

Clementine Tutorial

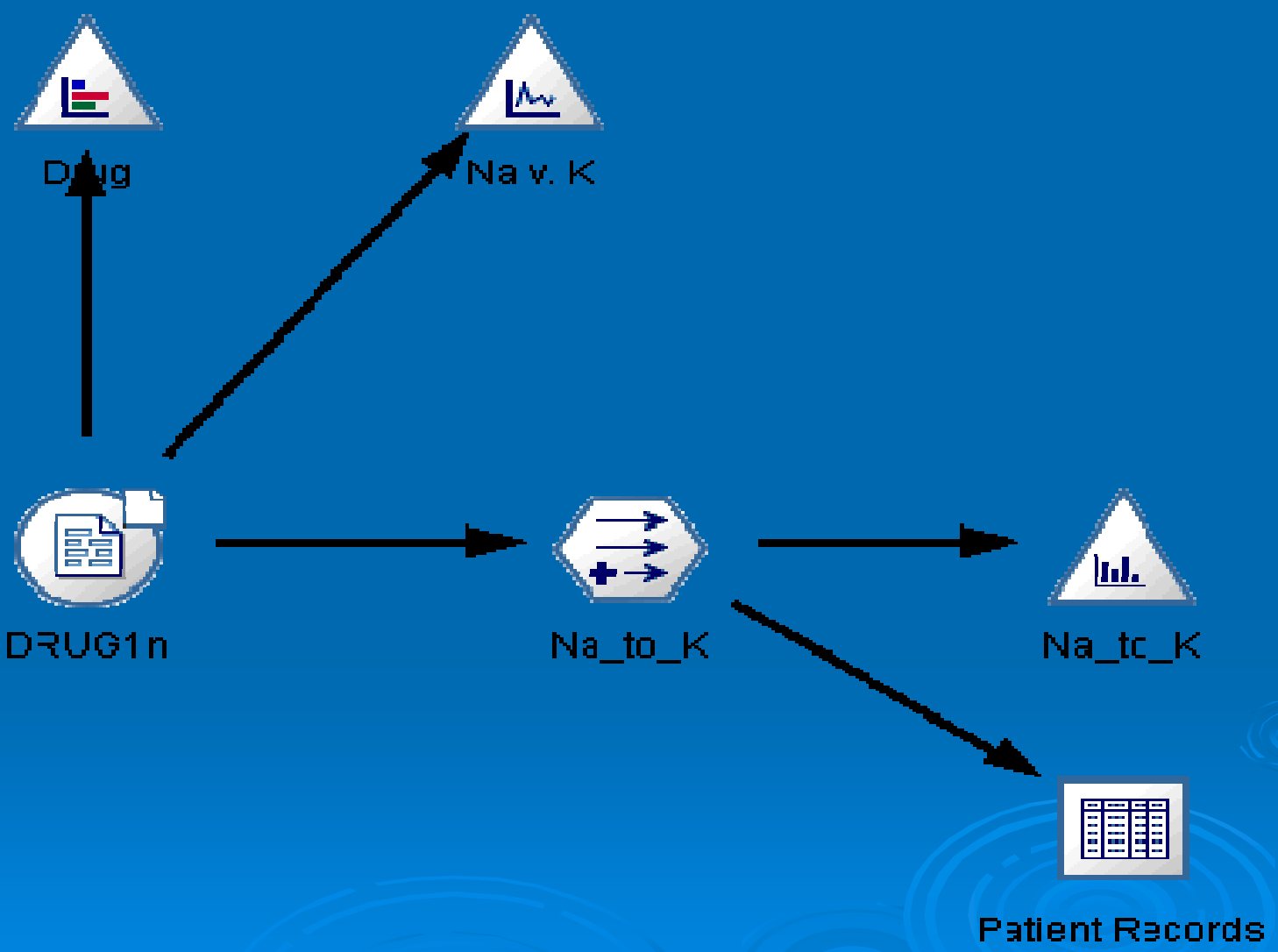
Zdroj: Dr. Teh Ying Wah
<http://fsktm.um.edu.my/~tehyw/6317_lab1.ppt>

- This tutorial will introduce you to the Clementine toolkit for data mining and show you how to get started with your own data mining project.



- The first part provides a tour of the workspace, including an update of what's new in this version of Clementine.
- The second part is a step-by-step guide to data mining in Clementine. All of the files shown in the examples are installed with Clementine so that you can follow along.

- Clementine uses a visual approach to data mining that provides a tangible way to work with data.
- Each process in Clementine is represented by an icon, or **node**, that you connect to form a **stream** representing the flow of data through a variety of processes.



- Working in Clementine is essentially like using a visual metaphor to describe the world of data, statistics, and complex algorithms.

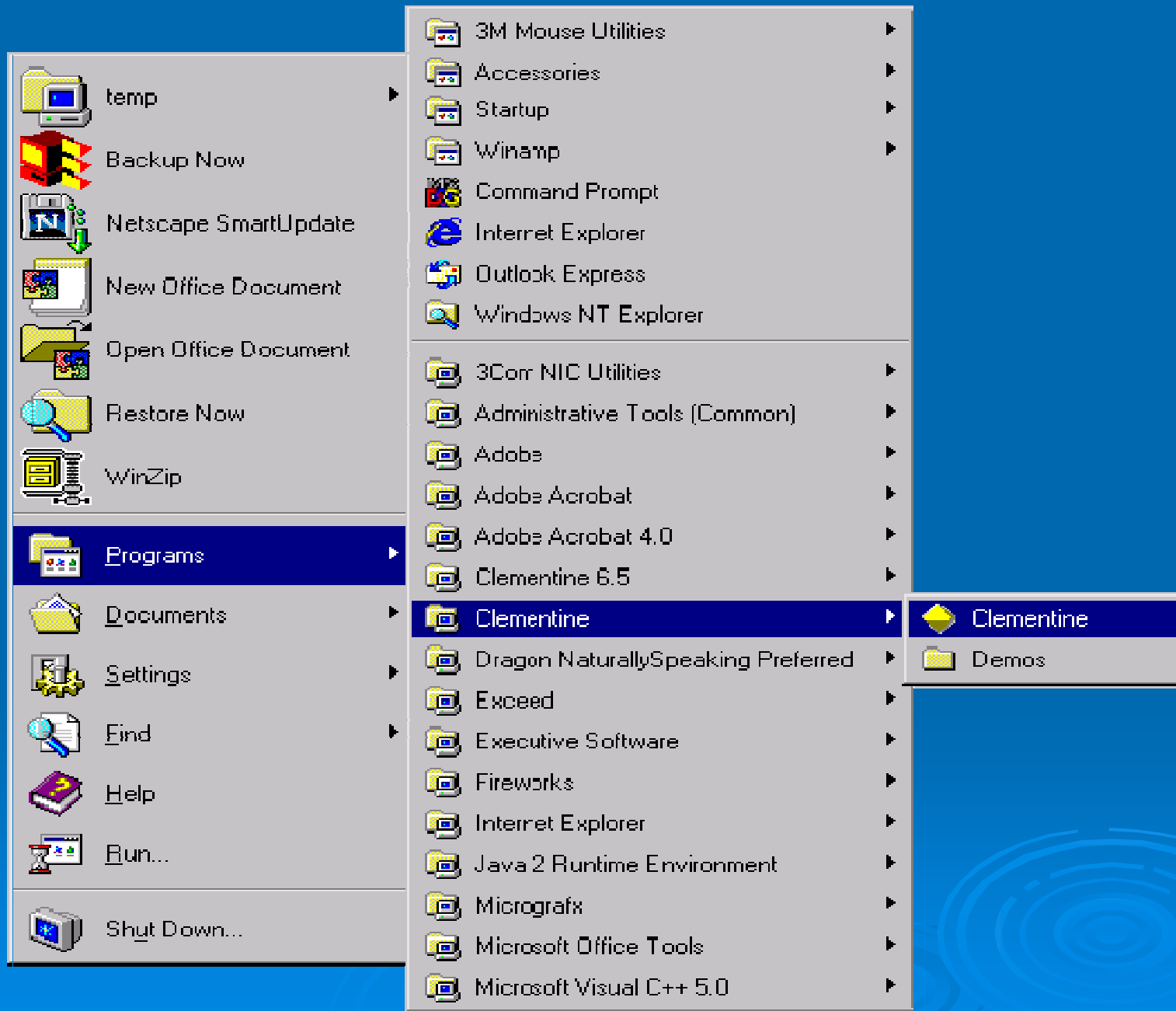


- Although it may take a minute to shift into this paradigm, you will soon find that Clementine's simplicity-of-use is exceedingly powerful. Let's take a closer look.



➤ To start Clementine:

- From the Windows Start menu choose:
 - Programs
Clementine



- When you first start Clementine, the workspace opens in the default view.
- The tools here are used to help you create a visual representation of data mining operations.



drugplot

File Edit Insert View Tools SuperNode Window Help

```
graph LR; DRUG1n[DRUG1n] --> Na_to_K[Na_to_K]; Na_to_K --> D_dp[D_dp]; Na_to_K --> Na_v_K[Na v. K]; Na_to_K --> Na_to_K_out[Na_to_K]; Na_to_K --> Patient_Records[Patient Records];
```

The diagram shows a workflow starting with a 'DRUG1n' source node. This node connects to a 'Na_to_K' transformation node. From 'Na_to_K', four arrows point to different output nodes: 'D_dp' (a plot icon), 'Na v. K' (a plot icon), 'Na_to_K' (a plot icon), and 'Patient Records' (a table icon).

Clementine

Streams Outputs Models

- Stream1
- drug
- drugplot
- druglearn
- fraud
- drugreport

CRISP-DM Classes

- Drug Discovery
 - Business Understanding
 - Data Understanding
 - Data Preparation
 - Modeling
 - Evaluation
 - Deployment

Favorites Sources Record Ops Field Ops Graphs Modeling Output

Database Var. File Select Sample Aggregate Derive Type Filter Plot Distribution Histogram Neural Net Kohonen C5.0 C&R Tree K-Means

Server: Local Server 41MB / 67MB

- First, the area in the middle is called the **stream canvas**. This is the main area you will use to work in Clementine.



drugplot

File Edit Insert View Tools SuperNode Window Help

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Drug

Na v. K

DRUG1n

Na_to_K

Na_to_K

Patient Records

Favorites Sources Record Ops Field Ops Graphs Modeling Output

Database Var. File Select Sample Aggregate Derive Type Filter Plot Distribution Histogram Neural Net Kohonen C5.0 C&R Tree K-Means

Server: Local Server 41MB / 67MB

The screenshot displays the 'drugplot' software interface. At the top, there is a menu bar with options: File, Edit, Insert, View, Tools, SuperNode, Window, and Help. Below the menu is a toolbar with various icons for file operations and execution. The main workspace contains a workflow diagram with the following components and connections:

- DRUG1n**: A source node (cylinder icon) with a green status indicator.
- Na v. K**: A plot node (triangle icon) connected to DRUG1n by an arrow.
- Na_to_K**: A derive node (hexagon icon) connected to DRUG1n by an arrow.
- Na_to_K**: A plot node (triangle icon) connected to the Na_to_K derive node by an arrow.
- Patient Records**: An output node (grid icon) connected to the Na_to_K derive node by an arrow.

On the right side, there are two panels:

- Clementine**: A panel with tabs for 'Streams', 'Outputs', and 'Models'. The 'Streams' tab is active, showing a list of streams: Stream1, drug, drugplot, druglearn, fraud, and drugreport.
- CRISP-DM Classes**: A panel showing a hierarchical tree structure for the CRISP-DM process, including categories like Business Understanding, Data Understanding, Data Preparation, Modeling, Evaluation, and Deployment.

At the bottom, there is a toolbar with tabs for 'Favorites', 'Sources', 'Record Ops', 'Field Ops', 'Graphs', 'Modeling', and 'Output'. The 'Field Ops' tab is active, showing icons for various operations: Database, Var. File, Select, Sample, Aggregate, Derive, Type, Filter, Plot, Distribution, Histogram, Neural Net, Kohonen, C5.0, C&R Tree, and K-Means.

The status bar at the very bottom indicates 'Server: Local Server' and '41MB / 67MB'.

- Most of the data and modeling tools in Clementine reside in **palettes**, the area below the stream canvas.



drugplot File Edit Insert View Tools SuperNode Window Help

The screenshot displays the **drugplot** software interface. The main workspace contains a workflow diagram with the following components and connections:

- DRUG1n** (Source icon) connects to **Na v. K** (Graph icon) and **Na_to_K** (Process icon).
- Na v. K** connects to **Drug** (Graph icon).
- Na_to_K** connects to **Na_to_K** (Graph icon) and **Patient Records** (Table icon).

The right sidebar, titled **Clementine**, shows the project structure:

- Streams**: Stream1, drug, drugplot, druglearn, fraud, drugreport
- CRISP-DM Classes**: Drug Discovery, Business Understanding, Data Understanding, Data Preparation, Modeling, Evaluation, Deployment

The bottom toolbar includes the following categories and icons:

- Favorites**
- Sources**: Database, Var. File
- Record Ops**: Select, Sample, Aggregate
- Field Ops**: Derive, Type, Filter
- Graphs**: Plot, Distribution, Histogram
- Modeling**: Neural Net, Kohonen, C5.0, C&R Tree, K-Means

Server: Local Server | 41MB / 67MB

- Each tab contains groups of nodes that are a graphical representation of data mining tasks, such as accessing and filtering data, creating graphs, and building models.
- To add nodes to the canvas, double-click icons from the node palettes or drag and drop them onto the canvas. You then connect them to create a **stream**, representing the flow of data.



- You will learn more about building streams later in this tutorial. You can jump ahead now using the Contents button below.



- On the top right side of the window are the output and object **managers**. These tabs are used to view and manage a variety of Clementine objects.

drugplot

File Edit Insert View Tools SuperNode Window Help

```
graph LR; DRUG1n((DRUG1n)) --> Drug[Drug]; DRUG1n --> Na_v_K[Na v. K]; DRUG1n --> Na_to_K1[Na_to_K]; Na_to_K1 --> Na_to_K2[Na_to_K]; Na_to_K1 --> Patient_Records[Patient Records];
```

Clementine

Streams Outputs Models

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CRISP-DM Classes

- Drug Discovery
 - Business Understanding
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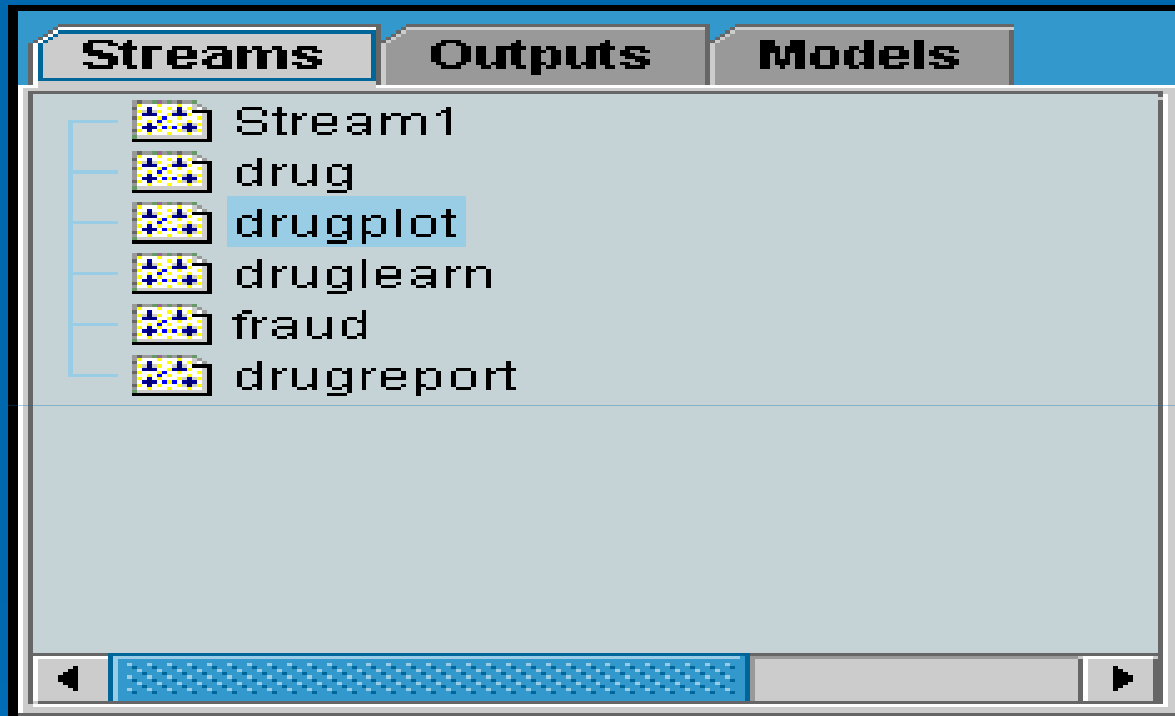
Favorites Sources Record Ops Field Ops Graphs Modeling Output

Database Var. File Select Sample Aggregate Derive Type Filter Plot Distribution Histogram Neural Net Kohonen C5.0 C&R Tree K-Means

Server: Local Server 41MB / 67MB











- The Streams tab contains all streams open in the current session. You can save and close streams as well as add them to a project.





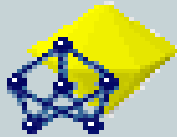
- The Outputs tab contains a variety of files produced by stream operations in Clementine. You can display, rename, and close the tables, graphs, and reports listed here

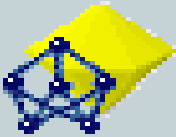
Streams **Outputs** **Models**

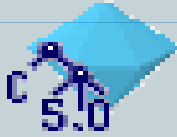
-  Patient Records (8 fields, 200 recor...
-  Distribution of Drug
-  Histogram of Na_to_K
-  Plot of Na v. K
-  table (10 fields, 300 records)
-  **Distribution of name**
-  Web of [region maincrop claimtype] ...
-  Histogram of diff
-  Plot of estincome v. claimvalue
-  Histogram of claimdiff

- The Models tab is a powerful tool that contains all generated models (models that have been built in Clementine) for a session. Models can be examined closely, added to the stream, exported, or annotated.

Streams Outputs Models

 Drug

 claimvalue

 Drug

◀ ▶

- *Note:* The Models tab replaces the Generated Models tab from earlier versions of Clementine.

- On the bottom right side of the window is the **projects** tool, used to create and manage data mining projects.
- There are two ways to view projects you create in Clementine--Classes view and CRISP-DM view.

drugplot

File Edit Insert View Tools SuperNode Window Help

```
graph TD; DRUG1n((DRUG1n)) --> Drug[Drug]; DRUG1n --> NavK[Na v. K]; DRUG1n --> NaToK[Na_to_K]; NaToK --> NaToK_Plot[Na_to_K]; NaToK --> PatientRecords[Patient Records];
```

Streams Outputs Models

- Stream1
- drug
- drugplot
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- drugreport

CRISP-DM Classes

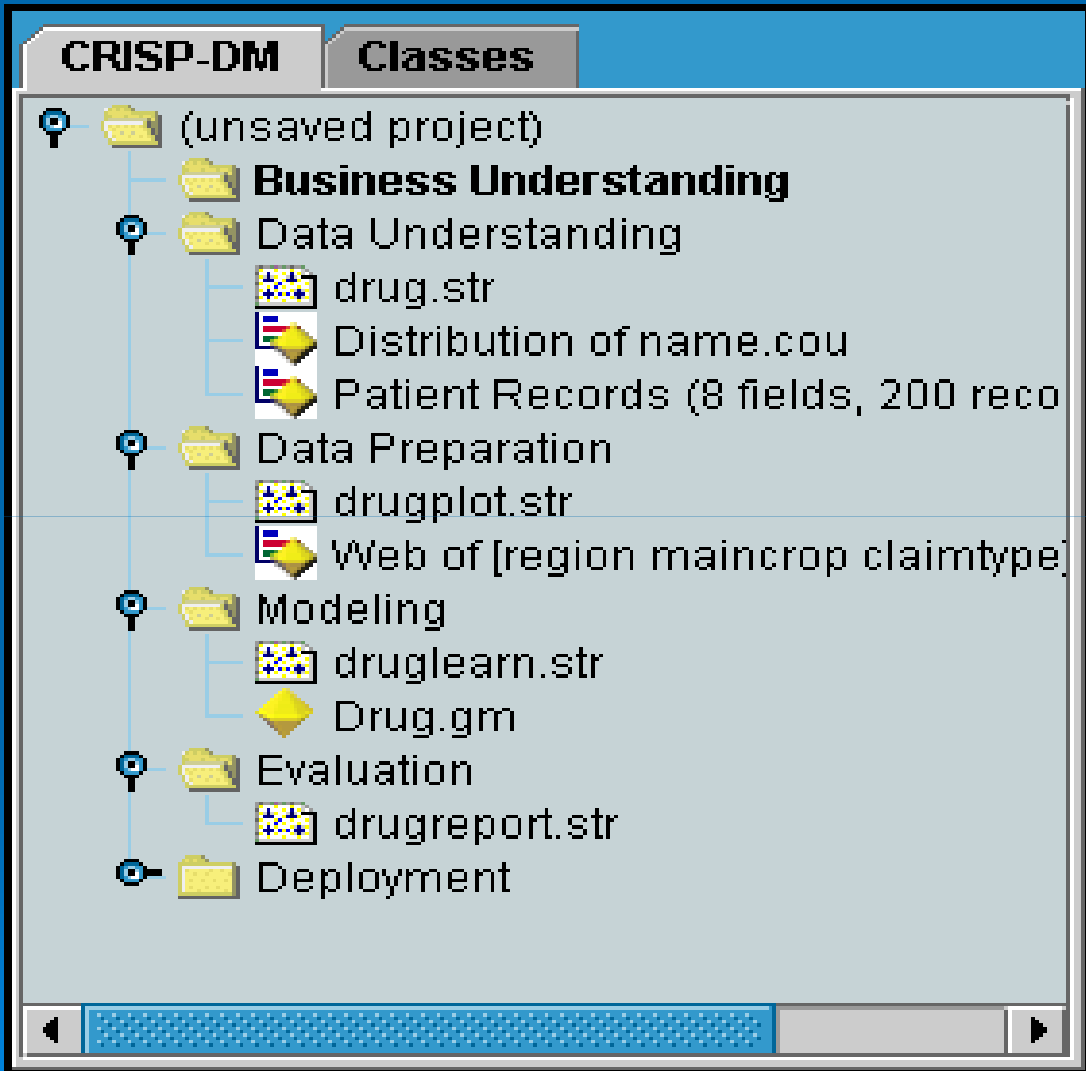
- Drug Discovery
 - Business Understanding
 - Data Understanding
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 - Deployment

Favorites Sources Record Ops Field Ops Graphs Modeling Output

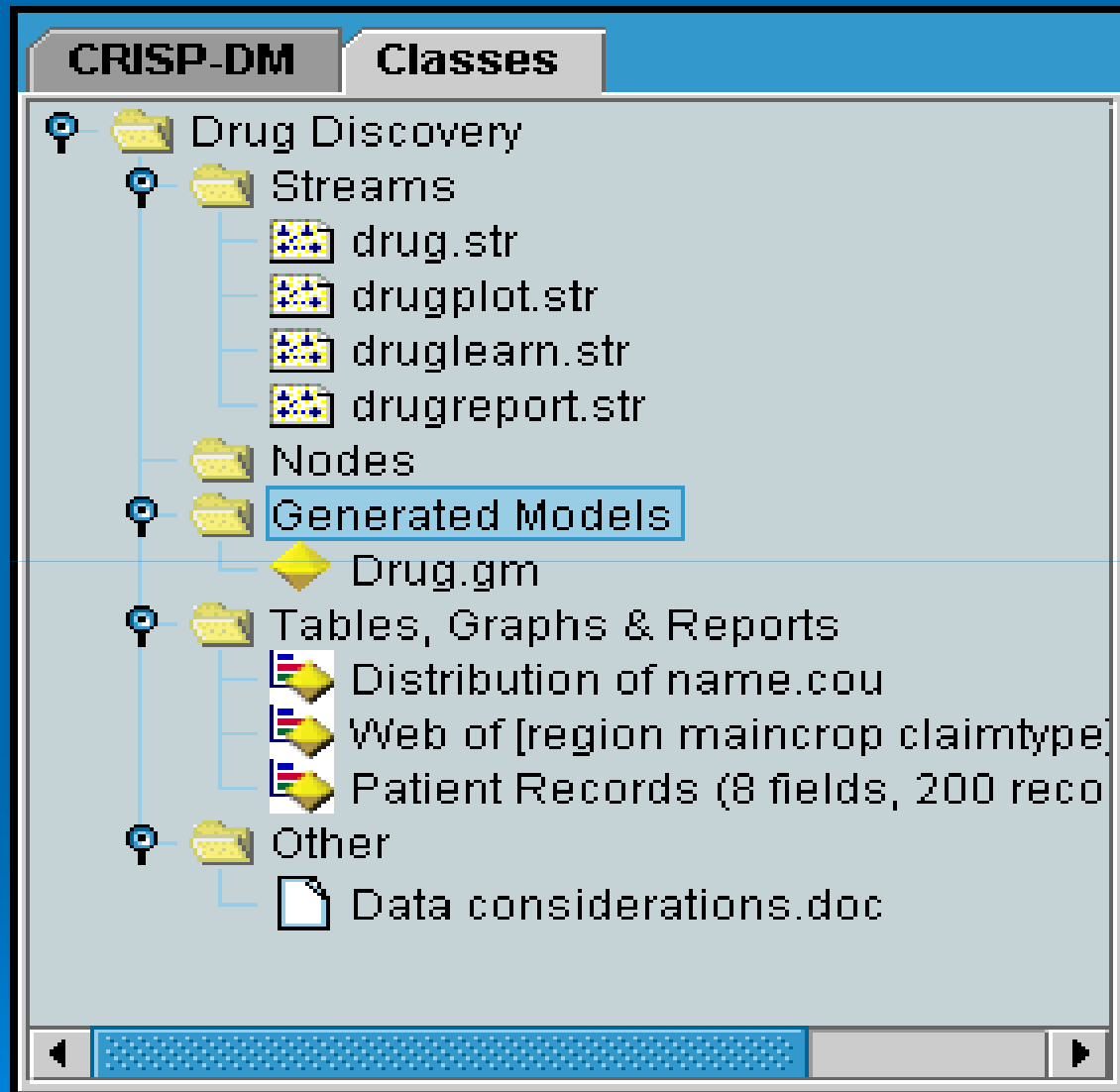
Database Var. File Select Sample Aggregate Derive Type Filter Plot Distribution Histogram Neural Net Kohonen C5.0 C&R Tree K-Means

Server: Local Server 41MB / 67MB

- The CRISP-DM tab provides a way to organize projects according to the Cross-Industry Standard Process for Data Mining, an industry-proven, nonproprietary methodology. For both experienced and first-time data miners, using the CRISP-DM tool will help you to better organize and communicate your efforts.



- The Classes tab provides a way to organize your work in Clementine categorically--by the types of objects you create. This view is useful when taking inventory of data, streams, models, etc.



- As a data mining application, Clementine offers a strategic approach to finding useful relationships in large data sets. In contrast to more traditional statistical methods, you do not necessarily need to know what you are looking for when you start. You can explore your data, fitting different models and investigating different relationships, until you find useful information.

➤ This section provides:

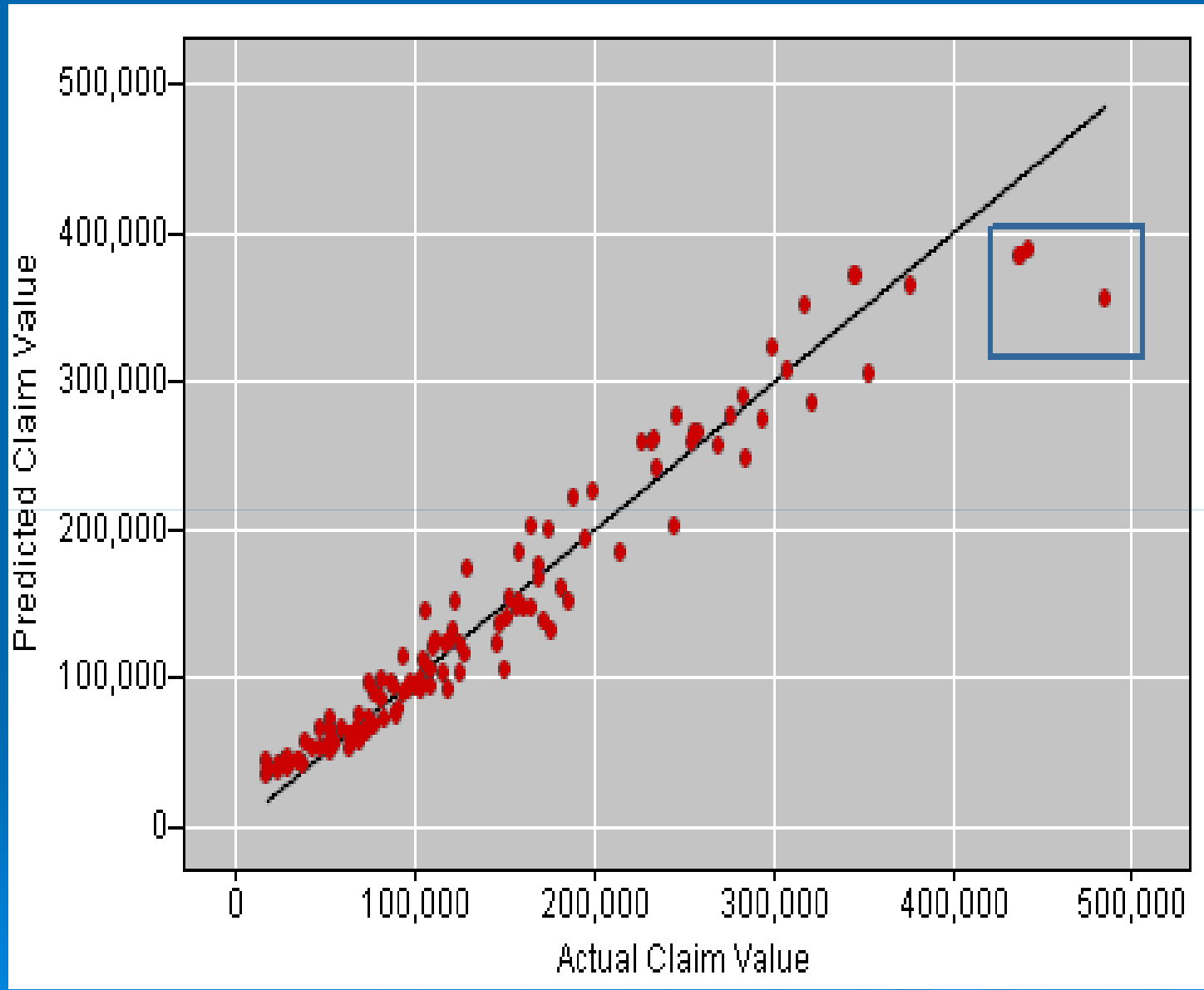
- An overview of the types of data-mining problems Clementine can help solve.
- A hands-on demonstration of building streams, deriving fields, using graphs, and modeling in Clementine.

- A wide variety of organisations use Clementine to help them mine vast repositories of data. Following is a sample of the types of problems data mining can help solve.



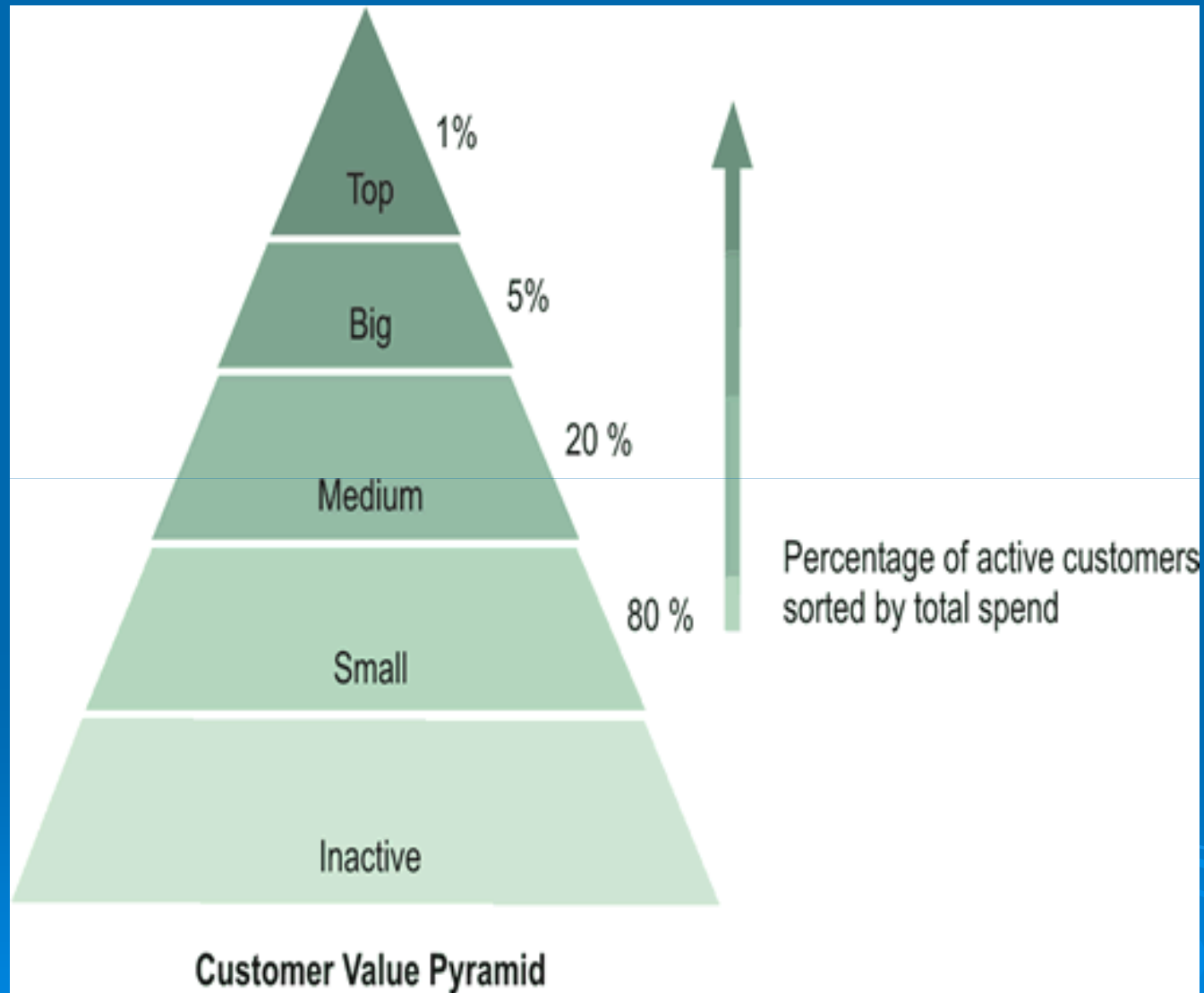
Public sector

- Governments around the world use data mining to explore massive data stores, improve citizen relationships, detect occurrences of fraud such as money laundering and tax evasion, detect crime and terrorist patterns, and enhance the expanding realm of e-government



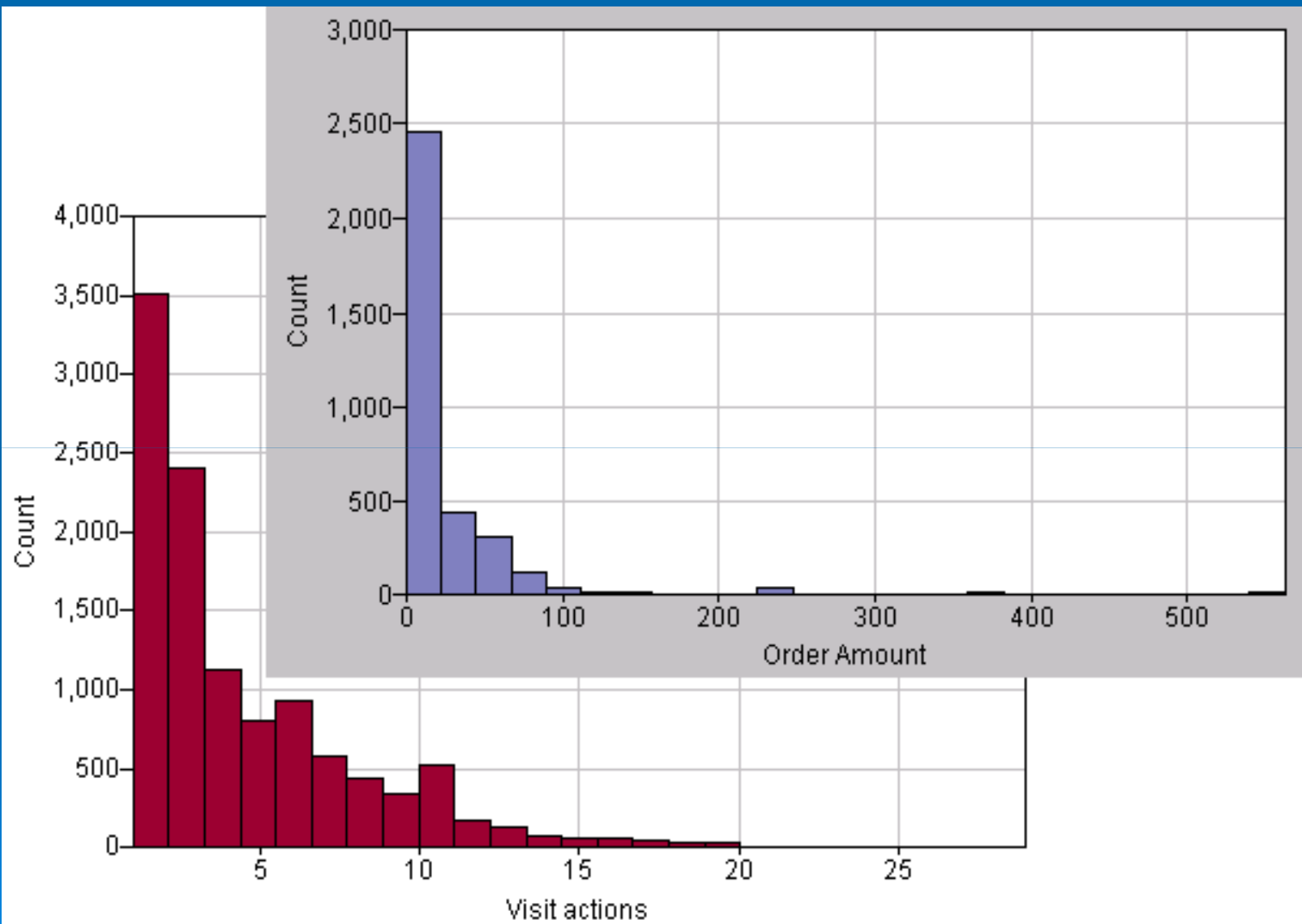
CRM

- Customer relationship management can be improved thanks to smart classification of customer types and accurate predictions of churn. Clementine has successfully helped businesses attract and retain the most valuable customers in a variety of industries.



Web mining

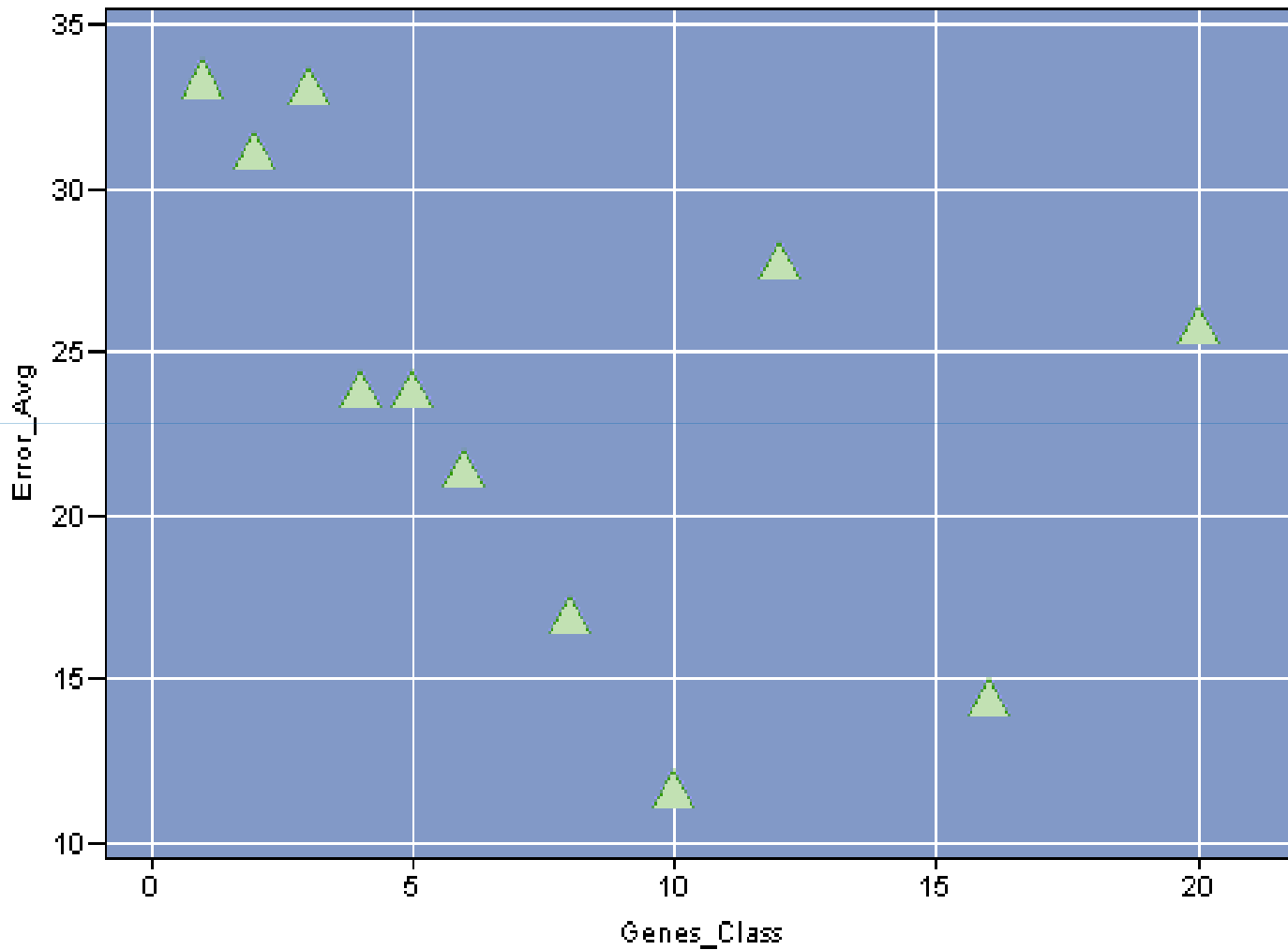
- With powerful sequencing and prediction algorithms, Clementine contains the necessary tools to discover exactly what guests do at a Web site and deliver exactly the products or information they desire. From data preparation to modeling, the entire data-mining process can be managed inside of Clementine.

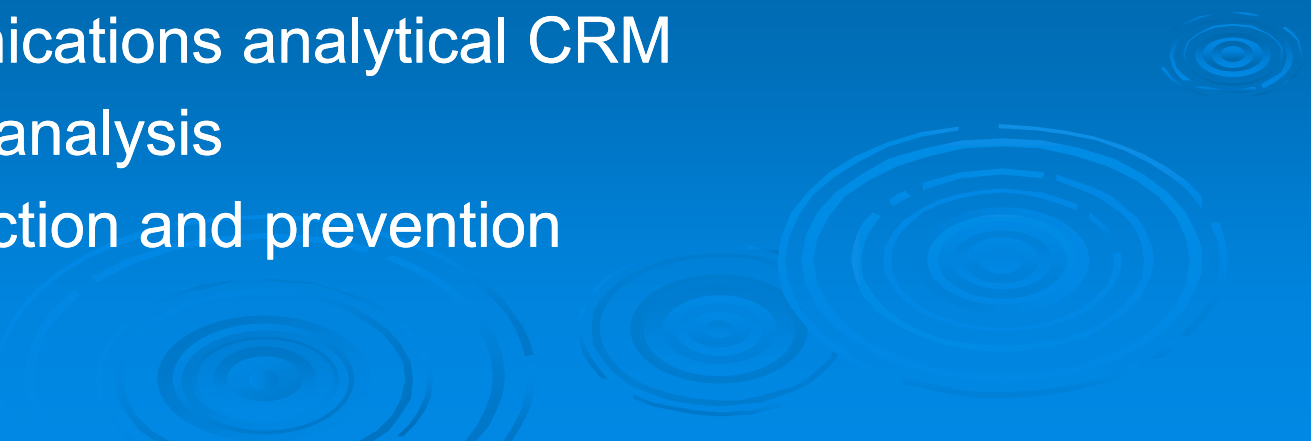


Drug discovery and bioinformatics

- Data mining aids both pharmaceutical and genomics research by analyzing the vast data stores resulting from increased lab automation. Clementine's clustering and classification models help generate leads from compound libraries while sequence detection aids the discovery of patterns.

Average Error vs. Genes per Class



- Clementine provides templates for many of these data-mining applications. Clementine Application Templates, also known as CATs, are available for the following types of activities:
 - Web-mining
 - Fraud detection
 - Analytical CRM
 - Telecommunications analytical CRM
 - Microarray analysis
 - Crime detection and prevention
- 

- Let's get started learning how Clementine can help you conduct your own data mining project.
- This section of the guide will show you how to build and execute simple streams using sample drug demonstration files that are included with Clementine. You will learn how to work with data in the various phases of data mining, including:
 - **Visualization**, which helps you gain an overall picture of your data. You can create plots and charts to explore relationships among the fields in your data set and generate hypotheses to explore during modeling.
 - **Manipulation**, which lets you clean and prepare the data for modeling. You can sort or aggregate data, filter out fields, discard or replace missing values, and derive new fields.
 - **Modeling**, which gives you the broadest range of insight into the relationships among data fields. Models perform a variety of tasks such as predict outcomes, detect sequences, and group similarities. These help your organization grow, streamline processes, detect fraud, and retain the most valuable customers.

- For this section, imagine that you are a medical researcher compiling data for a study.
- You have collected data about a set of patients, all of whom suffered from the same illness. During their course of treatment, each patient responded to one of five medications.
- Part of your job is to use data mining to find out which drug might be appropriate for a future patient with the same illness.

- The data fields used in this demo are:
 - Age (Number)
 - Sex M or F
 - BP Blood pressure: HIGH, NORMAL, or LOW
 - Cholesterol Blood cholesterol: NORMAL or HIGH
 - Na Blood sodium concentration
 - K Blood potassium concentration
 - Drug Prescription drug to which a patient responded

- The first step is to load the data file using a **Variable File node**. You can add a Variable File node from the palettes--either click the **Sources** tab to find the node or use the **Favorites** tab, which includes this node by default. Next, double-click the newly placed node to open its dialog box.



Var. File

Navigation bar with tabs: Favorites, Sources, Record Ops, Field Ops, Graphs, Modeling, Output.

Tool palette with icons and labels:

- Database (SQL icon)
- Var. File (document icon, highlighted with a dashed border)
- Select (hexagon with question mark and arrow)
- Sample (hexagon with three dots and arrow)
- Aggregate (hexagon with three arrows pointing right)
- Derive (hexagon with two arrows pointing right and a plus sign)
- Type (hexagon with four arrows pointing right and a plus sign)
- Filter (hexagon with two arrows pointing right and a star)
- Plot (triangle with a line graph)
- Distribution (triangle with a bar chart)
- Histogram (triangle with a bar chart)
- Neural (hexagon with a neural network diagram)

- Click the button just to the right of the File box marked with ellipses (...). This opens a dialog box for browsing to the directory in which Clementine is installed on your computer (or server). Open the *demos* directory and select the file called *DRUG1n*.

Var. File

Refresh

(No current file selected)

File:

Read field names from file

Skip header characters:

Strip lead and trail spaces: N

Delimiters

Space Comma Tab

Newline Other

Non-printing characters

Allow multiple blank delimiters

File Data Filter Type

OK Cancel

Open

Look In: demos

bask.str	condlearn.str	DRUG4
BASKETS1n	condplot.str	DRUG4n
basklinks.str	derived_fields.str	drugcluster.str
baskrule.str	drug.str	druglearn.str
cluster.str	DRUG1	drugplot.str
cond.str	DRUG1n	drugplot.str-
COND1	DRUG2	drugplot_graphs.s
COND1n	DRUG2n	drugreport.str
COND2	DRUG3	factor.str
COND2n	DRUG3n	fixed.dat

File Name: DRUG1n

Files of Type: All Files

Open Cancel

- Select **Read field names from file** and notice the fields and values that have just been loaded into the dialog box. Before clicking **OK** to close the dialog box, take a moment to look at the data using the other tabs on the Source node.

Var. File [X]

Refresh [?]

C:\Program Files\Clementine\7.0\demos\DRUG1n

File: C:\Program Files\Clementine\7.0\demos\DRUG1n

```
Age,Sex,BP,Cholesterol,Na,K,Drug
23,F,HIGH,HIGH,0.792535,0.031258,drugY
47,M,LOW,HIGH,0.739309,0.056468,drugC
47,M,LOW,HIGH,0.697269,0.068944,drugC
```

Read field names from file **Specify number of fields** 1

Skip header characters: 0 EOL comment characters:

Strip lead and trail spaces: **None** **Left** **Right** **Both**

Delimiters

Space **Comma** **Tab**

Newline **Other** []

Non-printing characters

Allow multiple blank delimiters

Quotes

Single quotes: **Discard** [v]

Double quotes: **Discard** [v]

Decimal symbol: **Stream default** [v]

Lines to scan for type: 50

File | **Data** | **Filter** | **Types** | **Annotations**

OK Cancel Apply Reset

- Click the **Data** tab to override and change **storage** for a field. Note that storage is different than **type**, or usage of the data field.

Var. File [X]

Refresh [?]

C:\Program Files\Clementine\7.0\demos\DRUG1.n

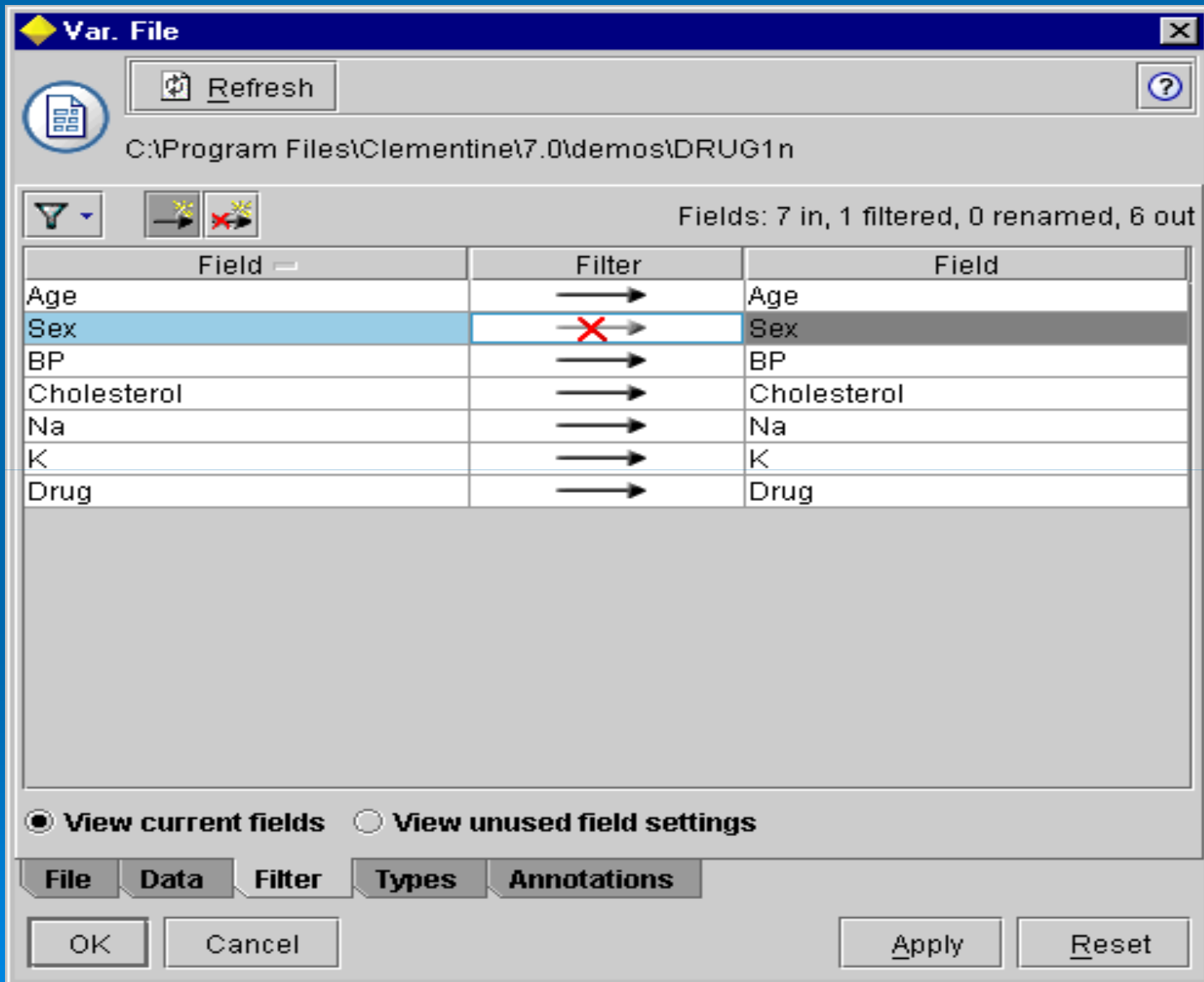
Field	Override	Storage
Age	<input checked="" type="checkbox"/>	Integer
Sex	<input checked="" type="checkbox"/>	String
BP	<input checked="" type="checkbox"/>	String
Cholesterol	<input checked="" type="checkbox"/>	String
Na	<input type="checkbox"/>	(Unknown)
K	<input type="checkbox"/>	String
Drug	<input checked="" type="checkbox"/>	Integer

View current fields
 View unused field settings

File | Data | Filter | Types | Annotations

OK Cancel Apply Reset

- The **Filter** tab can be used to remove any fields from the data that is brought into Clementine. Clicking on a field's arrow will mark it with a red X and filter it out. For this tutorial, though, we want to keep all fields.



- The **Types** tab helps you learn more about the type of fields in your data. You can also choose **Read Values** to view the actual values for each field based on the selections that you make from the *Values* column. This process is known as **instantiation**.

DRUG1n [X]

Refresh [?]

C:\Program Files\Clementine\7.0\demos\DRUG1n

Read Values Clear Values

Field	Type	Values	Missing	Check	Direction
Age	Range	[15,74]		None	In
BP	Set	HIGH,LO...		None	In
Cholesterol	Flag	NORMAL...	Off	None	In
Na	Range	[0.500169,...	On (*)	None	In
K	Range	[0.020022,...	Off	None	In
Drug	Set	drugA,dru...	Specify...	None	In















View current fields
 View unused field settings

File Data Filter Types Annotations

OK Cancel Apply Reset

- Now that you have loaded the data file, you may want to glance at the values for some of the records.
- One way to do this is by building a stream that includes a Table node. To place a Table node in the stream, either double-click the icon in the palette or drag and drop it on to the canvas.

Favorites Sources Record Ops Field Ops Graphs Modeling Output

													
Table	Matrix	Analysis	Statistics	Quality	Report	Set Globals	Publisher	Database	Flat File	SPSS Export	SAS Export	Excel	SPSS Procedure

- *Note:* Double-clicking a node from the palette will automatically connect it to the selected node in the stream canvas. However, you can not connect to terminal nodes like tables and graphs.

- Next, if the nodes are not already connected, you can use your middle mouse button to connect the Source node to the Table node. To simulate a middle mouse button, click the Alt key while using the mouse.



DRUG1n



Table

- Now that you have built a stream, you must execute it in order to view its output. Click the green arrow button on the toolbar to execute the stream and view an output table showing all of the records in the data file.



drug - Clementine

File Edit Insert View Tools SuperNode Window Help



DRUG1r



Table

Table [7 fields, 200 records]

File Edit Generate

	Age	Sex	B ^p	Cholesterol	Na
1	23	F	HIGH	HIGH	0.793
2	47	M	LOW	HIGH	0.739
3	47	M	LOW	HIGH	0.697
4	28	F	NORMAL	HIGH	0.564
5	61	F	LOW	HIGH	0.559
6	22	F	NORMAL	HIGH	0.677
7	49	F	NORMAL	HIGH	0.790
8	41	M	LOW	HIGH	0.767
9	60	M	NORMAL	HIGH	0.777
10	43	M	LOW	NORMAL	0.526
11	47	F	LOW	HIGH	0.896
12	34	F	HIGH	NORMAL	0.668
13	43	M	LOW	HIGH	0.627
14	74	F	LOW	HIGH	0.793
15	50	F	NORMAL	HIGH	0.828
16	16	F	HIGH	NORMAL	0.834
17	69	M	LOW	NORMAL	0.849
18	43	M	HIGH	HIGH	0.656
19	23	M	LOW	HIGH	0.559
20	32	F	HIGH	NORMAL	0.643
21	57	M	LOW	NORMAL	0.537
22	63	M	NORMAL	HIGH	0.616
23	47	M	LOW	NORMAL	0.809