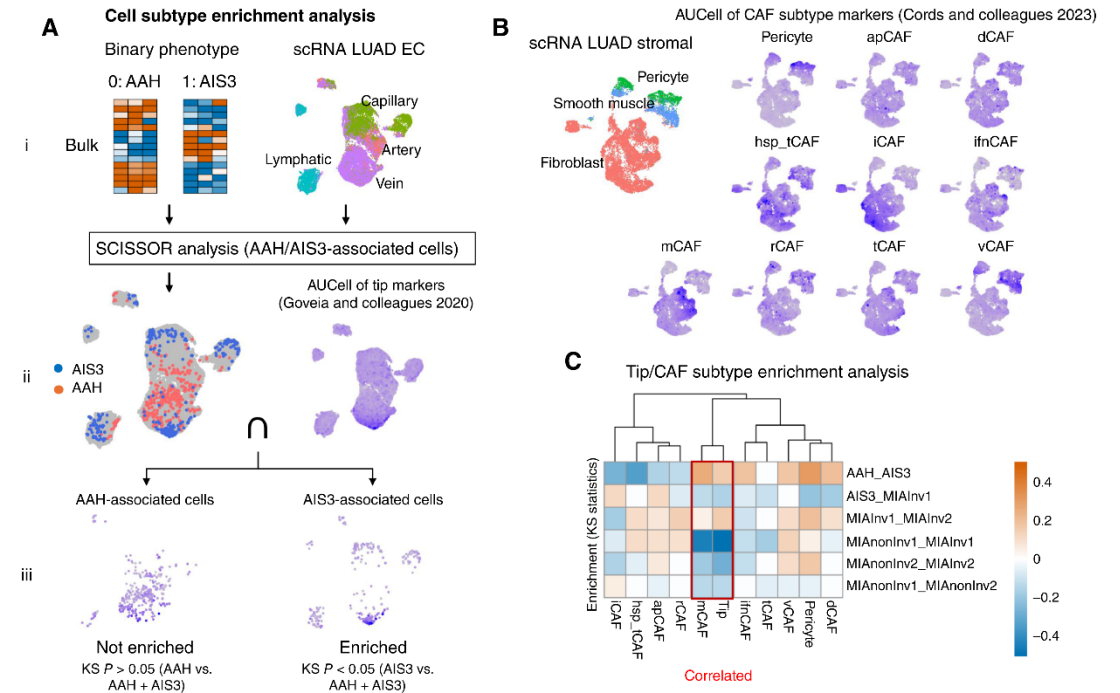
> [Cancer Res.](#) 2025 Feb 1;85(3):602-617. doi: 10.1158/0008-5472.CAN-24-0821.

Multiomics Analysis Reveals Molecular Changes during Early Progression of Precancerous Lesions to Lung Adenocarcinoma in Never-Smokers

Yun-Ching Chen ^{#1}, Chia-Lang Hsu ^{#2}, Hui-Min Wang ^{#1}, Shang-Gin Wu ^{#3},
 Yih-Leong Chang ⁴, Jin-Shing Chen ^{5 6}, Yu-Ching Wu ², Yen-Ting Lin ³, Ching-Yao Yang ⁷,
 Mong-Wei Lin ⁶, Jang-Ming Lee ⁶, Shuenn-Wen Kuo ⁶, Ke-Cheng Chen ⁶, Hsao-Hsun Hsu ⁸,
 Pei-Ming Huang ⁶, Yen-Lin Huang ⁴, Chong-Jen Yu ^{7 9}, Mehdi Pirooznia ¹, Bevan E Huang ¹,
 Rob Yang ¹, Jin-Yuan Shih ⁷, Pan-Chyr Yang ^{7 10}

Affiliations + expand

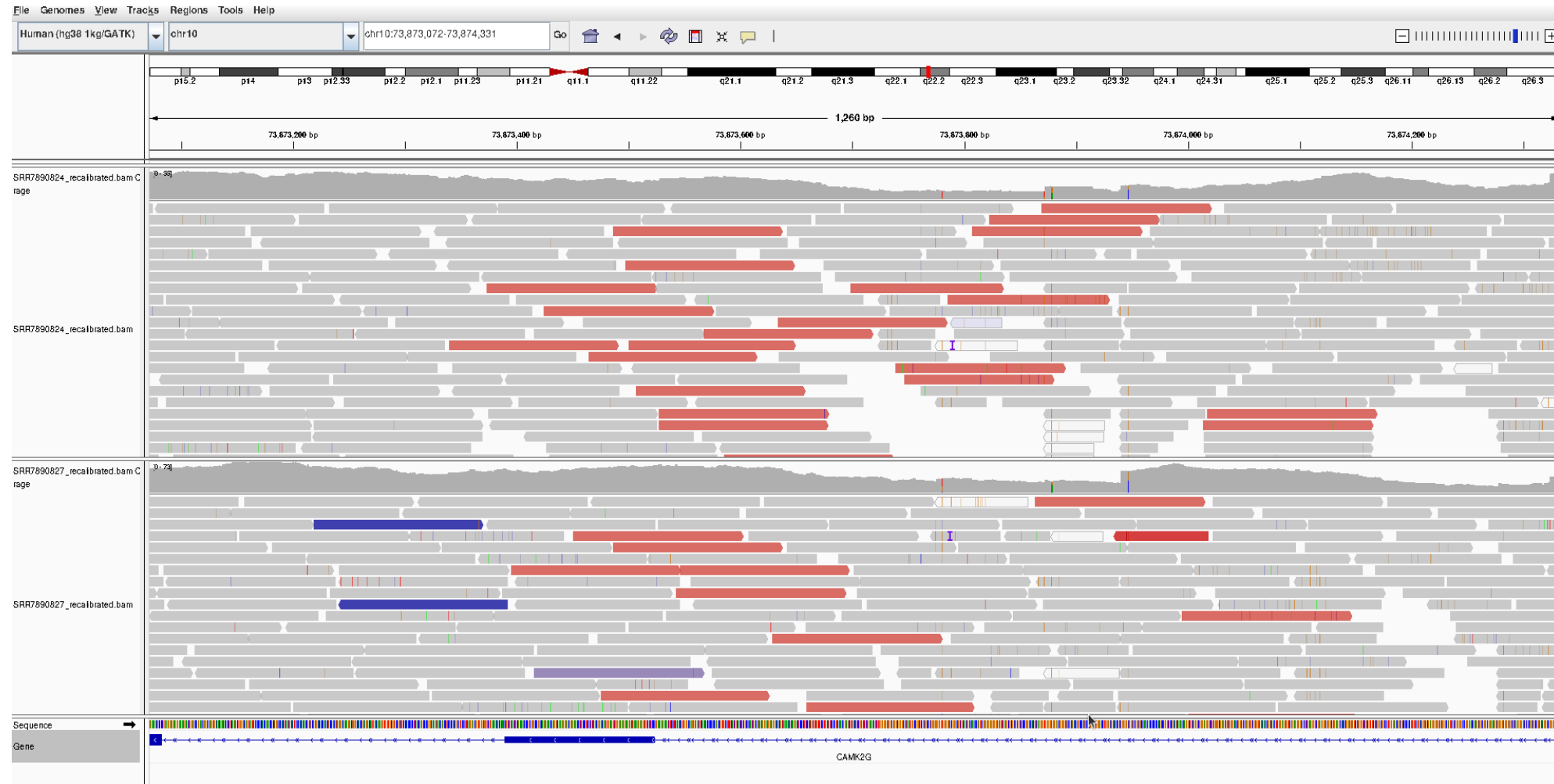
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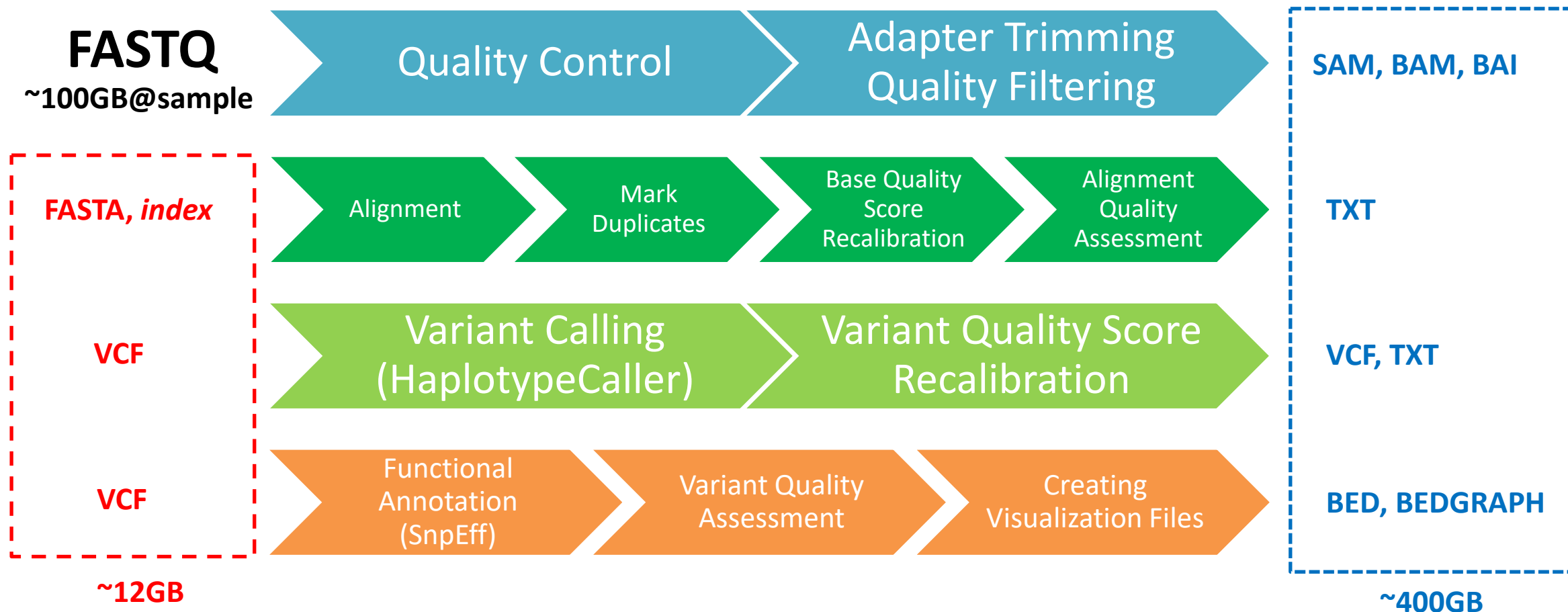
NGS data files

normal

tumor



GATK WGS pipelines & data files



NGS raw data

Platform	Primary Format	File Size	Read Length	Error Profile	Use Cases
Illumina	FASTQ	1-50 GB	50-300bp	Low substitution	Genome sequencing, RNA-seq, ChIP-seq
Nanopore	FAST5/POD5	10-500 GB	1kb-2Mb	Indels, homopolymer	Long-read assembly, structural variants
PacBio	BAM/FASTQ	5-200 GB	1kb-100kb	Random errors	High-quality assembly, isoform analysis

FASTQ/FASTA

FASTA: Simple Sequence Storage

[illegible]

FASTQ: The Universal Sequence Format

[illegible]

SAM/BAM

SAM: Sequence Alignment Map
BAM: Compressed Binary Alignments

[illegible]

VCF/BCF

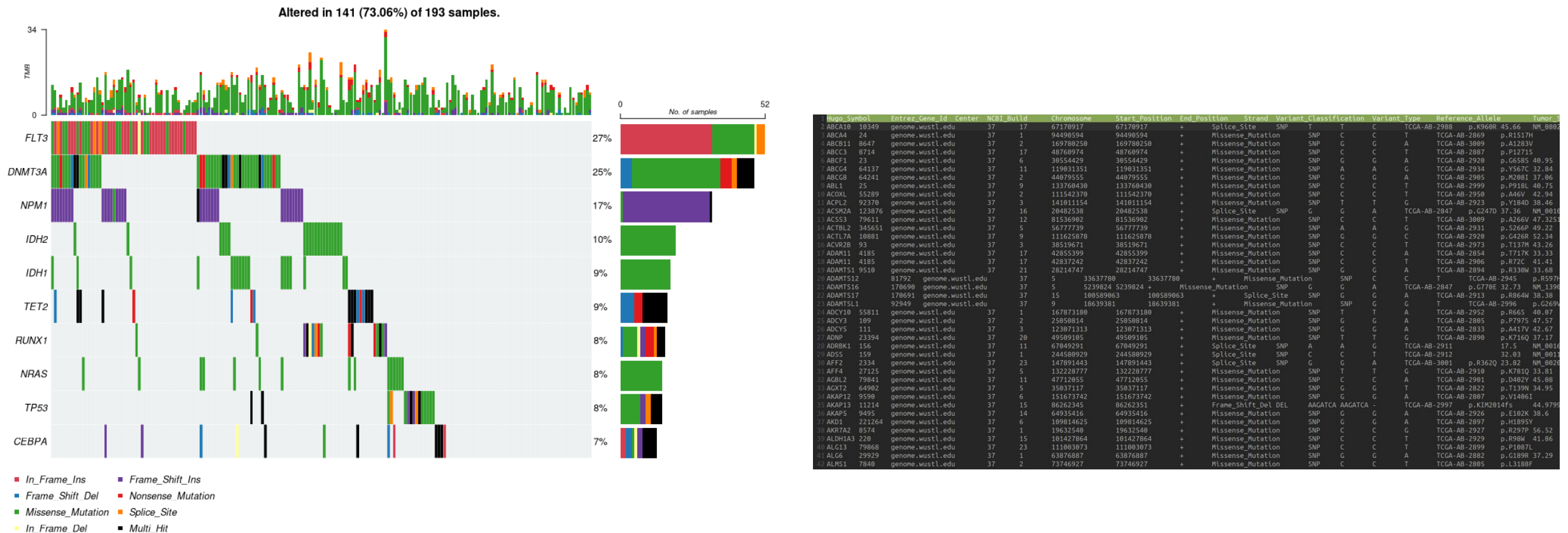
VCF: Variant Call Format

BCF: Binary Variant Call Format

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```

MAF

MAF: Mutation Annotation Format



resources

1. <https://genohub.com/resources/>
2. <https://info.abmgood.com/next-generation-sequencing-ngs>
3. <https://ngs101.com/tutorials/>

Logging to T3



國網中心GP1生醫核心設施...
 申請加入GP1核心設施服務...
 登入台灣杉三號生醫專用節...
 資料上傳
 生醫計算雲端節點與資源...
 高速計算儲存空間
 巨量資料儲存空間
 儲存空間管理政策與使用通...
 公用軟體安裝位置與使用通...
 Partition(Queue) 資源設定
 工作指令碼
 查看job狀態/刪除工作
 進階
 桌面環境、圖形環境
 軟體使用說明
 修改記錄
 Last updated: 2025/06/12 0...

全部展開
 回到頂部
 移至底部

國網中心GP1生醫核心設施 - 台灣杉三號生醫專用節點使用說明

申請加入GP1核心設施服務計畫

- 若您尚未申請GP1核心設施計算服務，請參考[申請服務流程](#)。
- 若您已經申請計算服務，但尚未加入核心設施Service服務計畫，請參考[申請加入說明](#)。

登入台灣杉三號生醫專用節點

- 生醫專用節點主機位置：t3-c4.nchc.org.tw 或 203.145.216.54。
- 請勿使用台灣杉1號進行計算，如此會衍生出額外的費用，請使用者配合。
- 亦請勿使用登入節點主機的CPU與GPU進行計算，以免影響登入節點運作與排程系統效能，敬請配合。
- 帳號密碼：iservice內 會員中心->會員資訊->主機帳號資訊，可以找到您的帳號或修改密碼
- One Time Password(OTP)請參閱：<https://man.twcc.ai/@TWCC-III-manual/SJwbCxxqO#取得-OTP-認證碼>

資料上傳

- 請使用 t3-c4.nchc.org.tw 節點上傳資料，可以使用sftp、scp、rsync上傳資料。

- **GP1 使用手冊:**
<https://man.twcc.ai/cV1vwW9GRTql6ODnTREPhw>
- **Demo examples:**
https://github.com/nchcgp1/workshop/tree/main/2025_1104

Prerequisite

- Win11/Mac/Linux
- iService/T3主機帳號
- Internet
- Mobile app: IDExpert
- FileZilla

iOS



Android



Secure SHell

Windows

cmd



powershell

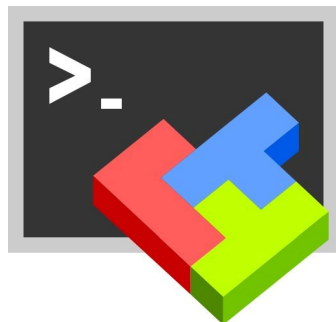


Mac/Linux

terminal



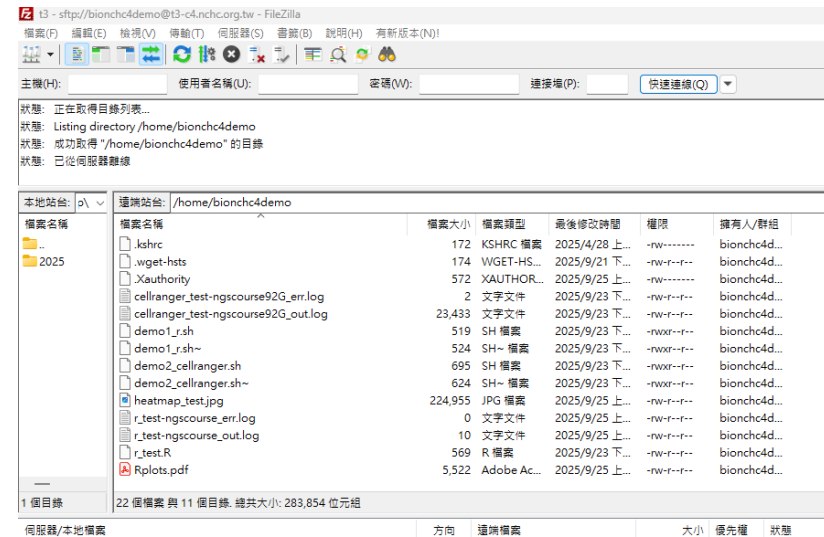
MobaXterm (freemium)



Terminal + FileZilla

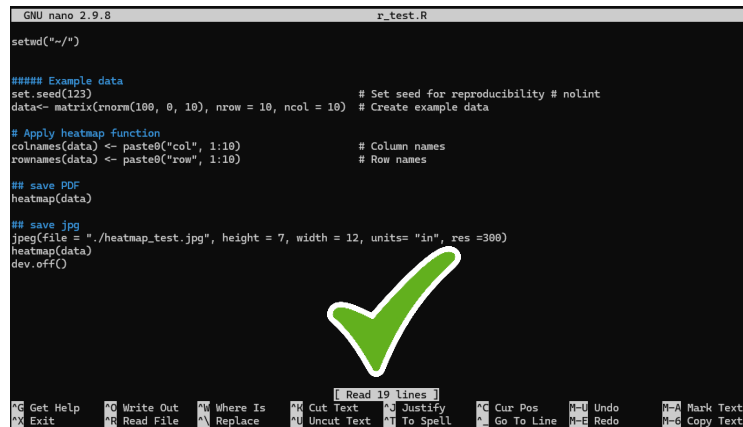
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-rw-r--r-- 1 bionchc4demo ACD114107 2 Sep 23 21:58 cellranger_test-ngscourse92G_err.log
-rw-r--r-- 1 bionchc4demo ACD114107 23433 Sep 23 22:06 cellranger_test-ngscourse92G_out.log
-rwxr--r-- 1 bionchc4demo ACD114107 519 Sep 23 15:13 demo1_r.sh
-rwxr--r-- 1 bionchc4demo ACD114107 524 Sep 23 15:11 demo1_r.sh~
-rwxr--r-- 1 bionchc4demo ACD114107 695 Sep 23 15:51 demo2_cellranger.sh
-rwxr--r-- 1 bionchc4demo ACD114107 624 Sep 23 15:40 demo2_cellranger.sh~
-rw-r--r-- 1 bionchc4demo ACD114107 224955 Sep 25 08:42 heatmap_test.jpg
-rw-r--r-- 1 bionchc4demo ACD114107 5522 Sep 25 08:42 Rplots.pdf
-rw-r--r-- 1 bionchc4demo ACD114107 0 Sep 25 08:42 r_test-ngscourse_err.log
-rw-r--r-- 1 bionchc4demo ACD114107 10 Sep 25 08:42 r_test-ngscourse_out.log
-rw-r--r-- 1 bionchc4demo MST109178 569 Sep 23 12:17 r_test.R
bionchc4demo@lgn304:~$
  
```



Text-based editors

nano



```

GNU nano 2.9.8                                r_test.R
setwd("~/")

#### Example data
set.seed(123)
data<- matrix(rnorm(100, 0, 10), nrow = 10, ncol = 10) # Set seed for reproducibility # nolint
# Create example data

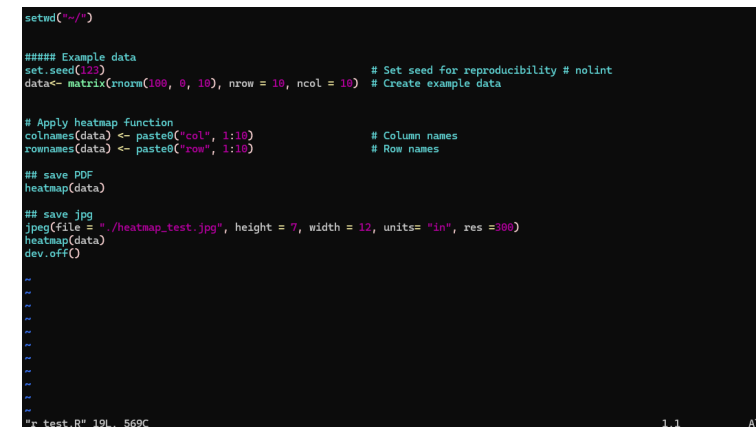
# Apply heatmap function
colnames(data) <- paste0("col", 1:10)           # Column names
rownames(data) <- paste0("row", 1:10)            # Row names

## save PDF
heatmap(data)

## save jpg
jpeg(file = "/heatmap_test.jpg", height = 7, width = 12, units= "in", res =300)
heatmap(data)
dev.off()

[ Read 19 lines ]
Get Help  Write Out  Where Is  Cut Text  Justify  Cur Pos  Undo  Mark Text
Exit      Read File  Replace  Uncut Text  To Spell  Go To Line  Redo  Copy Text
  
```

vi/vim



```

setwd("~/")

#### Example data
set.seed(123)
data<- matrix(rnorm(100, 0, 10), nrow = 10, ncol = 10) # Set seed for reproducibility # nolint
# Create example data

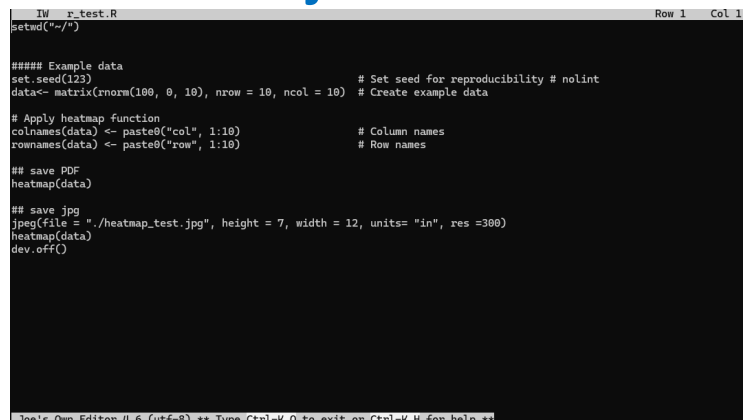
# Apply heatmap function
colnames(data) <- paste0("col", 1:10)           # Column names
rownames(data) <- paste0("row", 1:10)            # Row names

## save PDF
heatmap(data)

## save jpg
jpeg(file = "/heatmap_test.jpg", height = 7, width = 12, units= "in", res =300)
heatmap(data)
dev.off()

r_test.R" 19L, 569C                                1,1      All
  
```

joe



```

IV  >: test.R                                     Row 1  Col 1
setwd("~/")

#### Example data
set.seed(123)
data<- matrix(rnorm(100, 0, 10), nrow = 10, ncol = 10) # Set seed for reproducibility # nolint
# Create example data

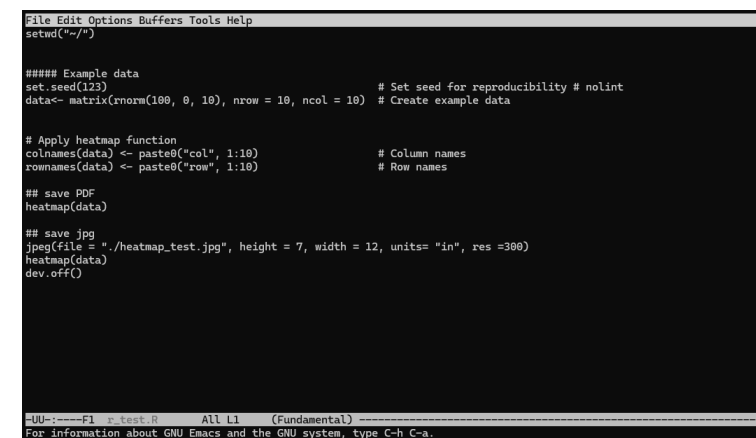
# Apply heatmap function
colnames(data) <- paste0("col", 1:10)           # Column names
rownames(data) <- paste0("row", 1:10)            # Row names

## save PDF
heatmap(data)

## save jpg
jpeg(file = "/heatmap_test.jpg", height = 7, width = 12, units= "in", res =300)
heatmap(data)
dev.off()

Joe's Own Editor 4.6 (utf-8) ** Type Ctrl-K Q to exit or Ctrl-K H for help **
  
```

emacs



```

File Edit Options Buffers Tools Help
setwd("~/")

#### Example data
set.seed(123)
data<- matrix(rnorm(100, 0, 10), nrow = 10, ncol = 10) # Set seed for reproducibility # nolint
# Create example data

# Apply heatmap function
colnames(data) <- paste0("col", 1:10)           # Column names
rownames(data) <- paste0("row", 1:10)            # Row names

## save PDF
heatmap(data)

## save jpg
jpeg(file = "/heatmap_test.jpg", height = 7, width = 12, units= "in", res =300)
heatmap(data)
dev.off()

--F1 r_test.R      All L1  (Fundamental)
For information about GNU Emacs and the GNU system, type C-h C-a.
  
```

Basic Linux commands

Rocky Linux release 8.5 (Green Obsidian)

- top/htop
- ls du
- cd pwd mkdir
- mv cp rm rename
- **man** more clear
- wget
- pipeline: |
- grep
- tar gzip zip/unzip

鳥站 基礎篇 訓練教材 伺服器篇 環工篇 討論區 49971419 Linux 基礎學習篇訓練教材 - 目錄彙整 5分鐘內線上有 981 人

Linux 基礎學習篇訓練教材 - RockyLinux 9.x

Linux 基礎學習篇訓練教材 - 目錄彙整

這個版本不是自學篇，這個是教師授課篇！許多的題目都建置在雲裡面，因此，只提供給校園教師呢！

最近更新時間：2023/03/10

老實說，基礎學習篇裡面的鳥哥講的廢話太多，雖然很多觀念就可以藉此強調同時強化學習，不過在學校上課時，就很容易發生找不到重點的問題！同時，因為上課時，老師經常都已經將環境整理好，因此也不太需要讓同學自己安裝系統。因此，在這個基礎學習訓練教材中，鳥哥比較強調在 15 周之內，將 Linux 基礎處理過，同時將環境整理好，讓朋友們能夠方便重點學習。當然啦，這個訓練教材真的只是一個『指引 (guide)』，要完整的學習，還是得要去基礎學習篇將所有的習作通通練習完才好囉！^_^

從 2021 年底，RHEL 衍生的 CentOS 8 系列就不再持續維護 (CentOS 7 則到 2024/06/30 結束營業)，由於 RHEL 算是業界使用廣泛的一個商品，因此，Red Hat 自己公司出產的 CentOS 系列，一向都是業界相當熱門使用的 Linux distribution 之一。在 2022 年中，由當初的 CentOS 共同創辦人提出 RockyLinux 的產品發表，同時於該年度推出 RHEL 9 的衍生版本。本次課程即使用 RockyLinux 9 作為介紹囉！

課前說明：

- 作業成績 30%，期中成績 30%，期末成績 40%
- 作業總共有 14+2 次 (前 14 周作業與期中、期末考前練習, practice1, practice2)。除特殊情況外，作業不許補交。
- 期末考前，如果通過 RHCSA 認證考試並取得證照，期末成績加 30 分。加權後期末成績若超過 100 分，則多的分數將累加至期中或平時作業。
- 每節課均會點名，但點名僅作為加分之用。
- 考試 (期中與期末考) 細節說明：
 - 考試期間沒有 Internet 可用，也不許攜帶任何電子用品 (不可使用手機、平板等)
 - 可以攜帶任何課本、手寫筆記、手寫小抄，但是不許攜帶任何影印筆記資料。

第 01 堂課：初次使用 Linux 與指令列模式初探

1.1：Linux 是什麼

https://linux.vbird.org/linux_basic_train/rockylinux9/

Demo #1: login + OTP + up/download

ssh t3-c4.nchc.org.tw

or

ssh 203.145.216.54

Running apps on T3

- Apps/reference genomes/databases
- Module
- 生資三本柱: R, python, java

400+ apps

/opt/ohpc/Taiwania3/pkg/biology

```

bionchc4demo@lgn304 biology]$ ls
AB-BLAST      Bracken      DRAGO        GTDBtk       libpng15     modkit        pigz          rust          tandem-genotypes
ABYSS         busco        drugbank     Gtftogenepred liboffice     MOP2          Pilon        SAIGE         T-Coffee
Admixture     BUSCO_phylogenomics Eagle         Guppy        libstdc      mosdepth     Pindel      salmon        TELL-seq
AfterQC       BWA         ECOLI       haddock      libsvm       Mothur       PLINK       sambamba      TelSeq
aggRSquare    bzip2       edlib       Haploview    libtool      MultiQC      PLINK2      samblaster    tensorflow
aldy          CAFES       Ensembl-API hashdeep     libuuid      MUMMER       SAMS2       SAMS2        terra
alevin-fry    Canu        Ensembl-VEP HDF5          llvmlite     MuPeXI       samsift     Scramble      tesseract
ALLPATHS-LG   cap3        ETE3        herro        llnlite      MUSCLE       SAMTOOLS    TETools      TEx
alphafold     cBioPortal EvidenceModeler hifiasm      Lmod         MusiteDeep   screen      TeX          TideHunter
AMP_GAN       CD-HIT      EXCAVATOR2tool HiPhase      LocusZoom   mutpred2     security    TopHat
Anaconda      CEAS        ExomeDepth  HISAT2       LocustZoom   NAMO         segemehl    Trans-ABYSS   TransDecoder
ANNOgesic     CellRanger  FALCON      HISAT2       loftee       nanocorr     seqOutBias  TRF
AnnotSV       Centrifuge  fast-bonito hladd        LongRanger   NanoPlot     SHAPEIT     TrimGalore   Trimmomatic
ANNOVAR       cget        fastp       HLA-LA       MMCopy       LTR_retriever Nanopolish   Trinity
ant           CheckM2     FastQC      HMMER        lua2env.py   nanosv       PyTorch     trust4
arcashHLA     chopper     FastQTL     HOMER        lumpy-sv     NBIS-meta    PyVCF       SIFT4G_Create_Genomic_DB
aria2         CIRCEXplorer FASTX-Toolkit MMER         lua2env.py~  NCBI-dataset-cli PyVCF       singularity
arriba        Circle-Map  FBAT        homopolish   lxml         NDATAtools   qctool      slivar
Aspera        CIRCLE-seq  fgbio       HTSLIB       m6anet      NeoFuse      QIIME2      slurm
Augustus      circniner   finemap     ICU          MACS         netMHCpan    Quallmap    smcp
autoconf      circos      firefox     IGV          MAFFT        nextflow     Quast       SMRT_LINK
autodock_vina clrcna_detection flye        Illumina_hap.py imputationserver mamba
auto_lua.sh   CLCBio     FREEC       IMPUTE2      Manta        manorm       napsplice   Snakemake
aws           ClinSV      FusionCatcher gATK-SV      MEGAN        Manta        Maven       Sniffles
axel          CNVkit      GapFiller   GATK         JBrowse     medaka       META        SnpEff
bamql         CNVnator    GapFiller   GATK         JBrowse     medaka       META        SOAP2
bam-readcount CNVpytor    IRESfinder  GATK-SV     JBrowse     medaka       META        SolexaQA
bantools      CNVRuler    iva         gcc          JDK          javafx       JBrowse     SPAdes
bamutil       CNV-Sim     CoLoGen     gcta         Jvarkit      kallisto     Kallisto    SpecHLA
bamUtil       Bases2Fastq CRISPRCasFinder gcta         Jvarkit      kallisto     Kallisto    SpliceAI
BaseSpaceCLI CoLoGen     CRISPRCasFinder gcta         Jvarkit      kallisto     Kallisto    splitp
Bazel         Cromwell    gdal         GEMMA        GEMMA        GEMMA        GEMMA        SRA_Toolkit
bbmap         cuda        GEMMA        GEMMA        GEMMA        GEMMA        GEMMA        SRA_Toolkit
BBTools       bcl2fastq2 Cufflinks   GemSIM       KING         MetaMinac2   MetaPhlAn   SRA_Toolkit
BCFtools      BCL_Convert custom       geNonad      kma          MetaPhlAn    pb-metagenomics-tools rhapsody
  
```

裡面沒有的，我們可以為您安裝

Reference genomes: ~4.2TB

/opt/ohpc/Taiwania3/pkg/biology/reference

```
[bionchc4demo@lgn304 reference]$ ls -l
total 6
drwxr-xr-x  5 biology biology 4096 Feb 21  2019 Caenorhabditis_elegans
drwxr-xr-x  5 biology biology 4096 Feb 22  2019 Drosophila_melanogaster
drwxr-xr-x 12 biology biology 4096 Dec 12  2024 Homo_sapiens
drwxrwxr-x  2 biology biology 4096 May  3  2022 Microbiota
drwxr-xr-x  7 biology biology 4096 Jul 15  2022 Mus_musculus
drwx----- 2 biology biology 4096 Aug 18  2021 Saccharomyces_cerevisiae
[bionchc4demo@lgn304 reference]$
```

Databases: ~7.8TB

/opt/ohpc/Taiwania3/pkg/biology/**DATABASE**

```
[bionchc4demo@lgn304 DATABASE]$ ls -l
total 79
drwxr-xr-x  4 biology biology 4096 Dec 28 2022 alphafold_DB
drwxr-xr-x  5 biology biology 4096 May 11 2018 BWA_Indices
drwxrwxr-x  3 biology biology 4096 Oct 26 2021 Centrifuge
-rw-rw-r--  1 biology biology  631 Oct 23 2023 download_nr.py
drwxr-xr-x  3 biology biology 4096 Oct  6 2021 FREEC
drwxrwxr-x  2 biology biology 4096 Aug 17 2023 gbdb
drwxrwxr-x  4 biology biology 4096 Oct 24 2023 Greengenes
drwxrwxr-x  2 biology biology 4096 May 11 2023 GTDB-Tk
drwxrwxr-x  2 biology biology 32768 Oct 23 2023 nr
drwxrwxr-x  2 biology biology 4096 Jul 11 2024 nr_new
drwxrwxr-x  2 biology biology 4096 Nov  1 2023 Pfam
drwxrwxr-x  2 biology biology 4096 Oct 24 2023 PlusPFP
drwxrwxr-x  4 biology biology 4096 Oct 24 2023 RDP
drwxrwxr-x 13 biology biology 4096 May  9 2022 release207_v2
drwxrwxr-x  5 biology biology 4096 Oct 24 2023 Silva
drwxrwxr-x  3 biology biology 4096 Oct  4 2021 VEP
[bionchc4demo@lgn304 DATABASE]$
```

/opt/ohpc/Taiwania3/pkg/biology/R

```
[bionchc4demo@lgn304 R]$ pwd
/opt/ohpc/Taiwania3/pkg/biology/R
[bionchc4demo@lgn304 R]$ ls -l
total 53
drwxrwxr-x 4 biology biology 4096 Jun 3 2024 Build
drwxr-xr-x 15 biology biology 4096 Mar 11 2022 R-4.0.0
drwxr-xr-x 16 biology biology 4096 Jun 3 2024 R-4.2.1
drwxr-xr-x 15 biology biology 4096 Aug 25 2023 R-4.3.0
drwxr-xr-x 15 biology biology 4096 Aug 1 2024 R-4.3.1
drwxr-xr-x 15 biology biology 4096 Mar 27 2024 R-4.3.2
drwxr-xr-x 15 biology biology 4096 May 31 2024 R-4.3.3
drwxr-xr-x 15 biology biology 4096 May 31 2024 R-4.4.0
drwxrwxr-x 18 biology biology 4096 Jul 12 2024 R_sequenza
drwxrwxr-x 5 biology biology 4096 Jun 5 2023 R_v3.3.0
drwxrwxr-x 5 biology biology 4096 Aug 26 2021 R_v3.6.3
lrwxrwxrwx 1 biology biology 16 Oct 19 2021 R_v3.6.3_gcc_8.3.0 -> R_v3.6.3_rstudio
drwxrwxr-x 5 biology biology 4096 Aug 25 2021 R_v3.6.3_gcc_8.3.0.old
drwxrwxr-x 5 biology biology 4096 Sep 8 2021 R_v3.6.3_gcc_v7.5.0
drwxrwxr-x 5 biology biology 4096 Dec 15 2021 R_v3.6.3_rstudio
drwxrwxr-x 16 biology biology 4096 Nov 4 2024 R_v4.1.0
drwxrwxr-x 93 biology biology 4096 Jun 20 2022 R_v4.1.2
drwxrwxr-x 16 biology biology 4096 Oct 12 2022 R_v4.2.1
drwxrwxr-x 17 biology biology 4096 Dec 19 2023 R_v4.3.1
drwxr-xr-x 15 biology biology 16384 Mar 27 2024 R_v4.3.2_o
drwxr-xr-x 17 biology biology 4096 Mar 21 2024 R_v4.3.3
drwxrwxr-x 16 biology biology 4096 Oct 28 2024 R_v4.4.1
[bionchc4demo@lgn304 R]$ pwd
/opt/ohpc/Taiwania3/pkg/biology/R
[bionchc4demo@lgn304 R]$ |
```

R: 4.4.1

```
[bionchc4demo@lgn304 bin]$ pwd
/opt/ohpc/Taiwania3/pkg/biology/R/R_v4.4.1/bin
[bionchc4demo@lgn304 bin]$ /opt/ohpc/Taiwania3/pkg/biology/R/R_v4.4.1/bin/R

R version 4.4.1 (2024-06-14) -- "Race for Your Life"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-conda-linux-gnu

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 1+1
[1] 2
>
>
```

Module: 環境變數管理工具

Without module

```
[bionchc4demo@lgn304 bin]$ pwd
/opt/ohpc/Taiwania3/pkg/biology/R/R_v4.4.1/bin
[bionchc4demo@lgn304 bin]$
[bionchc4demo@lgn304 bin]$ ./R

R version 4.4.1 (2024-06-14) -- "Race for Your Life"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-conda-linux-gnu

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 1+1
[1] 2
>
```

With module

```
[bionchc4demo@lgn304 ~]$ pwd
/home/bionchc4demo
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$ R

R version 4.4.1 (2024-06-14) -- "Race for Your Life"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu

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'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 1+1
[1] 2
>
>
```

Module: R

Search module

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml spider R
```

R:

Description:

Versions:

- R/sequenza
- R/4.0.0
- R/4.1.0
- R/4.1.2
- R/4.2.1
- R/4.3.1
- R/4.3.2
- R/4.3.3
- R/4.4.0
- R/4.4.1**

Other possible modules matches:

.gromacs-2021.2 .rcec 2018R 2018R1 2021R ANNOVAR

To find other possible module matches execute:

\$ module -r spider '.*R.*'

Load/unload module

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml load R/4.4.1  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml list
```

Currently Loaded Modules:

1) R/4.4.1


```
[bionchc4demo@lgn304 ~]$ ml unload R/4.4.1  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml list  
No modules loaded  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$
```

Module: python

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml spider python
```

```
python:
```

```
Versions:  
python/fv3web  
python/stack  
python/ufs_env  
python/ufspost  
python/wrfpost  
python/3.5.10-intel19  
python/3.10.8-ocu4rdj  
python/3.10.12  
python/3.12.2
```

Other possible module matches:
Python biology/Python pkg/Python py-python-dateutil

```
To find other possible module matches execute:  
  
$ module -r spider '.*python.*'
```

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml load python/3.12.2  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml list
```

Currently Loaded Modules:
1) python/3.12.2

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml unload python/3.12.2  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$
```

Python/conda

anaconda

```
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$ ml spider anaconda
```

Anaconda:

Description:
Anaconda - conda package management system.

Versions:
Anaconda/Anaconda3
 Anaconda/22.10

For detailed information about a specific "Anaconda" package name.
Note that names that have a trailing (E) are extensions provided.
For example:

\$ module spider Anaconda/22.10

biology/Anaconda:

Description:
Anaconda - conda package management system.

Versions:
 biology/Anaconda/Anaconda3
 biology/Anaconda/22.10

miniconda

```
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$ ml spider miniconda3
```

miniconda3:

Versions:
 miniconda3/4.8.4
 miniconda3/22.11.1-6zzs5sq
 miniconda3/24.1.2
miniconda3/24.5.0

Other possible module matches:
pkg/miniconda3

To find other possible module matches execute:

\$ module -r spider '.*miniconda3.*'

For detailed information about a specific "miniconda3" name.
Note that names that have a trailing (E) are extensions provided.
For example:

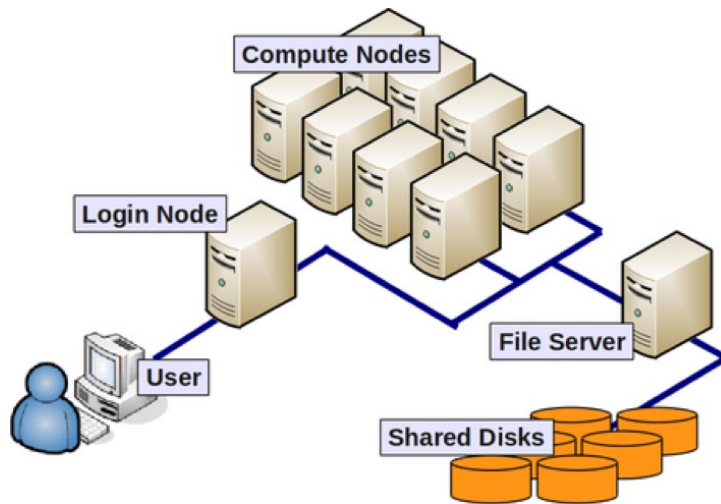
\$ module spider miniconda3/24.5.0

Python/venv

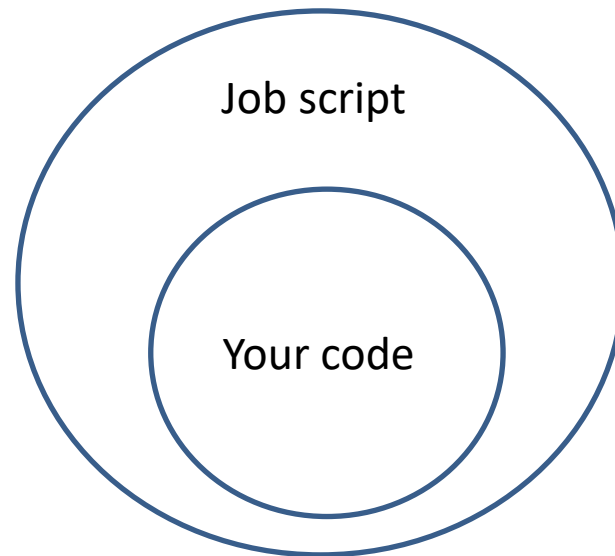
```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml load miniconda3  
(base) [bionchc4demo@lgn304 ~]$  
(base) [bionchc4demo@lgn304 ~]$  
(base) [bionchc4demo@lgn304 ~]$ conda env list  
# conda environments:  
#  
base * /opt/ohpc/Taiwania3/pkg/miniconda3/24.1.2  
(base) [bionchc4demo@lgn304 ~]$  
(base) [bionchc4demo@lgn304 ~]$  
(base) [bionchc4demo@lgn304 ~]$
```

```
(base) [bionchc4demo@lgn304 ~]$  
(base) [bionchc4demo@lgn304 ~]$ conda env list  
# conda environments:  
#  
base * /opt/ohpc/Taiwania3/pkg/miniconda3/24.1.2  
(base) [bionchc4demo@lgn304 ~]$ conda create -n myenv  
Channels:  
- defaults  
Platform: linux-64  
Collecting package metadata (repodata.json): done  
Solving environment: done  
## Package Plan ##  
  
environment location: /home/bionchc4demo/.conda/envs/myenv  
  
Proceed ([y]/n)? y  
  
Preparing transaction: done  
Verifying transaction: done  
Executing transaction: done  
#  
# To activate this environment, use  
#  
# $ conda activate myenv  
#  
# To deactivate an active environment, use  
#  
# $ conda deactivate  
(base) [bionchc4demo@lgn304 ~]$ conda activate myenv  
(myenv) [bionchc4demo@lgn304 ~]$
```

Submitting jobs



Job script



N: T/P: 周初查

★人氣推薦 ●新品上市

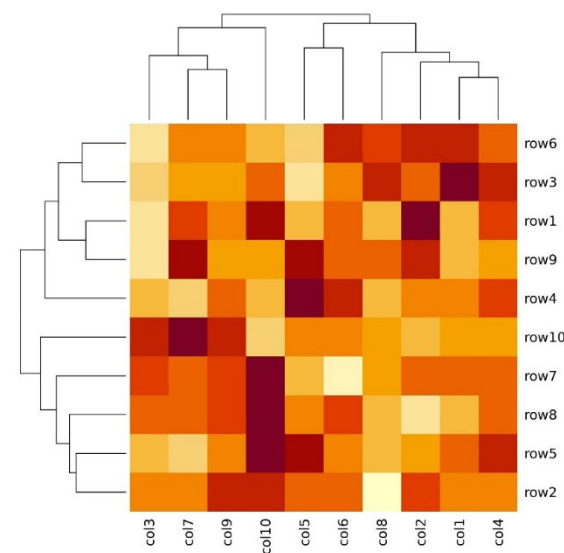
☐ S ☐ I ☐ W ☐ I

★62 乾扁四季豆(時菜)	180	★03 紅燒牛肉麵	280
61 涼拌雲耳	110	01/02 元氣雞絲麵/元氣牛肉麵	280/270
★500 小菜/時蔬	100/110	04 紅燒牛肉湯麵	140
★58 辣味黃瓜	100	051 香茅肉燥湯麵	170
60 寧式黃芽菜	110	1043 鹹酥麵(週四/週五)	210/180
★57 甜酸雞絲	350	0760 蝦仁麵/肉燥麵	260/240
45/53 炸排骨/滷菜	150/100		
64 紅燒茄子(冷菜)	140	15 炸醬麵	120
48/4 糖醋排骨	260	1160 香茅肉燥雞排麵	170
★47 蒜香粉蒸	260	12/15 豬蹄麵/麻婆麵	120
●600 香酥雞排	280	16 紅油抄手麵	120
●800 滷牛腱	240		
小籠包		★30 蝦仁蛋炒飯(時蔬)	270
★66 小籠包(5個)	125/250	31 肉燥蛋炒飯(時蔬)	220
67 蟹粉小籠包(5個)	200/400	29 蝦仁肉燥蛋炒飯(時蔬)	330
67 蟹粉小籠包(5個)	125/250	★32 排骨蛋炒飯(時蔬)	280
★65 韭菜蝦仁小籠包(5個)	180/360	338 什蔬蛋炒飯(時蔬)	230
★67 韭菜小籠包(5個)	450		
肉燥蛋炒飯		★35 紅燒獅子頭(時蔬)	210/180
71 菜肉蒸餃(5個)	130/260	106/90 鹹酥雞排麵(週四/週五)	200/170
72 蝦肉蒸餃(5個)	145/290	0580 砂子(雞肉/王沙)	100/90
74 鮮肉大蒸餃(5個)	135/270		
73 香酥素餃(5個)	135/270	335 清蒸海上鮮(時蔬/薑蔥)	90/120
★75 牛肉蒸餃(5個)	175/350	92 什蔬清炒時蔬	90
★78 蝦仁蒸餃(5個)	155/310	★64 韭菜炒小籠包(5個)	95/190
79 豬肉蒸餃(5個)	135/270	★69 芋泥小籠包(5個)	105/210
91 蝦肉蒸餃(6個)	240	★70 巧克力小籠包(5個)	175/350
		943 八寶飯	100
13/32 大腸麵線(原肉)	160	104/90 芝麻菜雞(原肉/薑蔥)	120
84 香酥素餃	110	★80 酥子(雞肉/王沙)	100
★86 韭菜大餃	110		
88 韭菜大餃	90	001/002 可樂/可樂 Zui	50
89 芝麻大餃	90	003/004 雪碧/可樂(必喝)	50
90 芋泥大餃	100	0021 天天好(時蔬/時蔬)	190
★90 黃金蛋炒飯	100	00002 命星(時蔬/時蔬)	300/600
80/80 蛋炒飯(時蔬/時蔬)	60	00000 蛋炒飯(時蔬/時蔬)	120/130
★90 蛋炒飯(時蔬/時蔬)	70/80	★002 上海大麵筋(時蔬/時蔬)	1200
★18 紅燒牛肉麵	230	冷湯麵	
19 元氣牛肉麵	230	9900 麵品麵	400
20 紅燒牛肉麵	250	0100 紅燒牛肉麵	280
22/21 鹹魚湯(原肉/菜肉)	200/70	★900 紅油抄手	210/140
★23 酸辣湯(小/中/大)	110/120/250	★900 (雞肉/菜肉)	
23/22 原肉/雞味	120/250	★980 蛋味手工水餃(20入)	200
23/22 蛋味/雞味(時蔬/時蔬)	120/250	★980 (韭菜/高麗菜)	
13 滷菜麵粉	160	★980 (雞肉/韭菜/蔬菜)	300/300
★90 松露雞絲麵	230	00000 鮮肉粉(5個)	380/100
26 蛋包飯(時蔬)	220	00000 蛋粉(5個)	450/900
		00000 元氣雞絲麵	400/130
★40 高麗菜	230	00000 元氣牛肉麵	440/130
41/57 清炒(原肉)	490	9904 蟹粉白灼麵	1390
★37 空心菜	230	9904 紅燒獅子頭	599
44 地瓜(原肉)	230	★980 櫻花蝦湯(時蔬/時蔬)	699
50/50 韭菜/韭菜(時蔬)	230/110		

內頁加註 10% 服務費 * 顧客請先告知

Submitting a demo job

- job script: demo1_r.sh
- your code: r_test.R
- partition: ngscourse
- 確定可執行: chmod
- 送job: sbatch
- 查詢job狀態: squeue --me



Job script: demo1_r.sh

```
#!/usr/bin/sh
#SBATCH -A ACD114107
#SBATCH -J r_test-ngscourse

## ngscourse
#SBATCH -p ngscourse
#SBATCH -c 2
#SBATCH --mem=13g

# Path to the standard output file
# Path to the standard error output file
# email
#####
# email
#####
# 指定送出email時機 可為NONE, BEGIN, END, FAIL, QUEUE, ALL
##### your scripts

ml load biology
ml load R/4.4.1

Rscript r_test.R --vanilla
```

核心設施用戶: MST109178

這裡填你的email

Your code

Partitions

Partition(Queue) 資源設定

Partition	記憶體配置 (--mem)	核心數搭配 (-c)	時間限制	個人Job上限	使用狀態
ngsTest	7G	1	10 mins	2	CPI
ngsConsole	7G	1	unlimit	2	CPI
ngs7G	7G	1	48 hrs	1000	CPI
ngs13G	13G	2	48 hrs	500	CPI
ngs26G	26G	4	96 hrs	250	CPI
ngs53G	53G	8	96 hrs	120	CPI
ngs92G	92G	14	unlimit	80	CPI
ngs186G	186G	28	unlimit	40	CPI
ngs372G	372G	56	unlimit	20	CPI
ngs224core	184G*4 (sbatch 不用指定mem)	56*4 (sbatch 參數使用： -c 56 - n 4)	unlimit	4	CPI
ngs448core	184G*8 (sbatch 不用指定mem)	56*8 (sbatch 參數使用： -c 56 - n 8)	unlimit	2	CPI
ngs512G	500G	9	unlimit	8	2,4TB大

核心設施專用
MST109178

教育訓練專用
ACD114107

ngscourse	13G	2	48 hrs	500
ngscourse92G	92G	14	unlimit	80

Your code: r_test.R

```
setwd("~/")

##### Example data
set.seed(123) # Set seed for reproducibility
data<- matrix(rnorm(100, 0, 10), nrow = 10, ncol = 10) # Create example data

# Apply heatmap function
colnames(data) <- paste0("col", 1:10) # Column names
rownames(data) <- paste0("row", 1:10) # Row names

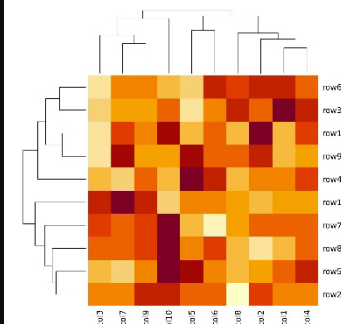
## save PDF 輸出pdf
heatmap(data)

## save jpg
jpeg(file = "./heatmap_test.jpg", height = 7, width = 12, units= "in", res =300)
heatmap(data) 輸出jpg
dev.off()

~
~
~
~
~
```

testing your code on login node

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml load biology R/4.4.1  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ R  
  
R version 4.4.1 (2024-06-14) -- "Race for Your Life"  
Copyright (C) 2024 The R Foundation for Statistical Computing  
Platform: x86_64-conda-linux-gnu  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
Natural language support but running in an English locale  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
  
> source("r_test.R")  
>  
>  
>
```



Executable job script

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ls -l  
total 2  
-rw-r--r-- 1 bionchc4demo ACD114107 672 Sep 26 10:09 demo1_r.sh  
-rw-r--r-- 1 bionchc4demo ACD114107 695 Sep 23 15:51 demo2_cellranger.sh  
-rw-r--r-- 1 bionchc4demo MST109178 569 Sep 23 12:17 r_test.R  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ chmod u+x demo1_r.sh  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ls -l  
total 2  
-rwxr--r-- 1 bionchc4demo ACD114107 672 Sep 26 10:09 demo1_r.sh  
-rw-r--r-- 1 bionchc4demo ACD114107 695 Sep 23 15:51 demo2_cellranger.sh  
-rw-r--r-- 1 bionchc4demo MST109178 569 Sep 23 12:17 r_test.R  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$
```

testing job script on login node

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml load biology R/4.4.1  
[bionchc4demo@lgn304 ~]$ ml list  
  
Currently Loaded Modules:  
  1) biology   2) libxml2/2.9.12   3) ImageMagick/7.1.0   4) libpng15/1.5.21   5) R/4.4.1  
  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ Rscript r_test.R  
pdf  
  2  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ls -l  
total 242  
-rwxr--r-- 1 bionchc4demo ACD114107    672 Sep 26 10:09 demo1_r.sh  
-rw-r--r-- 1 bionchc4demo ACD114107    695 Sep 23 15:51 demo2_cellranger.sh  
-rw-r--r-- 1 bionchc4demo ACD114107 224955 Sep 26 10:30 heatmap_test.jpg  
-rw-r--r-- 1 bionchc4demo ACD114107   5522 Sep 26 10:30 Rplots.pdf  
-rw-r--r-- 1 bionchc4demo MST109178    569 Sep 23 12:17 r_test.R  
[bionchc4demo@lgn304 ~]$
```

Submitting job

```

[bionchc4demo@lgn304 ~]$ sbatch demo1_r.sh
Submitted batch job 16701258
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$ squeue --me

```

sbatch: 送job

squeue: 顯示job狀態

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	ODELIST(Reason)
16701258	ngscourse	r_test-n	bionchc4	PD	0:00	1	(None)

```

[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$ squeue --me

```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	ODELIST(Reason)
-------	-----------	------	------	----	------	-------	-----------------

```

[bionchc4demo@lgn304 ~]$

```

收信匣

☐ 封存
 ☐ 回信
 ☐ 全回
 ☐ 轉寄
 ☐ 標籤
 ☐ 移至
 ☐ 廣告信
 ☐ 檢視
 ☐ 更多

☐ ☐ ☐ 標題

☐	✉	Slurm Job_id=16701258 Name=r_test-ngscourse Ended, Run time 00:00:01, C
☐	✉	Slurm Job_id=16701258 Name=r_test-ngscourse Began, Queued time 00:00:03

Demo #2: heatmap

ssh t3-c4.nchc.org.tw

or

ssh 203.145.216.54

Installing apps on T3

- App: Cellranger
- R package: ggplot2
- Python package: Scanpy

10x Genomics Cellranger

- 1st step of single-cell analysis
- Cellranger count + aggr



```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ml spider CellRanger
```

CellRanger:

Description:

Versions:

CellRanger/9.0.1

Other possible module matches:

biology/CellRanger

To find other possible module matches execute:

```
$ module -r spider '.*CellRanger.*'
```

For detailed information about a specific "CellRanger" package (including how to load the modules) use the module's full name.
Note that names that have a trailing (E) are extensions provided by other modules.
For example:

```
$ module spider CellRanger/9.0.1
```

Installing Cellranger in you dir

Cell Ranger 9.0.1 (Feb 6, 2025)

- Chromium Single Cell Software Suite
- Self-contained, relocatable tar file. Does not require centralized installation.
- Contains binaries pre-compiled for CentOS/RedHat 7.0 and Ubuntu 16.04.
- Runs on Linux systems that meets the minimum compute requirements.
- [View Cell Ranger source code on GitHub](#)

tar.gz compression

Download for Linux 64-bit (tar.gz)

File size: 807 MB

md5sum:

2efec98bff01f7a59edaf43724fae13f

```
[bionchc4demo@lgn304 ~]$
[bionchc4demo@lgn304 ~]$ curl -o cellranger-9.0.1.tar.gz "https://cf.10xgenomics.com/rele
tar.gz?Expires=1758900398&Key-Pair-Id=APKAI7S6A5RYOXBWRPDA&Signature=m0PWbF7Chc6AxAK56mR
RhZZ~RwZzV1iDw4Pv~QtPpLmsf4tLKVB1BEgmIOxkjfBmmMCCUtblQEmG2ERdX30lgwyHQJGw3ZITG3eXKly6oLF
LeIMubah1heJAxhVjYMRylZdHkSaU~oj8fFmKWLjSu5ET6CL4KS04aZGNUMYVfe04fJSofdcPBJeMzXY1VLjyPON2
94asFRavukAWUH9ckDIMN0HNRp2lQAdCuqrlyLH~gslVq2bJGFW..."
% Total    % Received % Xferd  Average Speed   Time    Time     Time  Current
           Dload  Upload   Total   Spent    Left     Speed
100 806M  100 806M    0     0  227M      0  0:00:03  0:00:03 --:--:-- 227M
[bionchc4demo@lgn304 ~]$ ls -l
total 825378
-rw-r--r-- 1 bionchc4demo ACD114107 845171096 Sep 26 11:28 cellranger-9.0.1.tar.gz
-rwxr--r-- 1 bionchc4demo ACD114107    678 Sep 26 10:56 demo1_r.sh
-rwxr--r-- 1 bionchc4demo ACD114107    672 Sep 26 10:09 demo1_r.sh~
-rw-r--r-- 1 bionchc4demo ACD114107    695 Sep 23 15:51 demo2_cellranger.sh
-rw-r--r-- 1 bionchc4demo MST109178    569 Sep 23 12:17 r_test.R
[bionchc4demo@lgn304 ~]$
```

安裝: 下載 & 解壓縮

```
[bionchc4demo@lgn304 bin]$ pwd
/home/bionchc4demo/cellranger-9.0.1/bin
[bionchc4demo@lgn304 bin]$
[bionchc4demo@lgn304 bin]$ ls
cellranger _cellranger_in_... ..ma tenkit
[bionchc4demo@lgn304 bin]$ ./cellranger
cellranger cellranger-9.0.1

Process 10x Genomics Gene Expression, Feature Barcode, and Immune Profiling data

Usage: cellranger <COMMAND>

Commands:
count      Count gene expression and/or feature barcode reads from a single sample and GEM well
multi      Analyze multiplexed data or combined gene expression/immune profiling/feature barcode data
multi-template  Output a multi config CSV template
vdj        Assembles single-cell VDJ receptor sequences from 10x Immune Profiling libraries
aggr       Aggregate data from multiple Cell Ranger runs
annotate   Annotate cell-types from outputs of a CellRanger run
reanalyze  Re-run secondary analysis (dimensionality reduction, clustering, etc)
mkvdjref   Prepare a reference for use with CellRanger VDJ
mkfastq    Run Illumina demultiplexer on sample sheets that contain 10x-specific sample index sets
testrun    Execute the 'count' pipeline on a small test dataset
cloud      Invoke cloud commands
mat2csv    Convert a feature-barcode matrix to CSV format
mkref      Prepare a reference for use with 10x analysis software. Requires a GTF and FASTA
mkgtf      Filter a GTF file by attribute prior to creating a 10x reference
upload     Upload analysis logs to 10x Genomics support
sitecheck  Collect Linux system configuration information
telemetry  Configure and inspect telemetry settings and data
help       Print this message or the help of the given subcommand(s)
```

Installing R package: ggplot2

/home/你的主機帳號/R/x86_64-conda-linux-gnu-library/4.4

```
[bionchc4demo@lgn304 ~]$ R

R version 4.4.1 (2024-06-14) -- "Race for Your Life"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-conda-linux-gnu

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> install.packages("ggplot2")
Warning in install.packages("ggplot2") :
  'lib = "/work/opt/ohpc/Taiwania3/pkg/biology/R/R_v4.4.1/lib/R/library"' is not writable
Would you like to use a personal library instead? (yes/No/cancel) yes
Would you like to create a personal library
' /home/bionchc4demo/R/x86_64-conda-linux-gnu-library/4.4 '
to install packages into? (yes/No/cancel) yes
--- Please select a CRAN mirror for use in this session ---
|
```

選擇下載來源

```
11: Canada (MB) [https]
13: Canada (ON 2) [https]
15: China (Beijing 1) [https]
17: China (Beijing 3) [https]
19: China (Hong Kong) [https]
21: China (Lanzhou) [https]
23: China (Shanghai 2) [https]
25: China (Wuhan) [https]
27: Costa Rica [https]
29: Czech Republic [https]
31: East Asia [https]
33: Finland (Helsinki) [https]
35: France (Lyon 2) [https]
37: Germany (Erlangen) [https]
39: Germany (Leipzig) [https]
41: Greece [https]
43: Iceland [https]
45: India (Bhubaneswar) [https]
47: Iran (Mashhad) [https]
49: Italy (Padua) [https]
51: Korea (Gyeongsan-si) [https]
53: Morocco [https]
55: New Zealand [https]
57: Saudi Arabia (Riyadh) [https]
59: Spain (Madrid) [https]
61: Switzerland (Zurich 1) [https]
63: UK (Bristol) [https]
65: USA (IA) [https]
67: USA (OH) [https]
69: USA (PA 1) [https]
71: USA (UT) [https]
73: Uruguay [https]
12: Canada (ON 1) [https]
14: Chile (Santiago) [https]
16: China (Beijing 2) [https]
18: China (Hefei) [https]
20: China (Jinan) [https]
22: China (Nanjing) [https]
24: China (Shenzhen) [https]
26: Colombia (Cali) [https]
28: Cyprus [https]
30: Denmark [https]
32: Ecuador (Cuenca) [https]
34: France (Lyon 1) [https]
36: France (Paris 1) [https]
38: Germany (Göttingen) [https]
40: Germany (Münster) [https]
42: Hungary [https]
44: India (Bengaluru) [https]
46: Indonesia (Banda Aceh) [https]
48: Italy (Milano) [https]
50: Japan (Yonezawa) [https]
52: Mexico (Mexico City) [https]
54: Netherlands (Dronten) [https]
56: Norway [https]
58: Spain (A Coruña) [https]
60: Sweden (Umeå) [https]
62: Taiwan (Taipei) [https]
64: UK (London 1) [https]
66: USA (MI) [https]
68: USA (OR) [https]
70: USA (TN) [https]
72: United Arab Emirates [https]
74: (other mirrors)
```

Selection: 62

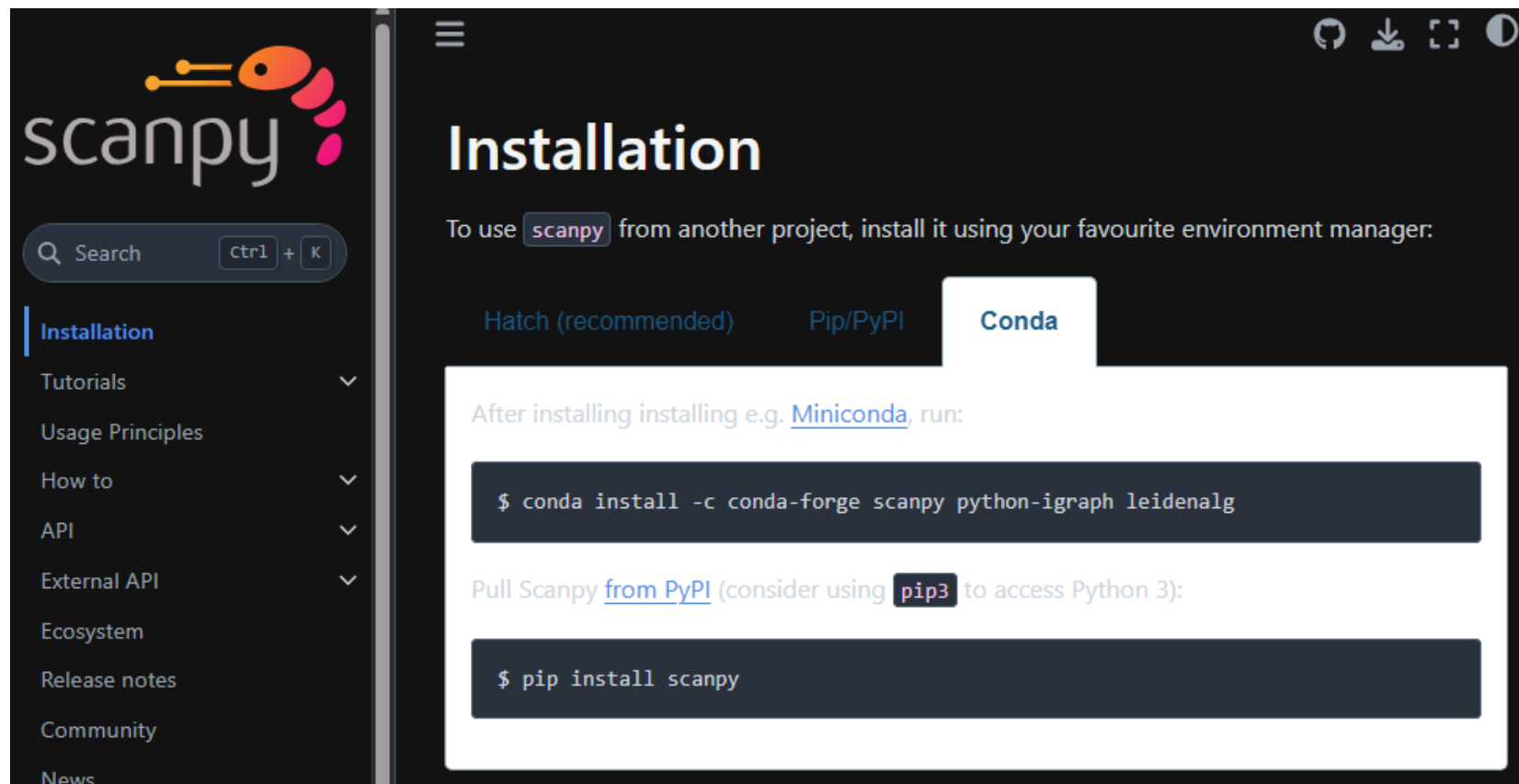
編譯&安裝

```
* DONE (S7)
* installing *source* package 'scales' ...
** package 'scales' successfully unpacked and MD5 sums checked
** using staged installation
** R
** byte-compile and prepare package for lazy loading
** help
*** installing help indices
*** copying figures
** building package indices
** testing if installed package can be loaded from temporary location
** testing if installed package can be loaded from final location
** testing if installed package keeps a record of temporary installation path
* DONE (scales)
* installing *source* package 'ggplot2' ...
** package 'ggplot2' successfully unpacked and MD5 sums checked
** using staged installation
** R
** data
*** moving datasets to lazyload DB
** inst
** byte-compile and prepare package for lazy loading
** help
*** installing help indices
*** copying figures
** building package indices
** installing vignettes
** testing if installed package can be loaded from temporary location
** testing if installed package can be loaded from final location
** testing if installed package keeps a record of temporary installation path
* DONE (ggplot2)
```

```
The downloaded source packages are in
' /tmp/Rtmpy4CPOX/downloaded_packages'
> |
```

Installing python package: scanpy

Single-Cell Analysis in Python



The screenshot shows the scanpy website's installation page. On the left is a dark sidebar with the scanpy logo and a search bar. The sidebar menu includes: Installation (highlighted), Tutorials, Usage Principles, How to, API, External API, Ecosystem, Release notes, Community, and News. The main content area has a dark header with the title 'Installation'. Below the title, it says 'To use `scanpy` from another project, install it using your favourite environment manager:'. There are three tabs: 'Hatch (recommended)', 'Pip/PyPI', and 'Conda' (which is selected). Under the 'Conda' tab, it says 'After installing installing e.g. [Miniconda](#), run:' followed by a terminal code block containing the command: `$ conda install -c conda-forge scanpy python-igraph leidenalg`. Below this, it says 'Pull Scanpy [from PyPI](#) (consider using `pip3` to access Python 3):' followed by another terminal code block containing the command: `$ pip install scanpy`.

scanpy

Search `ctrl + K`

Installation

Tutorials

Usage Principles

How to

API

External API

Ecosystem

Release notes

Community

News

Installation

To use `scanpy` from another project, install it using your favourite environment manager:

Hatch (recommended) Pip/PyPI **Conda**

After installing installing e.g. [Miniconda](#), run:

```
$ conda install -c conda-forge scanpy python-igraph leidenalg
```

Pull Scanpy [from PyPI](#) (consider using `pip3` to access Python 3):

```
$ pip install scanpy
```

Installing python package in your venv

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ conda activate myenv  
(myenv) [bionchc4demo@lgn304 ~]$  
(myenv) [bionchc4demo@lgn304 ~]$  
(myenv) [bionchc4demo@lgn304 ~]$ conda env list  
# conda environments:  
#  
myenv          * /home/bionchc4demo/.conda/envs/myenv  
base           /opt/ohpc/Taiwania3/pkg/miniconda3/24.1.2  
  
(myenv) [bionchc4demo@lgn304 ~]$  
(myenv) [bionchc4demo@lgn304 ~]$  
(myenv) [bionchc4demo@lgn304 ~]$ conda install -c conda-forge scanpy python-igraph leidenalg  
Channels:  
- conda-forge  
- defaults  
Platform: linux-64  
Collecting package metadata (repodata.json): done  
Solving environment: done  
  
## Package Plan ##  
  
environment location: /home/bionchc4demo/.conda/envs/myenv  
  
added / updated specs:  
- leidenalg  
- python-igraph  
- scanpy  
  
The following packages will be downloaded:  
  
package | build  
-----|-----  
anndata-0.12.2 | pyhd8ed1ab_0 129 KB conda-forge
```

Submitting a real job: 為什麼橘貓是橘色的?

以下省略10,000字

Current Biology

CellPress

Article

Molecular and genetic characterization of sex-linked orange coat color in the domestic cat

Christopher B. Kaelin,^{1,2} Kelly A. McGowan,^{1,2} Joshaya C. Trotman,³ Donald C. Koroma,³ Victor A. David,⁴ Marilyn Menotti-Raymond,⁴ Emily C. Graff,⁵ Anne Schmidt-Küntzel,^{4,6} Elena Oancea,³ and Gregory S. Barsh^{1,2,7,*}

¹Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305, USA

²HudsonAlpha Institute for Biotechnology, Huntsville, AL 35806, USA

³Department of Neuroscience, Division of Biology and Medicine, Brown University, Providence, RI 02912, USA

⁴Laboratory of Genomic Diversity, National Cancer Institute, Frederick, MD 21701, USA

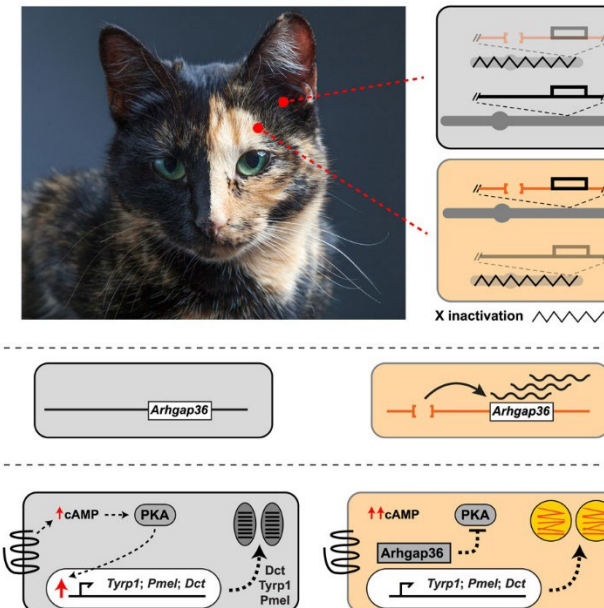
⁵Department of Pathobiology and Scott-Ritchey Research Center, College of Veterinary Medicine, Auburn University, Auburn, AL 36849, USA

⁶Cheetah Conservation Fund, Otjiwarongo, Namibia

⁷Lead contact

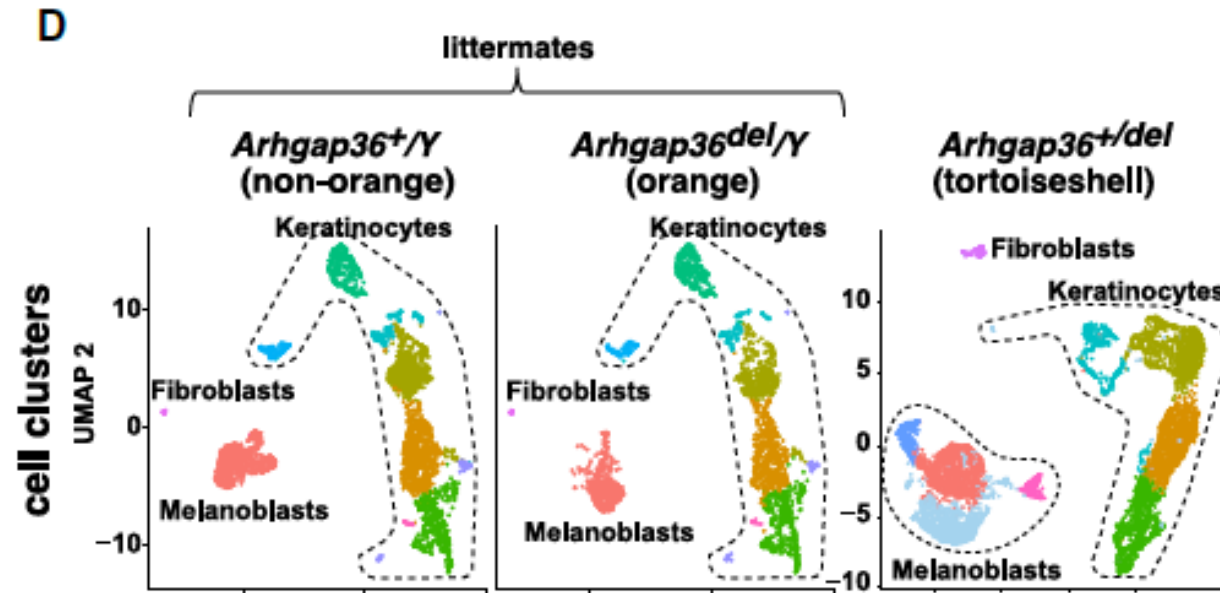
*Correspondence: gbarsh@stanford.edu

<https://doi.org/10.1016/j.cub.2025.04.055>



「橘貓，你為什麼是橘貓？」集結全球貓奴之力，科學家揭開貓咪橘毛的基因秘密
<https://dq.yam.com/post/16561>

量化基因表現量: Cellranger count



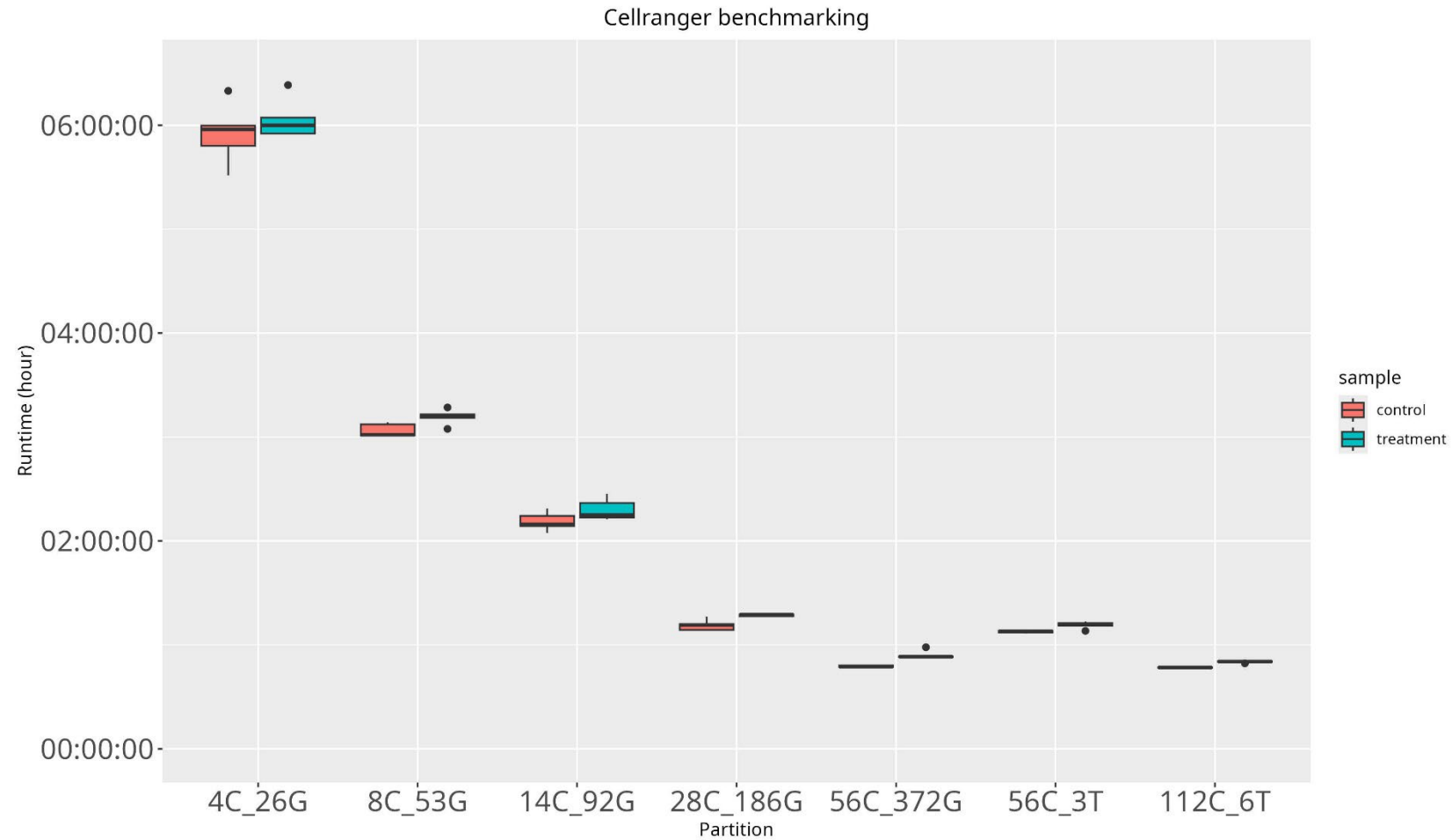
Found 3 Items

☒	☐	Run	BioSample	Bases	Bytes	Experiment	genotype	Library Name	create_date	Sample Name	sex
☐	1	SRR32481539	SAMN47003498	141.51 G	63.88 Gb	SRX27795448	Arhgap36del/Y	GSM8812388	2025-02-25 14:47:00Z	GSM8812388	male
☐	2	SRR32481540	SAMN47003499	141.63 G	63.84 Gb	SRX27795447	Arhgap36+/Y	GSM8812387	2025-02-25 15:01:00Z	GSM8812387	male
☐	3	SRR32481541	SAMN47003500	138.81 G	64.46 Gb	SRX27795446	Arhgap36+/del	GSM8812386	2025-02-25 14:40:00Z	GSM8812386	female

今日不宜demo

https://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP566189&o=acc_s%3Aa

Benchmarking: cellranger count

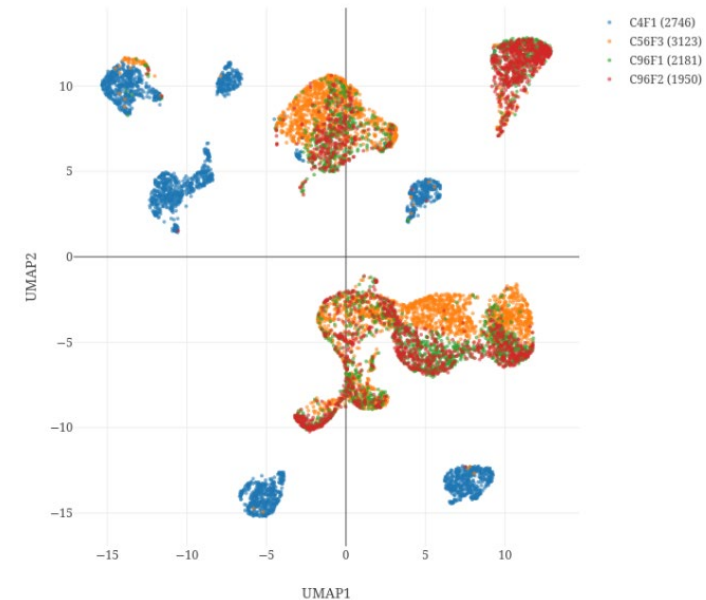


Raw sequences & counts

```
[bionchc4demo@lgn304 seq]$  
[bionchc4demo@lgn304 seq]$  
[bionchc4demo@lgn304 seq]$ pwd  
/opt/ohpc/Taiwania3/pkg/biology/zzz_sctest/seq  
[bionchc4demo@lgn304 seq]$  
[bionchc4demo@lgn304 seq]$  
[bionchc4demo@lgn304 seq]$ ls -l  
total 4  
drwxrwxr-x 4 biology biology 4096 Sep 23 17:08 C4F1  
drwxrwxr-x 4 biology biology 4096 Sep 23 21:55 C56F3  
drwxrwxr-x 4 biology biology 4096 Sep 23 19:57 C96F1  
drwxrwxr-x 4 biology biology 4096 Sep 23 14:29 C96F2  
[bionchc4demo@lgn304 seq]$  
[bionchc4demo@lgn304 seq]$  
[bionchc4demo@lgn304 seq]$ du -sh  
354G  
[bionchc4demo@lgn304 seq]$
```

Cellranger aggr: put the count together

- job script: demo2_cellranger.sh
- your code: cellranger + 一堆參數
- partition: ngscourse92G
- 確定可執行: chmod
- 送job: sbatch
- 查詢job狀態: squeue --me



Job script: demo2_cellranger.sh

```
#!/usr/bin/sh
#SBATCH -A ACD114107
#SBATCH -J cellranger_test-ngscourse92G

## ngscourse92G
#SBATCH -p ngscourse92G
#SBATCH -c 14
#SBATCH --mem=92g

#SBATCH -o cellranger_test-ngscourse92G_out.log
#SBATCH -e cellranger_test-ngscourse92G_err.log

#####
#####
##SBATCH --mail-user=xxx@yyy.zz
#####
#####

# email
# 指定送出email時機 可為 NONE, BEGIN, END, FAIL, QUEUE, ALL

#### your scripts

ml load biology
ml load CellRanger/9.0.1

cd

cellranger aggr --id=cat_aggr-test --output-dir=./cat_aggr-test --csv=/opt/ohpc/Taiwania3/pkg/biology/zzz_sctest/cat_lib
aries.csv
```

核心設施用戶: MST109178

這裡填你的email

Your code

Executable job script

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ls -l  
total 825380  
drwxr-xr-x 7 bionchc4demo ACD114107      4096 Feb  5  2025 cellranger-9.0.1  
-rw-r--r-- 1 bionchc4demo ACD114107 845171096 Sep 26 11:28 cellranger-9.0.1.tar.gz  
-rwxr--r-- 1 bionchc4demo ACD114107      23 Sep 26 13:56 del_all.sh  
-rwxr--r-- 1 bionchc4demo ACD114107     672 Sep 26 13:51 demo1_r.sh  
-rw-r--r-- 1 bionchc4demo ACD114107     845 Sep 26 15:17 demo2_cellranger.sh  
drwxr-xr-x 3 bionchc4demo ACD114107      4096 Sep 26 12:03 R  
-rw-r--r-- 1 bionchc4demo MST109178     569 Sep 23 12:17 r_test.R  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ chmod u+x demo2_cellranger.sh  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ ls -l  
total 825380  
drwxr-xr-x 7 bionchc4demo ACD114107      4096 Feb  5  2025 cellranger-9.0.1  
-rw-r--r-- 1 bionchc4demo ACD114107 845171096 Sep 26 11:28 cellranger-9.0.1.tar.gz  
-rwxr--r-- 1 bionchc4demo ACD114107      23 Sep 26 13:56 del_all.sh  
-rwxr--r-- 1 bionchc4demo ACD114107     672 Sep 26 13:51 demo1_r.sh  
-rwxr--r-- 1 bionchc4demo ACD114107     845 Sep 26 15:17 demo2_cellranger.sh  
drwxr-xr-x 3 bionchc4demo ACD114107      4096 Sep 26 12:03 R  
-rw-r--r-- 1 bionchc4demo MST109178     569 Sep 23 12:17 r_test.R  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$
```

Submitting job

```
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ sbatch demo2_cellranger.sh  
Submitted batch job 16706093  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$ squeue --me  
      JOBID PARTITION    NAME     USER ST       TIME  NODES NODELIST(REASON)  
      16706093 ngscourse cellrang bionchc4  R        0:10        1 cpn3896  
[bionchc4demo@lgn304 ~]$  
[bionchc4demo@lgn304 ~]$
```

⊕ 來源: no-reply@twcc.ai 

標題: Slurm Job_id=16706093 Name=cellranger_test-ngscourse92G Began, Queued time 00:00:01

日期: Fri, 26 Sep 2025 15:55:45

⊕ 來源: no-reply@twcc.ai 

標題: Slurm Job_id=16706093 Name=cellranger_test-ngscourse92G Ended, Run time 00:07:53, COMPLETED, ExitCode 0

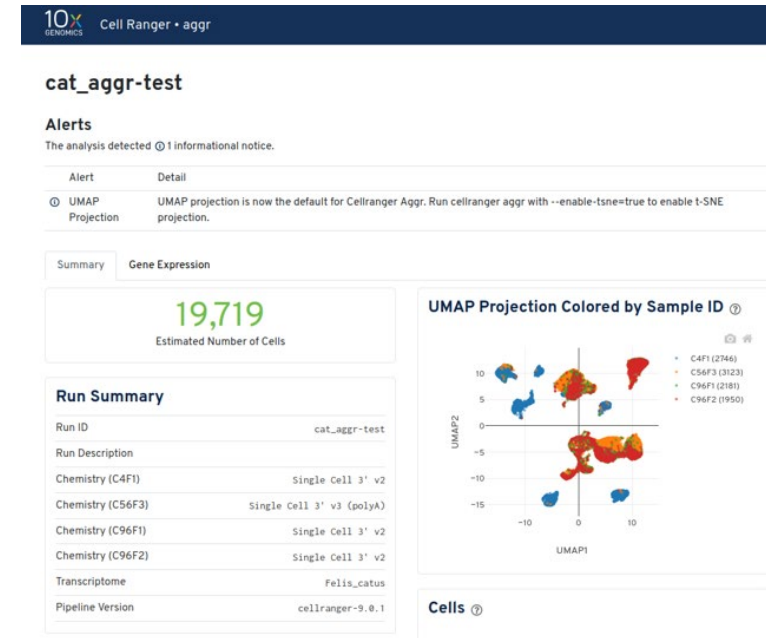
日期: Fri, 26 Sep 2025 16:03:38

Expected results: web_summary.html

~8 min

```

[bionchc4demo@lgn304 cat_aggr-test]$
[bionchc4demo@lgn304 cat_aggr-test]$ ls -l
total 5495
-rw-r--r-- 1 bionchc4demo ACD114107 4168594 Sep 26 16:03 cat_aggr-test.mri.tgz
-rw-r--r-- 1 bionchc4demo ACD114107 131 Sep 26 16:03 _cmdline
drwxr-xr-x 3 bionchc4demo ACD114107 4096 Sep 26 16:03 extras
-rw-r--r-- 1 bionchc4demo ACD114107 51205 Sep 26 16:03 _filelist
-rw-r--r-- 1 bionchc4demo ACD114107 589880 Sep 26 16:03 _finalstate
-rw-r--r-- 1 bionchc4demo ACD114107 843 Sep 26 15:55 _invocation
-rw-r--r-- 1 bionchc4demo ACD114107 5 Sep 26 15:55 _jobmode
-rw-r--r-- 1 bionchc4demo ACD114107 40297 Sep 26 16:03 _log
-rw-r--r-- 1 bionchc4demo ACD114107 297783 Sep 26 15:55 _mrosources
drwxr-xr-x 3 bionchc4demo ACD114107 4096 Sep 26 16:03 outs
-rw-r--r-- 1 bionchc4demo ACD114107 327918 Sep 26 16:03 _perf
drwxr-xr-x 7 bionchc4demo ACD114107 4096 Sep 26 16:02 SC_RNA_AGGREGATOR_CS
-rw-r--r-- 1 bionchc4demo ACD114107 16914 Sep 26 16:03 _sitecheck
-rw-r--r-- 1 bionchc4demo ACD114107 2 Sep 26 15:55 _tags
-rw-r--r-- 1 bionchc4demo ACD114107 51 Sep 26 16:03 _timestamp
-rw-r--r-- 1 bionchc4demo ACD114107 36 Sep 26 15:55 _uuid
-rw-r--r-- 1 bionchc4demo ACD114107 16799 Sep 26 16:03 _vdrkill
-rw-r--r-- 1 bionchc4demo ACD114107 65 Sep 26 15:55 _versions
[bionchc4demo@lgn304 cat_aggr-test]$ cd outs
[bionchc4demo@lgn304 outs]$ ls -l
total 6386
-rw-rw-r-- 1 bionchc4demo ACD114107 370 Sep 26 15:55 aggregation.csv
drwxr-xr-x 4 bionchc4demo ACD114107 4096 Sep 26 16:03 count
-rw-r--r-- 1 bionchc4demo ACD114107 6526052 Sep 26 16:02 web_summary.html
[bionchc4demo@lgn304 outs]$
  
```



Demo #3: cellranger

ssh t3-c4.nchc.org.tw

or

ssh 203.145.216.54

Summary

- Experimental design
- NGS data files
- Accessing T3
- Playing around with T3
- Running your code
- Installing your apps
- Submitting jobs

Thank you

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國網生科雲

