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*Supplementary Material*

***DiffExpress: a bespoke cloud-based interface for RNA-seq differential expression modeling and analysis***

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Diff Express <sup>beta</sup> RNA-seq reads differential expression analysis

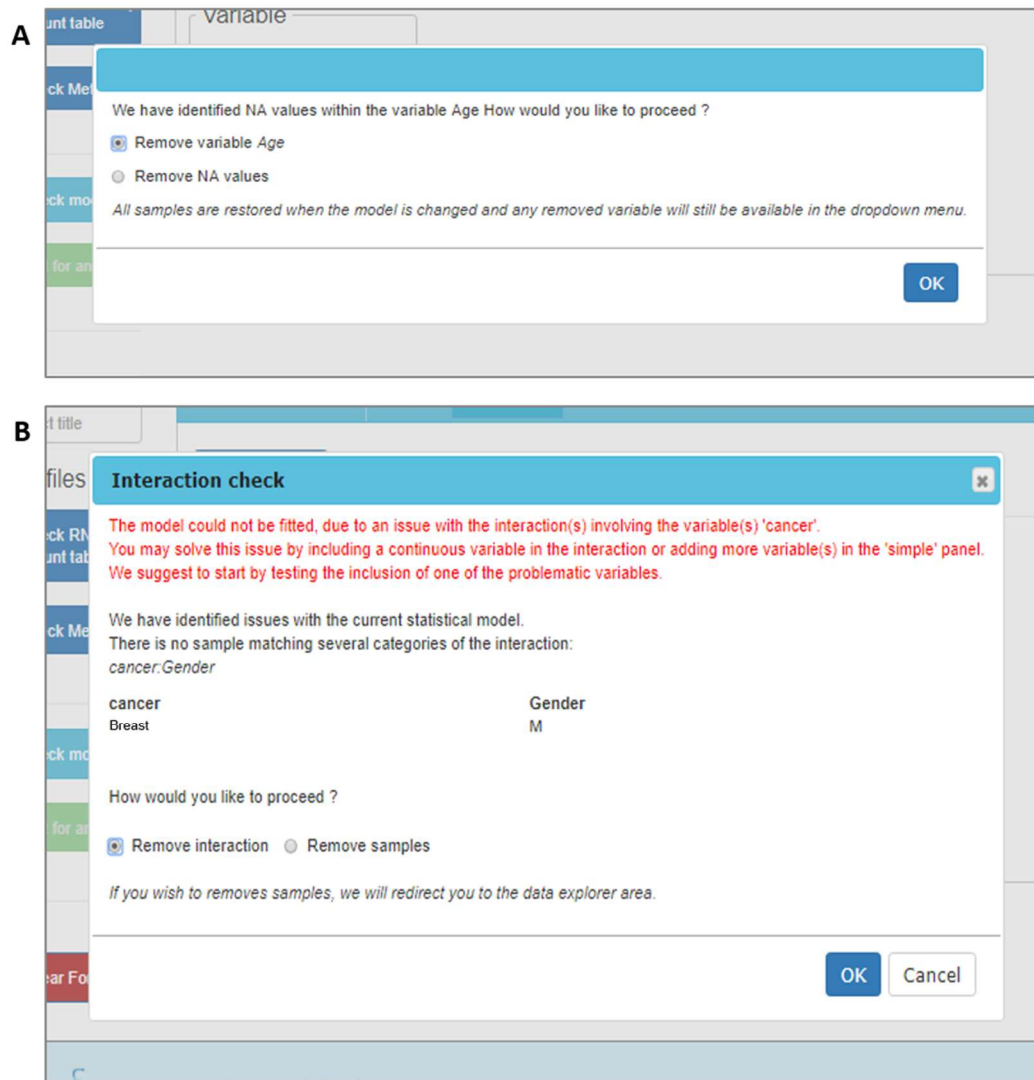
Project title

Input files

Statistical Design | Simple | Interaction | Removed samples | History | Statistics

Variable	Variable	Variable	Variable	Variable
batch	cancer	Gender	Age	Metastasis
<input checked="" type="checkbox"/> I want to remove this effect	<input type="checkbox"/> I want to remove this effect	<input checked="" type="checkbox"/> I want to remove this effect	<input checked="" type="checkbox"/> I want to remove this effect	<input type="checkbox"/> I want to remove this effect
<input type="checkbox"/> Continuous	<input type="checkbox"/> Continuous	<input type="checkbox"/> Continuous	<input checked="" type="checkbox"/> Continuous	<input type="checkbox"/> Continuous
Baseline (control) -- Select Value --	Baseline (control) HD	Baseline (control) -- Select Value --	Baseline (control) -- Select Value --	Baseline (control) N
<input type="button" value="Remove"/>	<input type="button" value="Remove"/>	<input type="button" value="Remove"/>	<input type="button" value="Remove"/>	<input type="button" value="Remove"/>

**Supplementary Figure 1.** Statistical design modeling. It shows the set-up used for the analysis presented as an example in the paper (model  $\sim batch + cancer + Gender + Age + Metastasis$ ). In this example, the focus is to look for genes differentially expressed in the samples from six cancer types and look for genes that could explain the metastasis occurrence. *Batch*, *Gender* and *Age* are considered bias sources and should be in the statistical model, but there is no need to test if there are differentially expressed genes due to those variables. Therefore the option ‘I want to remove this effect’ is selected for the variables. It is also important to inform which variables are continuous like was done *Age*. In the case of categorical variables that are not a source of bias, it is necessary to inform which level is the baseline. In the case of *cancer*, the aim is to identify changes in transcripts in relation to healthy donors, identified as ‘*HD*’ in this dataset. For *Metastasis* the baseline is ‘*N*’ because it indicates that no metastasis was observed in the patient. More details are presented at <https://www.youtube.com/watch?v=QKZu46c4HfU&feature=youtu.be>.



**Supplementary Figure 2.** Data validation. **(A)** The software can detect inconsistencies on the data upload and **(B)** when checking the model fitness.

**A**

Statistical Design   Simple   Interaction   Removed samples   History   **Statistics**

Remove genes with low counts, CPM <

Robustify dispersion estimative against potential outliers

Compare the gene expression between every category within the selected variables for the simple data model

Threshold criteria for plot generation

logFC

Adjusted p-value

[Reset statistics parameters to default value](#)

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**B**

Statistical Design   Simple   Interaction   **Removed samples**   History   Statistics

Samples removed from clinical data (no matching sample found in the count-table)

- SRR1982702

Samples removed due to lack of data for the variable(s) listed bellow

- Age : 9 samples have been removed
- cancer:Gender : 39 samples have been removed

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**C**

Statistical Design   Simple   Interaction   Removed samples   **History**   Statistics

- Checked model: ~Age+cancer + cancer:Gender  
No issues
- NA presence detected in variable ~cancer:Gender  
39 samples have been removed
- Checked model: ~Age + cancer:Gender  
cancer:Gender is invalid
- Checked model: ~Age + cancer:Gender  
cancer:Gender is invalid
- NA presence detected in variable ~Age  
9 samples have been removed

**Supplementary Figure 3.** Other features. **(A)** It is possible to choose the settings for filtering genes, statistical methods and the criteria for considering a gene differentially expressed. **(B)** The interface keeps track of the samples that needed to be removed and **(C)** tracks the tested models and changes done.

The screenshot shows the 'My Pipelines' menu in the NSilico software. The page has a blue header with the NSilico logo and navigation links: Home, My Pipelines, New Pipeline, Pipeline Studio, and Support. Below the header is a blue banner with the 'Simplicity' logo. The main content area is titled 'Finished Pipelines' and features a search bar and a 'Show 10 entries' dropdown. A table lists two pipeline entries:

ID	Name	Date Finished	Share	Remove
32925	TEP - SUCCESS	13 <sup>th</sup> August 2018 [12:33]	[Share icon]	[Remove icon]
32924	CD - SUCCESS	10 <sup>th</sup> August 2018 [09:36]	[Share icon]	[Remove icon]

Below the table, it indicates 'Showing 1 to 10 of 138 entries' and includes a pagination control with buttons for 'Previous', '1', '2', '3', '4', '5', '...', '14', and 'Next'. The footer contains copyright information: © 2018 - NSilico LifeScience Ltd. - Simplicity™ 1.5 - Home - Contact - Terms of use - NSilico.

**Supplementary Figure 4.** *Simplicity's 'My Pipelines' menu.* In this page, all submitted pipelines are listed. The pipeline ID is followed by the Project Title and completion status, with the finish date and the option to share the results with other users and delete the pipeline.