

Rapid exploration, interpretation, and comparison of discrete basis vectors contributing to transcriptional signatures of single cells at the scale of the HCA with ProjectoR

Personnel:		Role	Base	Cal. Mos.	% Effort	Salary Req.	Fringe	YR1 Total
Loyal Goff		PI	\$ 132,651	1.80	15%	\$19,898	\$6,765	\$ 26,663
Seth Blackshaw		Collaborator	\$ -	0.00	0%	\$0	\$0	\$ -
Brian Clark		Research Associate	\$ -	0.00	0%	\$0	\$0	\$ -
Genevieve Stein-O'Brien		Postdoctoral Fellow	\$ 47,853	6.00	50%	\$23,927	\$4,618	\$ 28,544
TBN		Graduate Student	\$ 31,936	9.00	75%	\$23,952	\$4,400	\$ 28,352
Briana Winer		Research Technologist	\$ 34,000	6.00	50%	\$17,000	\$5,780	\$ 22,780
<i>Subtotal</i>						\$84,776	\$21,563	\$ 106,339
Expenses:								
Supplies & Materials:								
10x V2 library kit (16 samples per kit; 2X \$21,000 each)								\$ 42,000
Chips (6*8 samples/chip, 2x \$1,440)								\$ 2,880
Barcode Index kit (96 samples, 1x \$805)								\$ 805
Nextera XT Library Prep Kits								\$ 2,000
Reagents for enzymatic dissociation of single cells and seq. library preparation								\$ 3,000
Computational storage space and Rstudio server (Amazon web services)								\$ 6,000
Laboratory Consumables (pipette tips, plasticware, etc)								\$ 4,867
RNAScope probes for model validations								\$ 4,000
Services								
Illumina 2500 Sequencing lanes (20*\$2,000)								\$ 40,000
Computers								
Laptop computer								\$ 3,000
Travel to HCA meetings								
Travel expenses								\$ 2,500
<i>Subtotal</i>								\$ 111,052
Total Direct Costs, Year 1:								\$ 217,391
<i>Facilities & Administration Costs 15%</i>								\$ 32,608.67
TOTAL COSTS, YEAR 1								\$ 250,000

- Loyal A. Goff, Ph.D. (PI) will be responsible for overall project design and coordination, direction on ProjectoR development and collaborative efforts on single cell collection and biological interpretation (Goff, Blackshaw).
- Seth Blackshaw, Ph.D. (Collaborator) Dr. Blackshaw is a renowned expert in the biology of mammalian retinal development. Drs. Goff, Blackshaw, and collaborative network member Dr. Fertig have an existing collaboration built around a detailed characterization of retinal cell developmental biology that has contributed much of the preliminary data for this proposed project. Dr. Blackshaw will continue to provide biological interpretations to learned basis vectors and will provide necessary resources for validations.
- Brian Clark, Ph.D. (Research Associate) Dr. Clark is a research associate (K99) jointly mentored in the labs of the PI (Goff) and collaborator (Blackshaw). He has years of experience in studying mouse retina development and has extensive experience working with RNA. He will be responsible for tissue acquisition, processing, and will continue to generate the bulk and single cell libraries in mouse and human retina. Dr. Clark will also be primarily responsible for validation of learned basis vectors through in situ fluorescence hybridization analysis.
- Genevieve Stein-O'Brien, Ph.D. (Postdoctoral Fellow) is the chief developer and maintainer of the ProjectoR package and will be responsible for implementing the transfer learning statistics into the software package. Dr. Stein-O'Brien is a postdoctoral fellow co-supervised by Dr. Goff and collaborative network member Dr. Fertig. She is listed in both proposals. In this proposal, Dr. Stein-O'Brien is listed as responsible for the algorithm development and analyses proposed in this award. Her work will be completed in collaboration with all key personnel on this proposal and co-supervised by Dr. Goff and Dr. Fertig. If both awards are funded, a TBN postdoc will be hired to collaborate with Dr. Stein-O'Brien on these efforts.
- TBN (Graduate Student) in conjunction with the research technologist will perform the required single cell library preparations and metadata aggregation and will be primarily responsible for generating and processing the human retinal single cell benchmark data.
- Briana Winer (Research Technologist). In conjunction with the TBN graduate student, Briana will be responsible for performing the additional 10x genomics and sci-RNA-Seq datasets under the direct supervision of the PI, as well as aggregation and organization of all associated metadata.