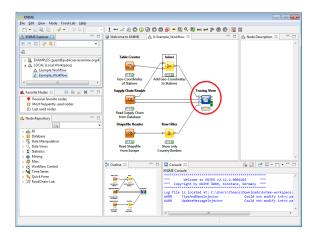
Clustering in FoodChain-Lab

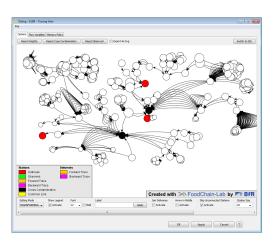
Tabl

## ${\sf Clustering} \,\, {\sf in} \,\, {\sf FoodChain\text{-}Lab}$

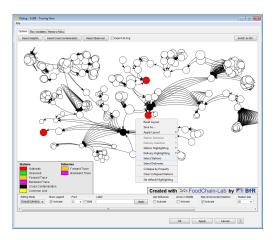
- Perform a clustering base the following workflow: https://github.com/SiLeBAT/ BfROpenLabResources/raw/master/GitHubPages/ workflows/Example\_Workflow.zip
- Cluster all French stations based on its city.
- That means all stations from the same city should be put into one meta-station.



- Import the Example Workflow from https://github. com/SiLeBAT/BfROpenLabResources/raw/master/ GitHubPages/workflows/Example\_Workflow.zip.
- Open the **Tracing View** by double-clicking on it.

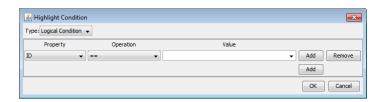


A window showing the delivery network should open now.



Right click in the graph to open the context menu and select Select Stations. Clustering in FoodChain-Lab

4

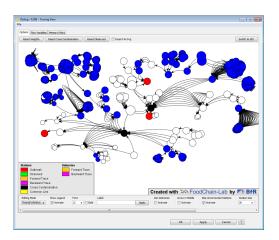


■ You should see this dialog now.

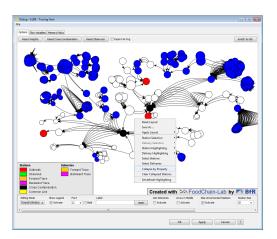


- For our clustering we only want to use the French stations, since most primary producers in this data set are French.
- Select "Country" as Property and "FR" as Value and press OK.

6



All French stations are seleted now, which is indicated by the blue color.



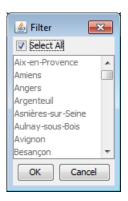
Right click in the graph to open the context menu and select Collapse by Property to cluster the selected stations.



Select Yes to only cluster selected stations.

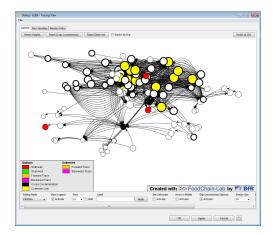


- The clustering will be done on city level. That means all stations from the same city will be merged.
- Select **City** and press **OK**.



■ Just press **OK**, since we do not want to exclude any cities.

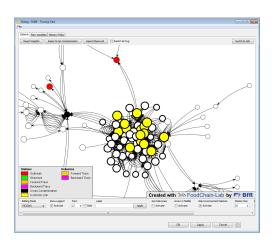
- All French stations have been clustered to cities.
- Each selected station (blue circle) is a French city.



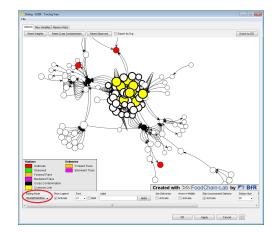
- Select "PICKING" as Editing Mode and click in the graph to unselect all stations.
- You can now see, that some of the stations are yellow. That means, that these stations (French cities) are connected to all outbreak spots (red circles).

- Since the graph looks confusing now, we should reapply the layout algorithm.
- Right click in the graph and select **Apply Layout** > **Fruchterman–Reingold** in the context menu.





- The stations should be arranged in better way now.
- The algorithm is not deterministic, therefore your result will look different from the screenshot.



- After applying the layout algorithm some stations might be outside the visible area.
- To see the whole graph select "TRANSFORMING" as **Editing Mode** and zoom/move the graph by using the mouse wheel and the left mouse button (works as in Google Maps).