

Request for Information (RFI): Characterizing and Understanding the Organization of Individual Cells within Human Tissues

Notice Number: NOT-RM-16-025

Key Dates

Release Date: May 26, 2016

Response Date: June 22, 2016

Related Announcements

None

Issued by

Office of Strategic Coordination ([Common Fund](#))

Purpose

This is a Request for Information (RFI) to solicit input regarding a proposal for a new Common Fund program aimed at characterizing and understanding organization of large numbers of primary cells in human tissues using high throughput approaches.

Background

The human body contains more than 10^{13} cells and more than 300 commonly recognized major cell types. Recent advances in multiplexed imaging, proteomics, genomics and transcriptomics are starting to reveal that cells in tissues and organs are more heterogeneous and have much richer organizational structure than previously thought.

There is now the opportunity to increase the throughput and apply these technologies to build a more robust and comprehensive molecular, morphological and functional characterization of major cells types in tissues and to identify spatial and temporal organization. Through the characterization of cell functional history, morphology, lineage mapping, and molecular characterization to develop more detailed maps, we have the opportunity to identify the foundational principles underlying cellular organization in human tissues that could lead to a new level of understanding in many scientific areas including developmental and aging processes, emergence of pathological states and how to engineer complex functional tissue.

Information Requested

The NIH seeks input from researchers, academic institutions, professional societies, businesses, non-profit organizations, other government agencies, and other stakeholders on the opportunities and challenges with applying methods, approaches and technologies to enable the study of entire organs at the individual cell level and cell interactions in situ that form a functional tissue.

Please provide perspectives, pertinent references (and hyperlinks if referencing papers / databases / repositories), as well as names of key experts related to a subset of the following questions that support your overall comments, though your comments are not limited to these topics:

- **Tissues and systems for studying cell organization and interactions**
 - This may include studies that have been conducted in small human tissue samples that would benefit from scaling up to study cell organization and interactions at the level of whole human tissues or organs and the key lessons learned from these studies or studies in model organisms.
 - Comments are welcome on existing human tissue repositories, molecular atlas and tissue expression projects that would be synergistic with an NIH program. [Please provide links to any existing projects or references mentioned]

- **Technical capabilities**
 - This may include technologies and approaches that can be scaled for whole organ studies and still maintain the molecular analysis of individual cells in their native environment and how efficiently these technologies can identify all cell types in a given tissue and be applied to different organs and tissues.
 - Comments are welcome on capturing the dynamic interactions of a cell with its neighboring cells, environment, and the extracellular matrix in a high throughput way to understand the origin of driving signals, and cooperative / competitive pressures on a cell within a tissue. Comments may include new computational methods that are under development to aid analysis and integration of large, disparate datatypes that would come out of these analyses.
- **Defining data needs**
 - This may include parameters that need to be collected about the function, structure, molecular composition and environment of all cells in a tissue to robustly classify them (e.g. immune system cells within solid tissues; somatic and germ cells; cell cycle, active differentiation, senescence or quiescence; and associated lineage and cell-cell interactions). This could also include estimates of the throughput at which we may currently collect these parameters potential limitations (e.g. compatibility with tissue preservation techniques, cell type, or molecular copy number).
 - Comments are welcome on to build a publicly accessible, standardized and interoperable dataset of cell types and human tissue atlases. This may include data and metadata standards, visualization, navigation, and analytical tools that are needed and engagement of the community to contribute data.
- **Other comments, suggestions, or considerations relevant to this RFI**

How to Submit a Response

Responses will be accepted through June 22, 2016.

Responses must be submitted via email to HUBMAP@MAIL.NIH.GOV.

This RFI is for planning purposes only and should not be construed as a solicitation for applications or as an obligation on the part of the Government to provide support for any ideas identified in response to it. Please note that the United States Government will not pay for the preparation of any information submitted or for its use of that information.

The NIH will use the information submitted in response to this RFI at its discretion and will not provide comments to any responder's submission. Proprietary, classified, confidential, or sensitive information should not be included in your response. The United States government reserves the right to use any non-proprietary technical information in any resultant solicitation(s). Responses to the RFI may be reflected in future funding opportunity announcements and will be used in the long-term planning for the Common Fund. Responses will be compiled and shared internally and with working groups convened by the NIH, as appropriate. In all cases where responses are shared, unless the respondent indicates otherwise, the names of the respondents will be withheld. We look forward to your input and hope that you will share this request with your colleagues.

Inquiries

Please direct all inquiries to:

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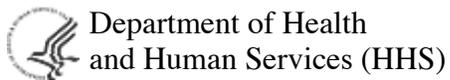
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