**CoExp Webpage, a web tool for the exploitation of co-expression networks as annotation models of genes and their role in transcription.**

**Abstract**

**Summary** *[this section should summarize the purpose/novel features of the program in one or two sentences].*

[what is a co-expression network]

Here, we present CoExp Webpage, a web tool the exploit the co-expression networks available at []. Users can upload their list of genes, to obtain annotation information from them.

**Availability and Implementation:**

The user interface (UI) code of CoExp is fully available for download on GitHub at <https://github.com/SoniaRuiz/CoExp_Web>.

The docker images of CoExp Webpage are available for download on Docker Hub at <https://hub.docker.com/r/soniaruiz/coexp>.

**Contact:** *[full E-mail address to be supplied, preferably an institution address.]*

**Supplementary information:** *[in case we have any supplementary data, here we will include links to additional figures/data available on a web site, or reference to online-only Supplementary data available at the journal's web site]*

**Introduction**

Gene co-expression network analysis has been widely used to investigate how different genes may cooperatively influence the development of complex human1. The main idea behind co-expression network analysis is that genes whose expression levels are highly correlated, are also likely to share functional and biological linkages2,3. In this sense, co-expression network approach consists into clustering together highly co-expressed genes in a number of modules, generally by using graph-based models to reveal their similarities4.

Previous works have successfully achieved this clustering effort. Some of them include different R software packages such as km2gcn4, which offers an additional k-means clustering step to classical WGCNA, and CoExpNets, which includes several co-expression networks generated through the beforementioned km2gcn R package.

However, the usage of the R language raises an important drawback: it requires coding skills to be able to use it in an effective way. On the other hand, its command-line environment reduces its usability in a world where the web-page format has become the most well-known and accepted way of browsing information. For those users with no expertise in the R language, we generated CoExp Webpage, a web-page application to make CoExpNets easily usable and accessible to every potential user around the world, at any time and from anywhere they decide to do so, regardless the coding level skills that they may present. In addition to the Network Catalog and Gene Set Annotation options that CoExpNets natively offers, CoExp Webpage provides a Plot Network option, which generates a directed graph to visualise the most important co-expressed genes that belong to the same module and network selected by the user.

[final sentence]

**Description**

**[]**

**Data preparation**

To be able to use the ‘Gene Set Annotation’ option, users are required to prepare their genes of interest in a comma-separated or blank-space-separated fashion. That list will be required to be pasted within the ‘Genes’ text area enabled for that purpose. In case the format introduced end up being not fully correct, a prompt message will inform the user with a user-friendly message.

**Co-expression networks available**

CoExp Webpage offers the management and exploitation of several co-expression networks that have been classified in five different categories: (1) ROSMAP, composed of four case and control Frontal Cortex co-expression networks; (2) GTEx V6, which contains 47 co-expression networks in control tissue, including 13 brain areas; (3) 10UKBEC, which are 10 Illumina microarray-based gene expression profiling networks from brain control tissue; (4) GTEx V7, which contains a beta version of the same 47 co-expression networks from GTExV6; (5) NABEC, composed of one gene co-expression network created from RNA-seq control Cortex samples, which have been quantified at transcript level with Salmon module.

**Network Catalogue**

a

**Gene Set Annotation**

s

PLOT NETWORK

**Conclusions**

Lastly, CoExp Webpage is a convenient web platform for the gene co-expression community, which offers the exploitation of co-expression networks in a web-page format, making it easily usable and accessible despite the coding level skills that they may present.

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Conflict of Interest: none declared.

**References**