Comparison of Liberality Between Melanocyte Stem Cells and Differentiated Cells in Mice

Norichika OGATA, norichik@nbiodata.com, https://orcid.org/0000-0002-6856-6655
Nihon BioData Corp., Kawasaki, Japan
Osaka University, Graduate School of Engineering, Department of Biotechnology, Osaka, Japan
Manufacturing Technology Association of Biologics, Kobe, Japan

Abstract

Liberality refers to the degree of cellular dedifferentiation/differentiation, quantified through the estimation of information entropy from numeric transcriptome data and Lempel-Ziv complexity from transcriptome sequence data. In a previous study, single-cell RNA-seq data for melanocyte stem cells (McSCs) and melanocytes were obtained. Based on the definition of liberality, McSCs are expected to exhibit higher liberality than differentiated melanocytes. In this study, we estimated and compared the liberality between these two cell types.

Keywords *- Liberality, Transcriptome, Melanocyte, differentiation, dedifferentiation, single-cell RNA-seq*

Introduction

Cells change their phenotypes in response to their environment and fate. A cellular phenotypic change, first discovered in 1913, was termed dedifferentiation, which represents morphological alterations and changes in proliferation observed in primary culture [1]. Initially, dedifferentiation was discussed as a qualitative phenomenon. A study published in 2023 distinguished stem cells and differentiated cells based on the presence of specific “marker” proteins [2]. Since 2010, we have been working on quantifying the processes of differentiation and dedifferentiation [3]. Over the past decade, we successfully developed and published methods to quantify these phenomena by estimating liberality as the information entropy of numeric gene expression data [4–11] and the Lempel-Ziv complexity of gene expression sequence data[12,13]. In this study, we aim to estimate and compare the liberality of McSCs and melanocytes [2]. We also used data from a previous study [14]. In total, we compared four groups of single-cell RNA-seq data: activated McSCs and melanocytes from the 2023 study [2], as well as McSCs and melanoma cells from the 2019 study [14].

Results and Discussion

We estimated the liberality of the cells and plotted it against the number of genes measured for expression in each cell during the experiment. Cells with fewer than 2000 genes measured (likely due to failed experiments) were abundant in the 2019 McSC dataset and common in the 2023 activated McSC dataset. These data are unsuitable for further analysis, as they are expected to have low liberality. We found that the liberality of differentiated melanocytes is lower than that of activated McSCs. Additionally, the number of genes measured

in differentiated melanocytes was fewer than in activated McSCs. The liberality of melanoma cells showed a wider distribution compared to that of differentiated melanocytes, with very few cells having fewer than 2000 genes measured. This may be due to the homogeneous phenotype of cancer cells, which simplifies single-cell RNA-seq preparations. In contrast, the McSC data from 2019 appears to have mostly failed. Melanoma cells may have higher liberality than McSC. There is a possibility that cancer cells have higher liberality than normal cells.

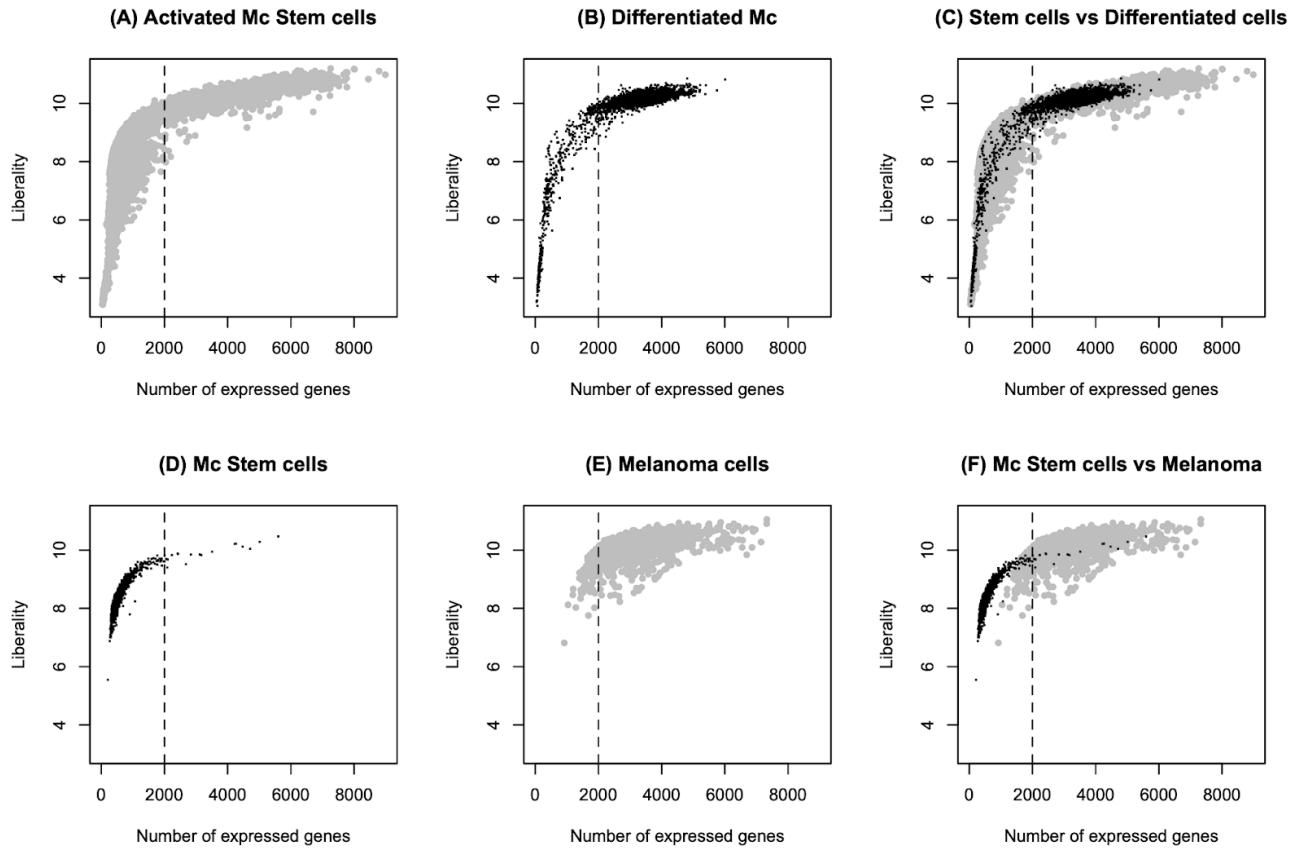

Figure 1. Liberality of Melanocyte Stem Cells, Differentiated Cells, and Cancer Cells
The number of expressed genes measured in each cell and their liberality were plotted. (A) Activated melanocyte stem cells from 2023. (B) Differentiated melanocytes from 2023. (C) Activated melanocyte stem cells and differentiated melanocytes from 2023. (D) Melanocyte stem cells from 2019. (E) Melanoma cells from 2019. (F) Melanocyte stem cells and melanoma cells from 2019.

Materials and Methods

The genome expression data were obtained from NCBI SRA (GSE113502 and GSE203051) [2,14]. The liberality was measured as previously described [8]. The implementation of the calculation method for liberality using the R language [15] is as follows.

```
entroshannon<-function(x){
x2<-x/sum(x)
x3<-x2*log2(x2)
x4<-x3[!is.na(x3)]
-sum(x4)
}
```

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