Data Mining SPSS Clementine 12.0

7. C5.0 Algorithm

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Outline

• Overview

- Deriving a New Field
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- Browsing the Model
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Overview

Overview

- The C5.0 node builds either a decision tree or a rule set.
- The model works by splitting the sample based on the field that provides the maximum information gain at each level.
- The target field must be categorical. Multiple splits into more than two subgroups are allowed.

Drug Treatments

- 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.
- This example uses the data file named DRUG1n.

Drug Treatments

• The data fields used in the demo are:

| Data field | Description |
|-------------|--|
| 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 |

Building Data Stream

- You can read in delimited text data using a Variable File node.
- You can add a Variable File node from Sources tab
- Next, double-click the newly placed node to open its dialog box.

Reading in Text Data

• Adding a Variable File node



Reading in Text Data

• Variable File dialog box

| 🔶 Yar. File | × |
|--|------|
| Refresh (| |
| C:\Program Files\SPSSInc\Clementine12.0\Demos\DRUG1n | |
| File: C:\Program Files\SPSSInc\Clementine12.0\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 | |
| Pead field names from file Peacify number of fields | |
| Skip header characters: 0 = EOL comment characters: | |
| Strip lead and trail spaces: 💿 None 🔘 Left 🔘 Right 🔘 Both | |
| nvalid characters: Discard Replace with | |
| Encoding: Stream default 👻 Decimal symbol: Stream default 💌 | |
| Delimiters Lines to scan for type: 50 🜩 | |
| □ Space ✔ Comma □ Tab | |
| Newline Other Single quotes: Discard | |
| □ Non-printing characters Double guotes: Discard | |
| Allow multiple blank delimiters | |
| File Data Filter Types Annotations | |
| OK Cancel Apply R | eset |

- Since the ratio of sodium to potassium seems to predict when to use drug *Y*, you can derive a field that contains the value of this ratio for each record.
- This field might be useful later when you build a model to predict when to use each of the five drugs.
- Add a Derive node into the stream, then double-click the node to edit it.



- Name the new field *Na_to_K*.
- Since you obtain the new field by dividing the sodium value by the potassium value, enter Na/K for the formula.

| ♦ Na_to_K | × |
|--|---------------|
| Derive as: Formula | 20 |
| Mode: 💿 Single 🔘 Multiple | |
| Derive field: | |
| Na_to_K | |
| Derive as: Formula 🔹 Field type: 🥜 <default> 👻 Formula:</default> | |
| Na/K | |
| Settings Annotations | |
| OK Cancel Apply | <u>R</u> eset |

• You can check the distribution of your new field by attaching a Histogram node to the Derive node.



• In the Histogram node dialog box, specify *Na_to_K* as the field to be plotted and *Drug* as the overlay field.

| 🔶 ? | X |
|--|-------|
| (Х: Na_to_К | 20 |
| Field: 🗳 Na_to_K | -1 |
| Overlay Color: 🖌 Drug 🚽 Panel: 🚽 Animation: | - |
| Plot Options Appearance Output Annotations | |
| OK Execute Cancel Apply E | Reset |

• Execute the stream. Based on the display, you can conclude that when the *Na_to_K* value is about 15 or above, drug *Y* is the drug of choice.



- By exploring and manipulating the data, you have been able to form some hypotheses.
- The ratio of sodium to potassium in the blood seems to affect the choice of drug, as does blood pressure.
- But you cannot fully explain all of the relationships yet.
- This is where modeling will likely provide some answers.
- In this case, you will use try to fit the data using a rulebuilding model, C5.0.

- Since you are using a derived field, *Na_to_K*, you can filter out the original fields, Na and K, so that they are not used twice in the modeling algorithm.
- You can do this using a Filter node.



- On the Filter tab, click the arrows next to Na and K.
- Red Xs appear over the arrows to indicate that the fields are now filtered out.

| | Fiel | lds: 8 in, 2 filtered, 0 renamed, 6 out | | | | |
|--|---------------|---|--|--|--|--|
| Field 🗁 | Filter | Field | | | | |
| Age | \rightarrow | Age | | | | |
| Sex | \rightarrow | Sex | | | | |
| BP | \rightarrow | BP | | | | |
| Cholesterol | | Cholesterol | | | | |
| Na | _ X → | Na | | | | |
| K | → | K | | | | |
| Drug | \rightarrow | Drug | | | | |
| Na_to_K | \rightarrow | Na_to_K | | | | |
| View current fields Oview unused field settings Filter Annotations OK Cancel Apply Reset | | | | | | |

• Change the default name of Filter node to Discard Fields

| 🔶 Filter | × |
|--|----------------------------|
| | 0 |
| Name: 🔷 Auto 💿 Custom Discard Fields | |
| Tooltip text: | |
| Keywords: | |
| | |
| Created on January 1, 2010 7:27 PM by Administrator. | ID: id5GYY15LYPD1 |
| This object has not been saved. | |
| Filter Annotations | |
| OK Cancel | <u>Apply</u> <u>R</u> eset |

- Attach a Type node connected to the Filter node.
- The Type node allows you to indicate the types of fields that you are using and how they are used to predict the outcomes.



- On the Types tab, set the direction for the Drug field to Out, indicating that Drug is the field you want to predict.
- Leave the direction for the other fields set to In so they will be used as predictors.

| 🔶 Туре | | | | | 1 |
|--|-------------------------|---------------|-----------------|-------|---------------|
| <u></u> | | | | | 0 |
| | D | efine Type | es | | |
| 🔧 🗸 😽 | ▶ Read Values | Clear Values | Clear All Value | s | |
| Field - | Туре | Values | Missing | Check | Direction |
| 今 Age | 🔗 Range | <read></read> | 1 | Jone | 📐 In |
| 🔥 Sex | 🐓 Discrete | ≺Read≻ | None | | 📐 In |
| A BP | 🐓 Discrete | ≺Read≻ | None | | 💊 In |
| 🔥 Cholesterol | 🐓 Discrete | ≺Read≻ | 1 | lone | 💊 In |
| A Drug | 🗳 Discrete | ≺Read≻ | 1 | lone | 🔨 In |
| 🌋 Na_to_K | 🞸 <default></default> | ≺Read≻ | 1 | lone | 📐 In |
| | | | | | 🙆 Out |
| | | | | | 🐌 Both |
| | | | | | None |
| View current | fields 🔘 View unused fi | eld settings | | | Partition |
| Types Format Annotations OK Cancel Apply | | | | | |
| | | | | | <u>R</u> eset |
| | | | | | |

• Change the default name of Type node to Define Types

| 🔶 Туре | × |
|--|-------------------|
| | 0 |
| Name: O Auto Custom Define Types | |
| Tooltip text: | |
| Keywords: | |
| | |
| | |
| | |
| | |
| Created on January 1, 2010 7:31 PM by Administrator. | ID: id14QY15LVTUF |
| This object has not been saved. | |
| Types Format Annotations | |
| OK Cancel | Apply Reset |

- To estimate the model, place a C5.0 node in the workspace and attach it to the end of the stream as shown.
- Then click the green Execute button to execute the stream.



- This node uses the C5.0 algorithm to build either a **decision tree** or a **rule set**.
- A C5.0 model works by splitting the sample based on the field that provides the maximum **information** gain.
- Each subsample defined by the first split is then split again, usually based on a different field, and the process repeats until the subsamples cannot be split any further.
- Finally, the lowest-level splits are reexamined, and those that do not contribute significantly to the value of the model are removed or **pruned**.

• The C5.0 node can predict only a categorical target (Set or Ordered Set fields).

• Requirements

- To train a C5.0 model, there must be one categorical (i.e., Set or Ordered Set) Out field, and one or more In fields of any type.
- Fields set to **Both** or **None** are ignored.
- Fields used in the model must have their types fully instantiated (their type can not be string or type less).

• Strengths

- C5.0 models are quite robust in the presence of problems such as missing data and large numbers of input fields.
- They usually do not require long training times to estimate.
- In addition, C5.0 models tend to be easier to understand than some other model types, since the rules derived from the model have a very straightforward interpretation.
- C5.0 also offers the powerful **boosting method** to increase accuracy of classification.

• C5.0 Node Model Options

| | → Drug |
|-----------------|---|
| | |
| | Model name: 💿 Auto 🔿 Custom |
| | ✓ Use partitioned data |
| | Output type: 💿 Decision tree 🔘 Rule set |
| | Group symbolics |
| | Use boosting Number of trials: 10 |
| | Cross-validate Number of folds: 10 |
| | Mode: Simple Expert |
| | Favor: 💿 Accuracy 🔾 Generality |
| | Expected noise (%): |
| | Fields Model Costs Analyze Annotations |
| | OK <u>Execute</u> Cancel <u>Apply R</u> eset |
| ie ⁻ | |

C5.0 Node Model Options

• Model name:

- Specify the name of the model to be produced.
- Auto
 - With this option selected, the model name will be generated automatically, based on the target field name(s). This is the default.
- Custom
 - Select this option to specify your own name for the model nugget that will be created by this node.

• Output type

 Specify here whether you want the resulting model nugget to be a Decision tree or a Rule set.

C5.0 Node Model Options

• Group symbolics

- If this option is selected, C5.0 will attempt to combine symbolic values that have similar patterns with respect to the output field.
- If this option is not selected, C5.0 will create a child node for every value of the symbolic field used to split the parent node.
- For example,
 - if C5.0 splits on a COLOR field (with values RED, GREEN, and BLUE), it will create a three-way split by default.
 - However, if this option is selected, and the records where COLOR = RED are very similar to records where COLOR = BLUE, it will create a two-way split, with the GREENs in one group and the BLUEs and REDs together in the other.

• When the C5.0 node is executed, the generated model node is added to the Models tab. To browse the model, right-click the icon and choose Browse from the context menu.

| | Add <u>T</u> o Stream | | 10 |
|---|-----------------------------|--------|--------------|
| | <u>B</u> rowse | | > <u>rug</u> |
| | <u>R</u> ename and Annotate | | |
| 8 | Generate Modeling Node | | |
| | <u>S</u> ave Model | | |
| | S <u>a</u> ve Model As | | |
| * | Sto <u>r</u> e Model | | |
| | Ex <u>p</u> ort PMML | | |
| | Add to Project | | ISP-DM |
| × | <u>D</u> elete | Delete | ⊁ (unsav |
| _ | | | 🛛 🌽 Bu: |

• The Rule browser displays the set of rules generated by the C5.0 node in a decision tree format.



• Initially, the tree is collapsed. To expand it, click the All button to show all levels.



- Now you can see the missing pieces of the puzzle. For people with an *Na-to-K* ratio less than 14.642 and high blood pressure, age determines the choice of drug.
- For people with low blood pressure, cholesterol level seems to be the best predictor.

- The same decision tree can be viewed in a more sophisticated graphical format by clicking the Viewer tab.
- Here, you can see more easily the number of cases for each blood pressure category, as well as the percentage of cases.



- You can assess the accuracy of the model using an Analysis node.
- First, attach the C5.0 model to the stream, and then attach an Analysis node.



• The Analysis node output shows that with this artificial dataset, the model correctly predicted the choice of drug for almost every record in the dataset.

| 🔍 Analysis | s of [Drug] | | | | |
|-------------------------------|--------------------|-----------|---------|--|----|
| [<mark>≣</mark> <u>F</u> ile | じ <u>E</u> dit 🛛 🔢 | 2 | | | ×0 |
| Colla | apse All | 🌳 Expa | and All | | |
| ⊡…Results | s for output field | d Drug | | | |
| . Ė…Cor | nparing \$C-Dr | ug with D |)rug | | |
| | Correct | 199 | 99.5% | | |
| | Wrong | 1 | 0.5% | | |
| | Total | 200 | | | |
| | | | | | |
| Analysis | Annotations | | | | |
| | | | | | ОК |

• With a real dataset you are unlikely to see 100% accuracy, but you can use the Analysis node to help determine whether the model is acceptably accurate for your particular application.

References

References

• Clementine® 12.0 Clementine Applications Guide, 2007. (Chapter 8)

• Clementine® 12.0 Clementine Modeling Nodes, 2007. (Chapter 6)

The end