

# IOSig: immuno-oncology signatures explorer in immunotherapy treated pancancer cohorts

Samuel Coleman<sup>1,2</sup>, Caroline Wheeler<sup>3</sup>, Rebecca Hoyd<sup>3</sup>, Louis Denko<sup>3</sup>, Ching-Nung Lin<sup>1,2</sup>, Muhammad Zaki Hidayatullah Fadlullah<sup>1</sup>, Siwen-Hu-Lieskovan<sup>1</sup>, Christine H. Chung<sup>4</sup>, Ahmad A. Tarhini<sup>5</sup>, Daniel Spakowicz<sup>3</sup>, and Aik Choon Tan<sup>1,2\*</sup>, 2022 Bioinformatics (In-Revision)



# Introduction

• Immuno-oncology signatures explorer (IOSig) is a web interface that allows users to query and explore immune checkpoint blockade treated cohorts with gene expression signatures for the purpose of predicting response to treatment.

• Users can upload their own gene expression signature, gene expression and clinical data, or query the data built in to IOSig.



The About page contains additional information about IOSig and the three analysis modules included in IOSIg

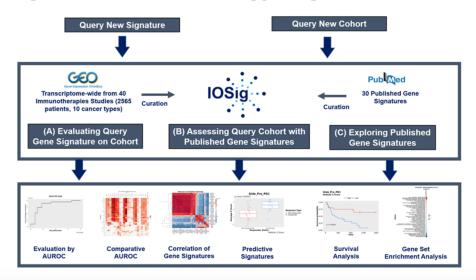




Dataset Overview

Immuno-Oncology Signatures Explorer (IOSig) is an interactive Shiny application meant to facilitate the investigation of immune checkpoint inhibitor (ICI) treated datasets with gene expression biomarker signatures for prediction of responder / non-responder. Previously published gene expression signatures have been collected in addition to publicly available ICI treated RNA-seq cohorts to allow for query their own datasets or signatures against. In addition, it also possible to explore the data within the application without providing your own.

## **IOSig: Immuno-Oncology Signatures Explorer**





### The Dataset Overview Tab details the RNA-seq datasets and Signatures included in IOSig



**Dataset Overview** 

**Dataset Analysis** 

**User Signature Analysis** Published Signature Analysis

**Expression Data Overview** 

Signature Overview

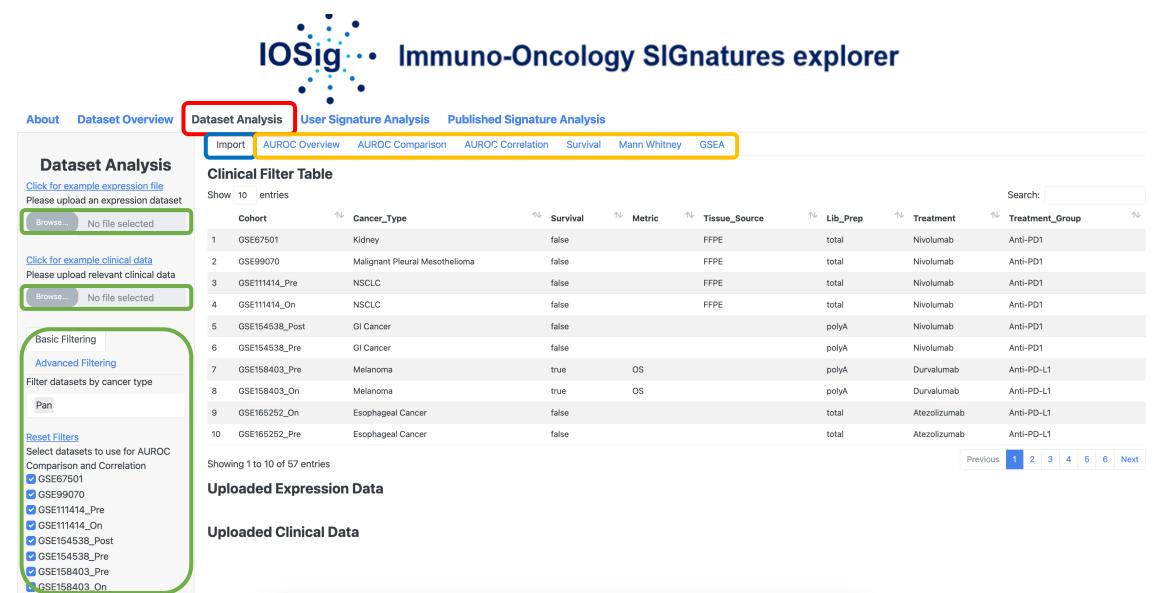
### **Expression data included in this application:**

				Show	10 entries							Search:		
	Data Set ID <sup>↑↓</sup> I	<b>V</b> ↑↓	Cancer Type <sup>↑↓</sup>	Pre On Post ↑↓	Drug	Treati Group	0.1	Survival Data <sup>↑↓</sup>	Library Prep <sup>↑↓</sup>	Tissue Source <sup>↑↓</sup>	Biosources <sup>↑↓</sup>	Clinical Trials ID	Platform <sup>↑↓</sup>	PMID ↑↓
1	GSE67501	11	Kidney	Pre	Nivolumab	Anti-P	PD1		total	FFPE	Tissue	NCT00441337, NCT00730639, NCT01354431, NCT01358721	Microarray	27491898
2	GSE99070	10	Malignant Pleural Mesothelioma	Pre	Nivolumab	Anti-P	PD1		total	FFPE	Tissue		Microarray	<u>29618661</u>
3	GSE111414	20	NSCLC	Pre/On	Nivolumab	Anti-P	PD1		total	FFPE	PBMC		RNA-seq	30765392
4	GSE154538	26	GI cancer	Pre/Post	Nivolumab	Anti-P	PD1		polyA		Tissue		RNA-seq	34014607
5	GSE158403	81	Melanoma	Pre/On	Durvalumab	Anti-P	PD-L1	os	polyA		Tissue	NCT02027961	RNA-seq	33288749
6	GSE165252	71	Esophageal	Pre/On/Post	Atezolizumab	Anti-P	PD-L1		total		Tissue	NCT03087864	RNA-seq	33504550
7	GSE165278	22	Melanoma	Pre/Post	Ipilimumab	Anti-C	CTLA4	OS	total		Tissue	NCT00796991,NCT00495066 NCT00920907, NCT00324155, NCT00162123, NCT0140045 and NCT00289640, NCT00495066, NCT00636168, NCT01515189, NCT00086489, NCT0047188		33588426
8	GSE173839	71	Breast	Pre	Durvalumab	Anti-P	PD-L1		total	FFPE	Tissue	NCT01042379	Microarray	34143979
9	GSE176307	87	Bladder	Pre	Atezolizumab/Pembrolizumab/Nivolumab/Durvalumab/Avelumab	Anti-		OS	total	FFPE	Tissue		RNA-sea	34294892



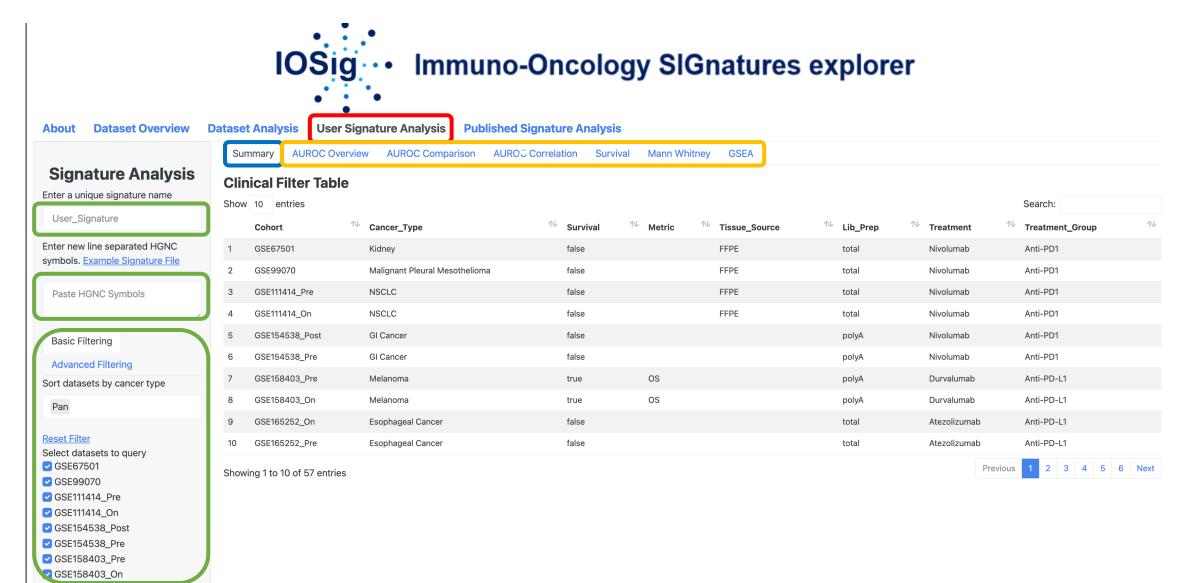
The Dataset Analysis module (red) allows the user to upload RNA-seq gene expression data with paired clinical data for analysis using the built-in IOSig signatures.

The data is loaded in on the Import tab (blue). Users upload their data and filter the comparison datasets on the side panel (green). The analysis results are located in the additional subtabs (yellow).





The user signature method (red) allows users to upload a list of genes that are used to predict response to immune checkpoint inhibitor treatment. Data is uploaded on the side panel (green) of the Summary tab (blue). Additional filtering of comparison datasets and gene signatures takes place on the side panel (green). The results of the analysis are found in the additional subtabs of the User Signature Analysis page (yellow).





The Published Signature Analysis method (red) allows users to query the gene expression and signature data built into IOSig. Users can filter the datasets and select gene signature sets on the side panel (green) of the Summary screen (blue). The results of the analysis can be found in the additional subtabs (yellow) of the Published Signature Analysis page (red).

