

# Clone-World: A Clone Analytics System

The main interface of Clone-World has four information-linked zoomable views: A, B, C, D, and a control panel E.

A. Clone Landscape: Here the dots correspond to the clones, red region corresponds to the highly changing clones over many software revisions. You can select a set of clones by drawing a rectangle with a right-click and drag operation.

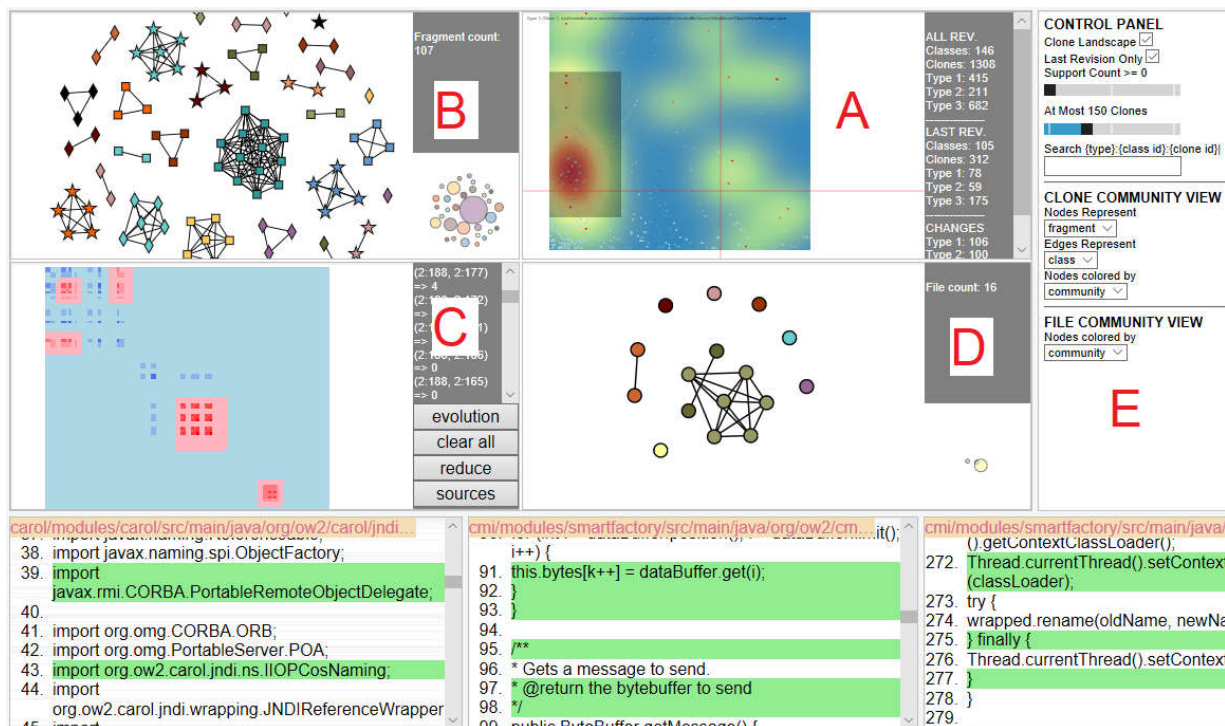
B. Clone Community: Clones are of three types 1(diamond), 2(square), and 3(star). Here you can see the highly changing clones from the selected region in the landscape. You can zoom in and right click on the clones to activate a context menu. Clone forms community based on edge relationships. Edge may represent class or file association, which you can choose from the control panel (E).

C. SPCP-Heatmap: This is a heatmap for pairwise relations of the clones shown in the clone community view. The darker the cell, the larger the SPCP (Similarity Preserving Change Pattern) score, or the number of times the pair of clones changed together in previous software revisions.

D. File Community: Each circle is a file, and each file contains at least one clone fragment from the clone community view. If you hover your mouse on a file node, the corresponding clones will be highlighted in the clone community. Two files are connected if they contain clones from the same class.

E. You can use this control panel to select the number of clones in the clone community view, their color, and pairwise relationships.

For best performance use a high-speed internet. Use Microsoft Edge, or Google Chrome, or a browser updated to its latest version.



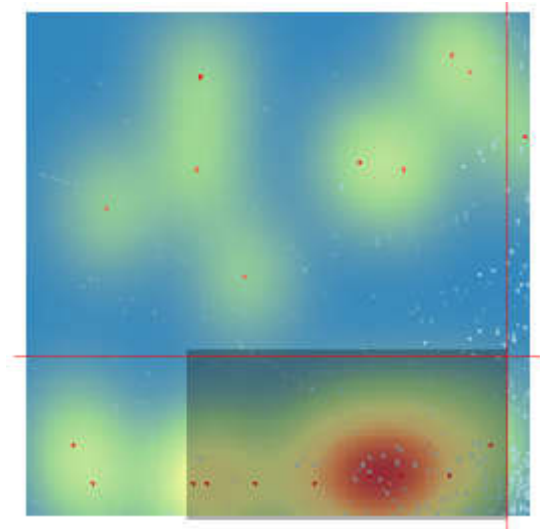
## Example 1

Find 5 clone classes among a set of highly changing clones such that each class contains clone pairs with SPCP-score at least 4. How many files correspond to these clone classes?

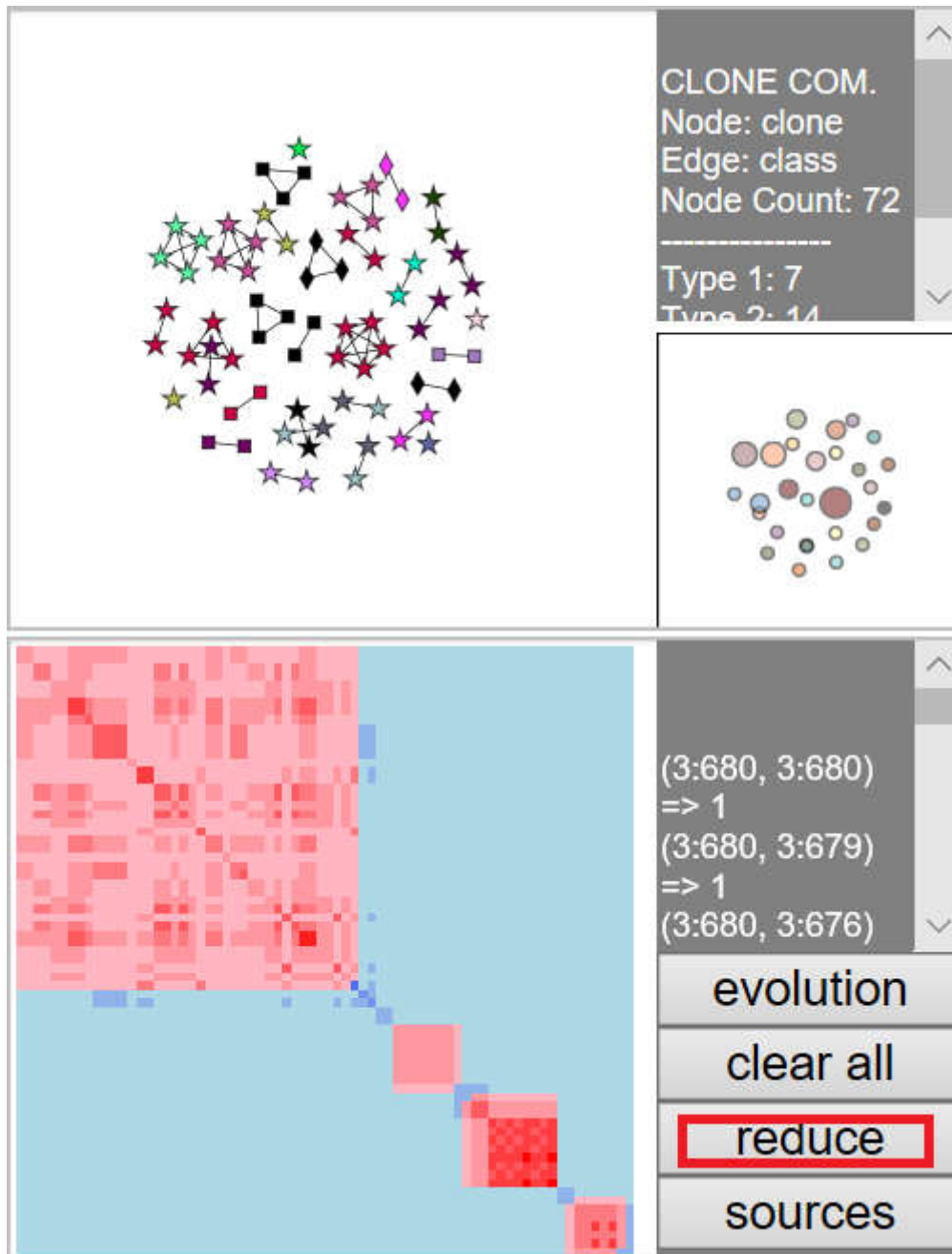
**Step 1. The user moves the support count (SPCP Score) slider to 4 (control panel)**



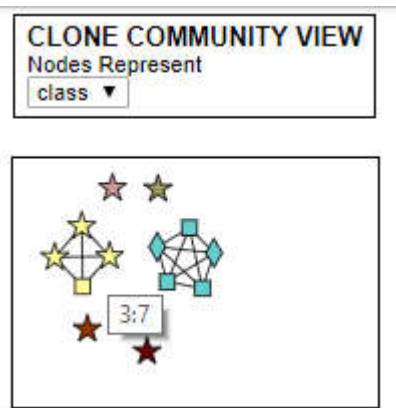
**Step 2. User selects a red region (RIGHT CLICK AND DRAG), a set of highly changing clones. (You can zoom and pan if needed.)**



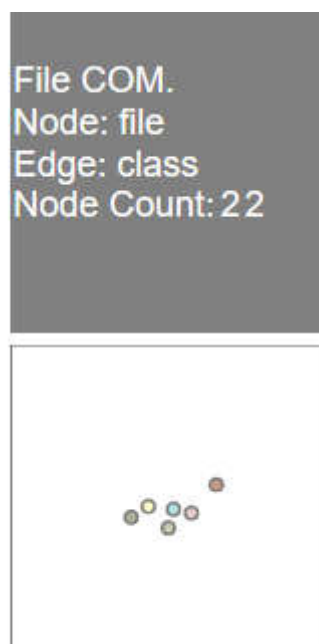
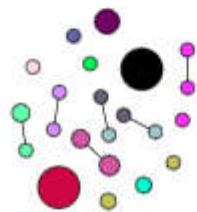
**Step 3. The user examines the clone-community view. He then selects clones that changed together from the Heatmap. Then he clicks on the Reduce button of the Heatmap view to focus only on co-changing clones. (The Heatmap is zoomable, you can right-click and drag to select; but mouse operations are only active on the cells; use clear all button if necessary.)**



**Step 4. The user selects "Nodes Represent: Class" in the Clone Community View control. Then he hovers on 5 random nodes (clone classes), and writes the information in the survey form. Example: 3:7, 5:12, 5:78, 9:56, 12:4**



**Step 5. The user examines the file community view to see how many files are associated with the clones in the clone community view. He reports the node count (number of files) from the information summary. Here the answer is 22.**

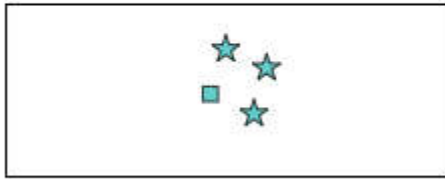


## Example 2

Search for the four clone classes 2:4,3:14,3:17,3:42, and report all within boundary relationships (clones that changed together and in the same class) and cross-boundary relationships (clones that changed together but in different classes).

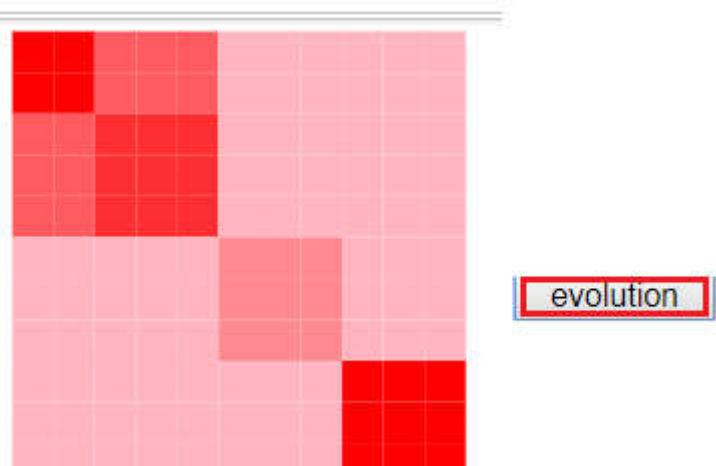
**Step 1. User searches for the clone classes in the search box located in the control panel. The clone community view shows these four classes.**

Search {type}:{class id}:{clone id}{{file path}}  
 2:4,3:14,3:17,3:42  
 Queried 25 clones.

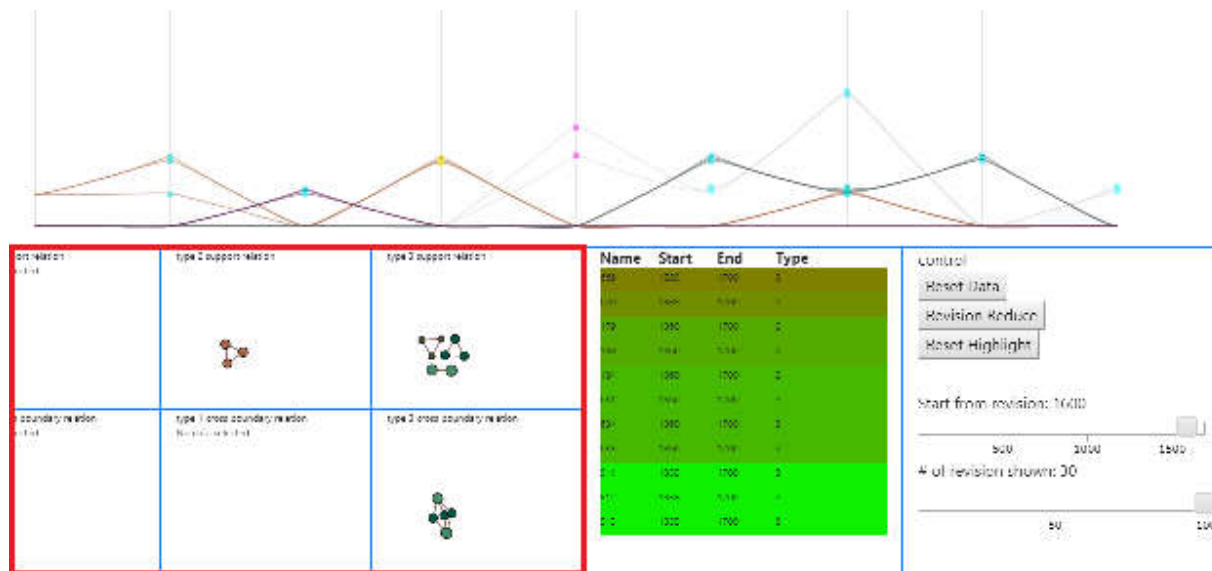


**Step 2. The user selects everything in the SPCP heatmap (you can zoom and pan; drag mouse only on cells; use clear all button if necessary). He then clicks the 'evolution button'. This opens the evolution viewer in the new tab.**

Search {type}:{class id}:{clone id}{{file path}}  
 2:4,3:14,3:17,3:42  
 Queried 25 clones.



**Step 3. The evolution viewer shows a 2 by 3 grid, some of them contain clone networks (graphs). These show whether different types of clones in the same/different clone classes changed together. The user reports the cells that contains graphs.**



### Example 3

Find the clone 3:12:698, and visualize all the clones that changed with 3:12:698 in previous revisions. Report 5 clones that changed closely with 3:12:698.

**Step 1. The user selects "Nodes Represent: Clone" in the Clone Community View control. Then the user searches for 3:12:698 in the search box located in the control panel.**

**CLONE COMMUNITY VIEW**  
Nodes Represent  
clone ▾

Search {type}:{class id}:{clone id}[(file path)]  
3:12:698  
Queried 1 clones.

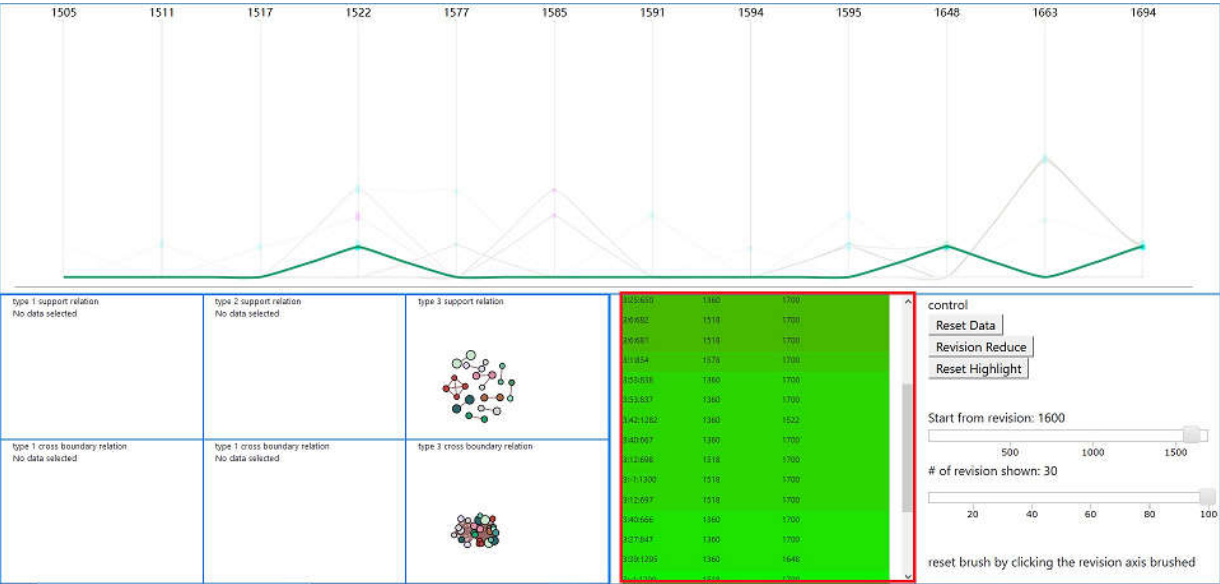
**Step 2. The user zooms in and right clicks on the node in clone community view, and then left clicks the "evolution of SPCP clones". This opens 'evolution viewer' in a new tab.**

- source of this clone
- sources of this class
- sources of this directory
- add other clones
- evolution of SPCP clones

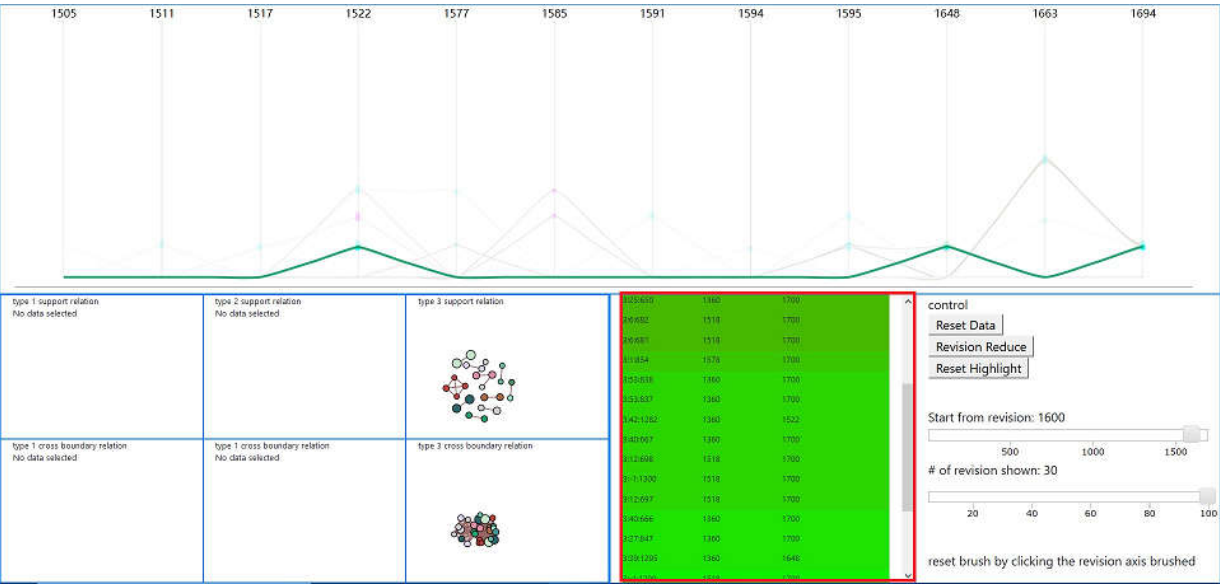
**Step 3. The user can see all clones that changed with clone 3:12:698 in a table. The user clicks on 'Revision Reduce' to see**



only the revisions where these clones changed together with clone 3:12:698.



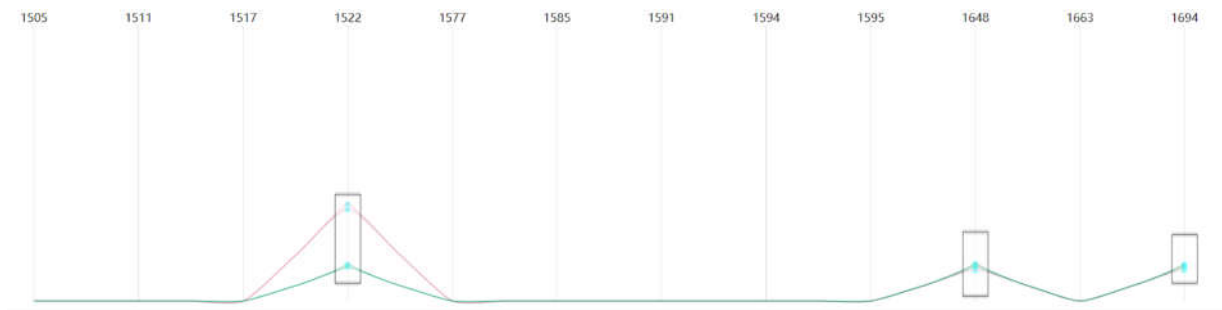
Step 5: To see the clone 3:12:698, the user finds the corresponding row in the table and clicks on that row. This highlights the clone, as shown in the figure. Here is an example where the clone changed in revisions 1522, 1648 and 1694.



Step 6: The user brushes (draw rectangles by left click and drag) on the revision axis to select other clones that changed closely with the selected clone. (If needed, you can remove a brushed rectangle, by clicking on the corresponding axis outside of the rectangle.)



**Step 7: The table now contains only the clones that intersect the rectangles drawn. The user then reports the names of the top 5 clones from the table.**



### Example 4

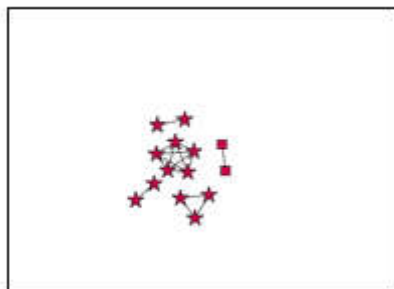
Find a file CMIAdmin.java, and examine all the clones contained in it. Report the software revisions where these clone codes were modified.

**Step 1. The user selects "Nodes Represent: Clone" in the clone community control. The user then searches for the file by typing "|CMIAdmin.java" (Note: there is a '|' symbol). This adds the clones contained in this file to the clone community view.**

Search {type}:{class id}:{clone id}:[file path]  
  
 Queried 0 clones.

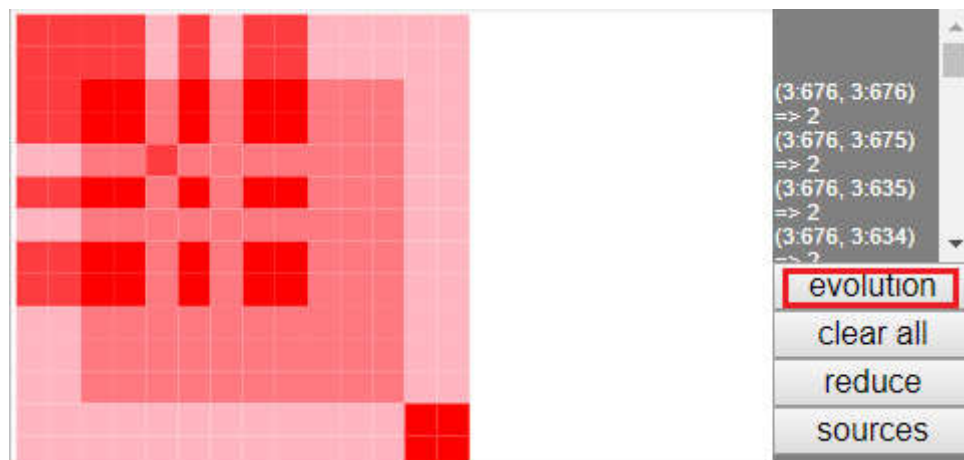
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**CLONE COMMUNITY VIEW**  
 Nodes Represent  
 clone ▼  
 Edges Represent  
 class ▼  
 Nodes colored by  
 directory ▼

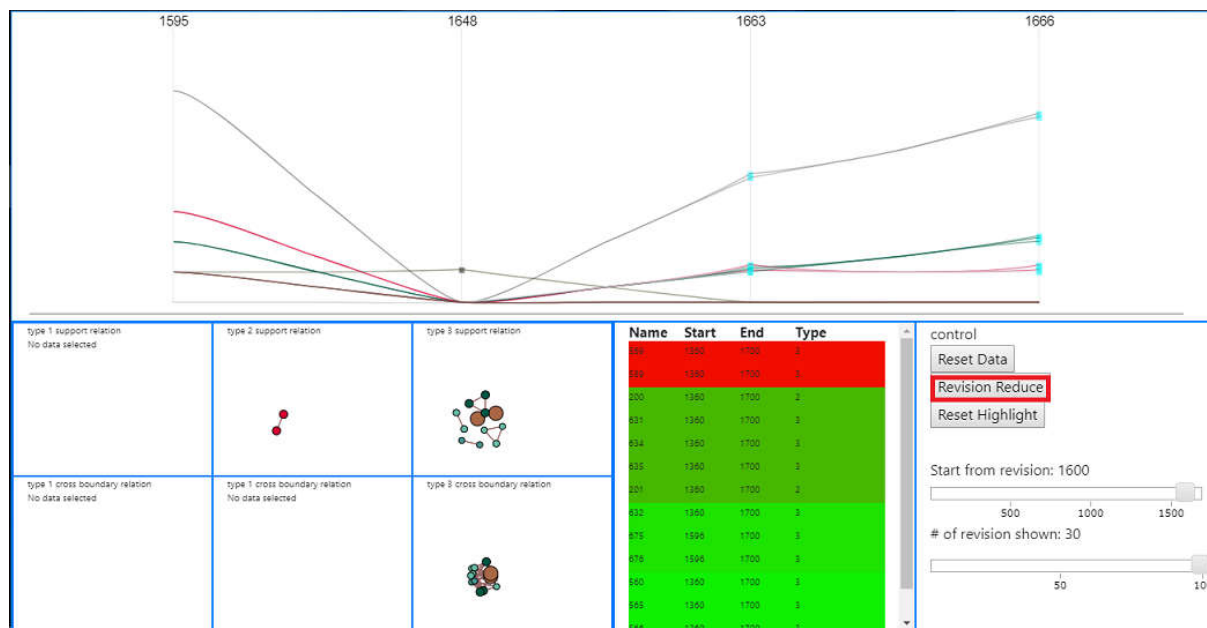




**Step 2.** The user then selects the entire Heatmap (you can drag mouse only on cells; use clear all button if necessary). Then he clicks on the 'Evolution button' to see the history of change for these clones.



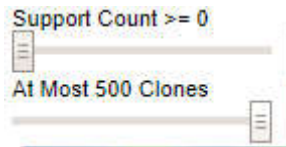
**Step 3.** In the evolution view, the user clicks on the 'Revision Reduce' button to focus only on the changes. Finally, the user reports the revision numbers, e.g., 1595, 1648, 1663, 1666



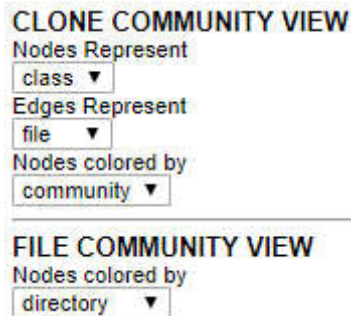
## Example 5

Select all clones in a change-prone landscape region. Find directories that show coupling (A set of directories are coupled if many files from these two directories are connected).

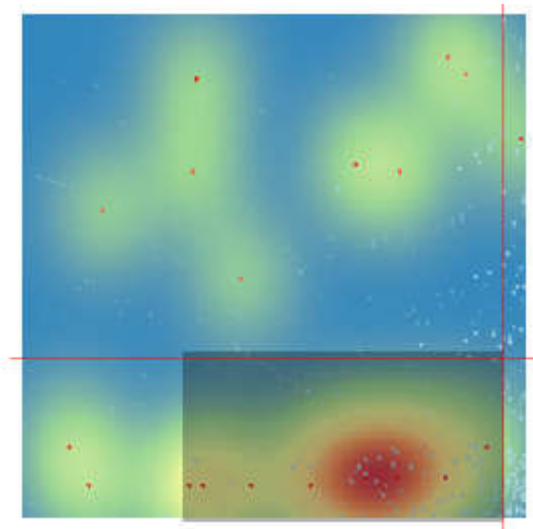
**Step 1.** The user decreases support count to the minimum and increases clone count to maximum (using the sliders located in the control panel).



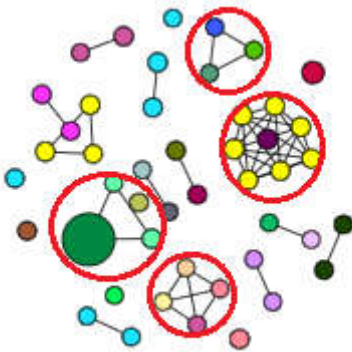
**Step 2. The user selects "Nodes Represent: Class" in the class community control and Nodes colored by: Directory" in the file community control.**



**Step 3. The user selects a red region (a set of highly changing clones). This may take some time depending on your selection and the browser.**



**Step 4. The user reports the number of communities (in the file community view) that contain nodes of different colors (an indication of coupling).**



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## JSON File Format

- `classes.json`
  - it contains a single list, and for each object of list:
    - `type`: the class type (1, 2, 3)
    - `id`: the class id
    - `cloneCount`: how many clones fragments in this class
- `files.json`
  - it contains a single list, and for each object of list:
    - `path`: the file path
    - `cloneCount`: how many clones fragments in this file
- `clones.json`
  - it contains a single list, and for each object of list: (all in string format)
    - `id`: the clone id
    - `chainId`: the chain id of this clone fragment
    - `classType`: the type of this clone (1, 2, 3)
    - `classId`: the class id of this clone
    - `filePath`: the file path of this clone
    - `startLine`: the start line of this clone in the source code
    - `endLine`: the end line of this clone in the source code
    - `sumChangeCount`: the sum of change counts in all revisions
    - `finalRevision`: the last revision that this clone exists
    - `x`: the x coordinate of the scatter plot
    - `y`: the y coordinate of the scatter plot
    - `DC`: the distinct color of the directory of this clone
    - `CC`: the distinct color of the class of this clone
- `support_count_map.json`
  - each object here contains the following parameters
    - `type id`
      - clone chain id x that evolved over previous revisions
        - chain id y and SPCP score of (x,y) [only if the score is non-zero]
- `system.json`
  - `name`: the name of the system (carol)
  - `finalRevision`: the last revision in the dataset