

Purpose: To request bioinformatics support from U of Washington Informatics, Systems immunology, and Data Omics in Medicine (U-WISDOM). This request is the beginning of the conversation and access to bioinformatics resources or personnel is subject to availability and funding.

Process: Please complete the following and send to Dr. Kim Dill-McFarland (<a href="mailto:kadm@uw.edu">kadm@uw.edu</a>) for review and scheduling of an initial consultation

Applica	nt		
Name			
PI nam	e (if different)		
Email			UW Department
Services	5		
Which	of the followin	ng best de	scribe your bioinformatic needs? Please select all that apply.
	Consultant	such as	study design, grant support, or code review
	Analyst	such as	data cleaning, quality-control, or other processing of raw data
	Statistician	such as	statistics, downstream analysis, or visualization of tidy data
	Training	such as v	workshops or mentoring another researcher
	Other		
Will yo	ou require long Yes No Unknown	-term sto	rage of data?
Funding	3		
At wha	nt stage is the f	unding fo	r this project?
	Unfunded		
	Funding in pr	ogress	such as grant in progress or submitted
	Funded		such as notice of funding or grant in hand
How m	nuch bioinform	atic fundi	ng is anticipated/available for this project? Please include all that apply.
	USD for	salary ov	er years
	USD for	computa	tional costs such as cloud resources over years
	☐ Unknow	/n	

2023-10-06



## **Project specifics**

<ul> <li>□ Amplicon sequencing (Please specify: 16S, 18S, ITS, or other)</li> <li>□ ATAC, DNase, or MNase-seq</li> <li>□ Flow cytometry</li> <li>□ Genetics array (Omni, MegaEx, or other chip)</li> <li>□ Genetics whole genome (exome, low pass or full WGS)</li> <li>□ Metagenomics</li> <li>□ Metatranscriptomics</li> <li>□ Methylation (Illumina EPIC or other chip)</li> <li>□ Proteomics</li> <li>□ RNA-seq (bulk)</li> <li>□ RNA-seq (single cell)</li> <li>□ Other:</li> </ul>	vhich of the following data types will be part of this project?			
<ul> <li>□ Flow cytometry</li> <li>□ Genetics array (Omni, MegaEx, or other chip)</li> <li>□ Genetics whole genome (exome, low pass or full WGS)</li> <li>□ Metagenomics</li> <li>□ Metatranscriptomics</li> <li>□ Methylation (Illumina EPIC or other chip)</li> <li>□ Proteomics</li> <li>□ RNA-seq (bulk)</li> <li>□ RNA-seq (single cell)</li> </ul>		Amplicon sequencing (Please specify: 16S, 18S, ITS, or other)		
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<ul> <li>□ Proteomics</li> <li>□ RNA-seq (bulk)</li> <li>□ RNA-seq (single cell)</li> </ul>		Metatranscriptomics		
<ul><li>□ RNA-seq (bulk)</li><li>□ RNA-seq (single cell)</li></ul>		Methylation (Illumina EPIC or other chip)		
☐ RNA-seq (single cell)		Proteomics		
		RNA-seq (bulk)		
□ Other:		RNA-seq (single cell)		
		Other:		

Please briefly describe the study including question/hypothesis, design, sample size, timeline for data generation, variables of interest, or any other relevant details.

If available, please provide the grant or project proposal associated with this study.

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