# User Manual of Muti-omic Acra Melanoma Altas

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MAMA (Multi-omic Acral Melanoma Atlas) is an interactive web server based on R package *shiny*. It is developed to showing the multi-omic analyze of Acral Melanoma in our research. We hope that our research will inspire future studies on acral melanoma by providing novel multi-omic perspectives.

#### 1. Overview

Multi-omic Acral Mela	<sup>ioma</sup> Atlas ≡ Website title	
A Home	Multi-omic Acral Melanoma Altas	Graphic Abstract –
Pathology Sections		
図 Clonal Evolution	Acta interationing (why is an aggressive soutppe or metanoma with a distinal progross. The distinct mont with a situ (AMis) to invasive AM (iAM) significantly decreases survival. Here we integrated data from <b>147 AM patients</b> using six omics approaches that identified four invasion-preferred drivers (NRAS, KRAS, NFf, and K/T) and suggested	Early detection     Early detection     Early detection     Vertical     Vertical     Secondary
III Single-cell RNA-seq	adnexal involvement as a potential invasive indicator. Two distinct invasion and expansion patterns were found in AM,	1 Invasion-preferred drivers
∰ Spatial Omics	and notably, one pattern showing enrichment of APOE/CD153** macrophages is associated with increased tumor progression and shorter patient survival. This particular macrophage profile promotes tumor cell transition through the GRT+IGF1R interaction. Our results shed light on the evolutionary dynamics during AM invasion and have important	ii) Adresal incluement Regional espansion Acral molanoma Casal Dependent
Molecular Subtypes	mplications for the early detection, prognosis, and treatment of AM.	(CD) Charles and Charles (SD)
Documents	Research Methodology and Pipeline –	APCE/201463 macrophage
🖂 About	Display area	C1 C2 C3 Readon Proffeesion
Menu bar	Discovery cohort (147 patients) Multi-omic profiling Integrative analysis Functional validation	Geconic instability Progression patien CE CE SD Low infiltration High
	Acrai melanoma VES scRNA.seq n = 92 n = 24	THE devinant of Cool During Pour Karalooge Board Appendix Control Technology Received
		Quick Start -
	LCM-WES Spatial RNA n = 33 n = 10	Search in:
	AM in situ (AMis) 56 patients Union	Single-cell Transcriptomic Atlas -
	Bulk RNA 222 plex Molecular Diagnostic Prognosis	Enter Genes (split by space, or comma):
	n = 81 n = 12 Early prediction Prognosis	APOE CD163
	Image: second	<b>⊘</b> Search
		Functional area
		discussion purposes only.

First let's take an overview of our website, which consists of **4** parts. Utilizing the Menu bar, users have the ability to switch to different pages. In the Functional area, you can interact with the server by modifying parameters or uploading data, finally controlling the Display area's figure. Furthermore, the abstract of the page is sometimes displayed in this section as supplement. Provided figures or texts are displayed in Display area, which helps get an in-depth understanding of our research.



Besides, via clicking this button, users can hide the Menu bar and the name of website. This function provides a better perspective for figure display.

We also realize the function that any functional module could be minimized by clicking the "-".

Uplo	bad Images For – Comparison
(	Choose Images
Browse	No file selected

# 2. Home Page

Quick Start	
Search in:	
gle-cell Transcriptomic Atlas	*
nes (split by space, or comma	):
	Search in: gle-cell Transcriptomic Atlas nes (split by space, or comma

Users should choose a wanted page , then fill in your target genes. By clicking the "Search" button, you will skip to the target page and our server will plot the corresponding figure for you. Attention! You can and only can split

genes with **comma(",")**, **space(" ")**, and **newline**. Please don't use other ways

### 3. Pathology Sections

Users can filter the pictures via patients or markers. Users can view and download images.

Filter	Images
Filter by	Patients:
Nothing selected	
Filter by	Markers:
Nothing selected	
Select All	Deselect All
APOE	
CD163	
NC	

Upload In	nages For Comparison	-
Choose Ima	ges	
Browse	No file selected	

Besides, we allow users o upload their own picture o contract with ours.

Filter or not, immunohistochemical pictures will be shown on the Display area. By clicking the "**Download**" button below a picture, users could download it. **All** of our pictures are **downloadable** for academic.

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	(Constraint)	

#### 4. Genomic Profiling

In the context of cancer, clonal evolution describes how tumor cells accumulate genetic alterations over time, leading to the formation of multiple subclones with differing genomic profiles. These subclones may have different



growth rates, responses to therapy, and metastatic potentials, contributing to the complexity and heterogeneity of cancer and posing challenges for effective treatment. Clonal evolution can be analyzed using techniques such as single- cell sequencing, multi-region

sampling, and phylogenetic analysis to reconstruct the evolutionary history of the tumor and identify the genetic alterations and evolutionary trajectories that give rise to different cellular subpopulations.

We provide our ComplexHeatMap figure in this page. Users can refer to it to decide the inputted genes in the functional area. In this way you can customize a heatmap you want about clonal evolution. Please pay attention to the way you split genes. **Only** comma(","), space(""), and newline can be used.

Іпрі	ut Gene(s) –
Input Genes	Upload Gene List
Enter multiple g space	genes (split by newline, e, or comma)
APOE FOXO3	в

# 5. Single-cell RNA-seq

Select Gene(s)	-
Input Gene(s)	
Upload Gene List	
Enter multiple genes (split by newline, spac or comma)	s :e,
APOE CD163	
A Plot	h.

Users can visualize gene expression features in single-cell RNA sequencing data by clicking the "Plot" button to submit your target genes. We'll provide the Featureplot figures and expression across subclusters in the corresponding dataset. (This function will be implemented in future website updates.) It allows researchers to quickly and intuitively view the

expression levels of different genes within individual cells, and can associate this information with cell clustering, subgroups, etc. Below the Image Generate Area, users can find provided reference marker genes and subclusters annotation, which can guide to choose the target genes. If you input unrecognized genes, our server will return "**No data**" rather than Feature plot figures. **Only** comma(","), space("") and newline are allowed. It will also influence our feedback.

#### 6. Spatial Omics

The conventional approach to studying tissue transcriptomes involves RNA-sequencing (RNA-seq) of homogenized biopsies, resulting in an averaged



transcriptome and the loss of spatial information. Spatial omics refers to a group of techniques that integrate traditional omics approaches, such as genomics, transcriptomics, proteomics, and metabolomics, with spatial information within biological systems. These technologies enable the characterization and analysis of biomolecules within the context of their precise location in tissues and cells.

Input Genes	Upload Gene List
nter multiple g r comma)	enes (split by newline, space,
CD163 CD4	
00100 001	

The same as Molecular Subtypes, we allow users to input or upload genes, resulting in corresponding Spatial Transcriptomics figures. Splitting by comma(","), space("") and newline is still a **must**. Reference spatial areas are also provided.

# 7. Molecular Subtypes



By inputting or uploading genes, users could get the corresponding Patient Survival Plot Regions. **Only** comma(","), space(""), and newline are allowed to use.

# 8. Document

Just read this.

# 9. About

We provide the used R package, citation, contact way. All resources are allowed to be used for academic. If you have any problems, please contact Hengkang Liu (<u>liuhengkang@pku.edu.cn</u>).