

BITS :: Call for Abstracts 2024 - Oral communication

<i>Type</i>	Oral communication
<i>Session</i>	High Resolution RNA Computational Biology
<i>Title</i>	Interactive exploration of cell-cell communication results from single-cell RNA sequencing data through a webapp
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Affiliation

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Motivation

Biological systems rely on the coordinated activity of multiple cells, responding to external stimuli by adapting their functional state. In the context of multicellular organisms, cell-cell communication (CCC) is fundamental to the proper functioning of tissues and organs, with aberrations often leading to pathological consequences. The elucidation of CCC thus represents a pivotal aspect in the comprehension of the physiopathology of biological systems[1].

In recent years, there have been extensive efforts in the development of computational methods with robust statistical foundations that can infer CCC from single-cell RNA sequencing data[2,3]. Despite the plethora of currently available computational tools in the field of CCC analysis, the challenge of elucidating the biological implications of the results persists. Moreover, addressing this challenge requires both deep computational and biological expertise.

Here we present CClens, an web app to empower laboratory scientists to analyse and explore the predicted CCC data, which are typically complex and highly-dimensional, without requiring programming skills.

Methods

CClens is implemented in R/shiny[4] using reactive programming paradigm, and it is released as an R package on GitLab[5]. The package includes a detailed vignette and provides the users with two example datasets that can be used to familiarise with the platform. The app supports input csv, tsv and RData files from the main CCC tools. Data may contain intercellular (i.e. ligand-receptor) and intracellular (e.g. pathway activation) scores, as well as user-defined scores. Additional info like statistical significance and gene lists is supported too, offering users flexibility to upload and display communication results regardless of the analysis tool used.

Results

CClens provides a user-friendly platform specifically designed for comprehensive analyses and visualisations of CCC data, deriving from either the analysis of a single biological condition or the analysis of differential communication between two biological conditions.

The design guides the exploration of results starting from a broad global perspective, then transitioning to a cell-centred analysis, and finally focusing on the molecular level (Fig 1). This approach empowers the capability to concentrate on specific ligands and receptors of interest, while maintaining a comprehensive understanding of the broader biological context.

The top panel is dedicated to the interactive filtering of data, achieved by setting custom thresholds for scores and the selection of specific cell types and molecules (ligand and receptors) that reactively subset the data visualised in the downstream panels of the app (Fig 1, top). Also, an additional tab with an interactive data frame permits the original data to be interrogated in a convenient yet advanced manner (Fig 1, top).

The first panel dedicated to visualisations provides an overview of all the ongoing communications, along with summary statistics about the cell types most involved in communication. This is achieved through interactive heatmaps, bar plots, chord diagrams and a network plot (Fig 1a).

The adjacent tab allows the user to focus on a single cell type of interest (Fig 1b). In order to facilitate the interpretation of the data, the communications are visualised separately according to the involvement of the cell type as a sender (i.e. expressing the ligand) or receiver (i.e. expressing the receptor).

For a deeper understanding of the results at a molecular level, interactive bubble plots allow the user to select specific ligand-receptor interactions and cell types to be included in the charts (Fig 1c). The interactivity also allows the inspection of the original data by clicking on the dots.

We believe that CClens is a valuable tool that will facilitate the interpretation of CCC results, enabling the formulation of new data-driven hypotheses on the underlying biological mechanisms.

Info

1. Armingol, E., Officer, A., Harismendy, O. & Lewis, N. E. Deciphering cell-cell interactions and communication from gene expression. *Nat. Rev. Genet.* 22, 71-88 (2021).
2. Almet, A. A., Cang, Z., Jin, S. & Nie, Q. The landscape of cell-cell communication through single-cell transcriptomics. *Curr. Opin. Syst. Biol.* 26, 12-23 (2021).
3. Dimitrov, D. et al. Comparison of methods and resources for cell-cell communication inference from single-cell RNA-Seq data. *Nat. Commun.* 13, 3224 (2022).
4. Winston Chang and Joe Cheng and JJ Allaire and Carson Sievert and Barret Schloerke and Yihui Xie and Jeff Allen and Jonathan McPherson and Alan Dipert and Barbara Borges. shiny: Web Application Framework for R. (2023).

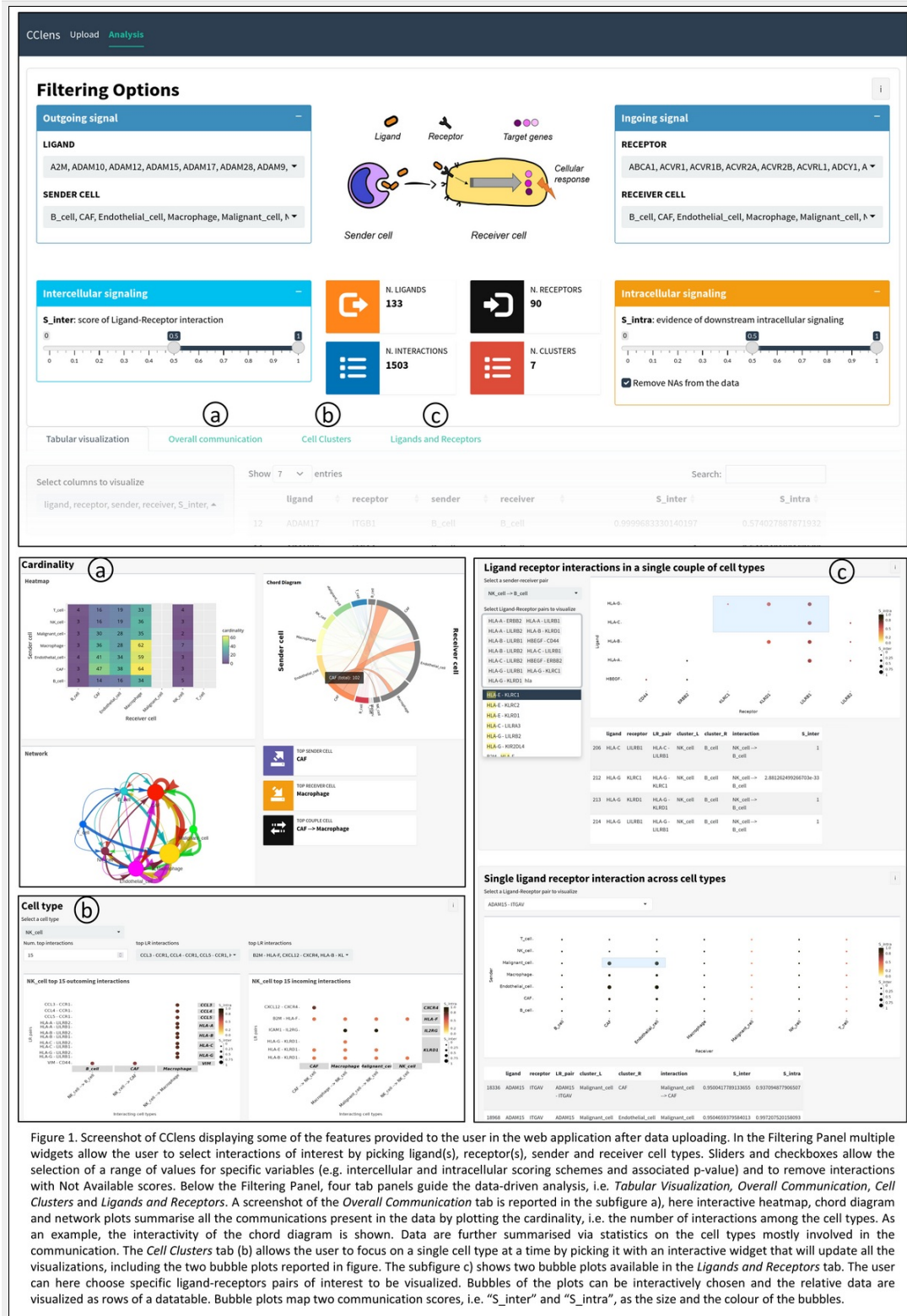


Figure 1. Screenshot of CClens displaying some of the features provided to the user in the web application after data uploading. In the Filtering Panel multiple widgets allow the user to select interactions of interest by picking ligand(s), receptor(s), sender and receiver cell types. Sliders and checkboxes allow the selection of a range of values for specific variables (e.g. intercellular and intracellular scoring schemes and associated p-value) and to remove interactions with Not Available scores. Below the Filtering Panel, four tab panels guide the data-driven analysis, i.e. *Tabular Visualization*, *Overall Communication*, *Cell Clusters* and *Ligands and Receptors*. A screenshot of the *Overall Communication* tab is reported in the subfigure a), here interactive heatmap, chord diagram and network plots summarise all the communications present in the data by plotting the cardinality, i.e. the number of interactions among the cell types. As an example, the interactivity of the chord diagram is shown. Data are further summarised via statistics on the cell types mostly involved in the communication. The *Cell Clusters* tab (b) allows the user to focus on a single cell type at a time by picking it with an interactive widget that will update all the visualizations, including the two bubble plots reported in figure. The subfigure c) shows two bubble plots available in the *Ligands and Receptors* tab. The user can here choose specific ligand-receptors pairs of interest to be visualized. Bubbles of the plots can be interactively chosen and the relative data are visualized as rows of a datatable. Bubble plots map two communication scores, i.e. "S_inter" and "S_intra", as the size and the colour of the bubbles.

Availability

<https://gitlab.com/sysbiobig/cclens>

Dissemination Material

Social

LinkedIn:

<https://www.linkedin.com/in/sysbiobig><https://www.linkedin.com/in/gaia-tussardi-029798291>

Twitter:

@sysbiobig

Summary

LinkedIn:

Engage with the complex world of cell-cell communication with CClens! ????. Our new web application simplifies the analysis of complex cell-cell communication data from single-cell RNA sequencing ????. With intuitive visualisation and no programming required, scientists can now delve deeper into understanding complex biological systems. ???????? Learn more:

<https://gitlab.com/sysbiobig/cclens> #CellCellCommunication #scRNAseq #cellbiology #bioinformatics #webapplication

Twitter:

Delve into complex #CellCellCommunication with #webapp CClens! Simplify #scRNAseq analysis with effective visualisations

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