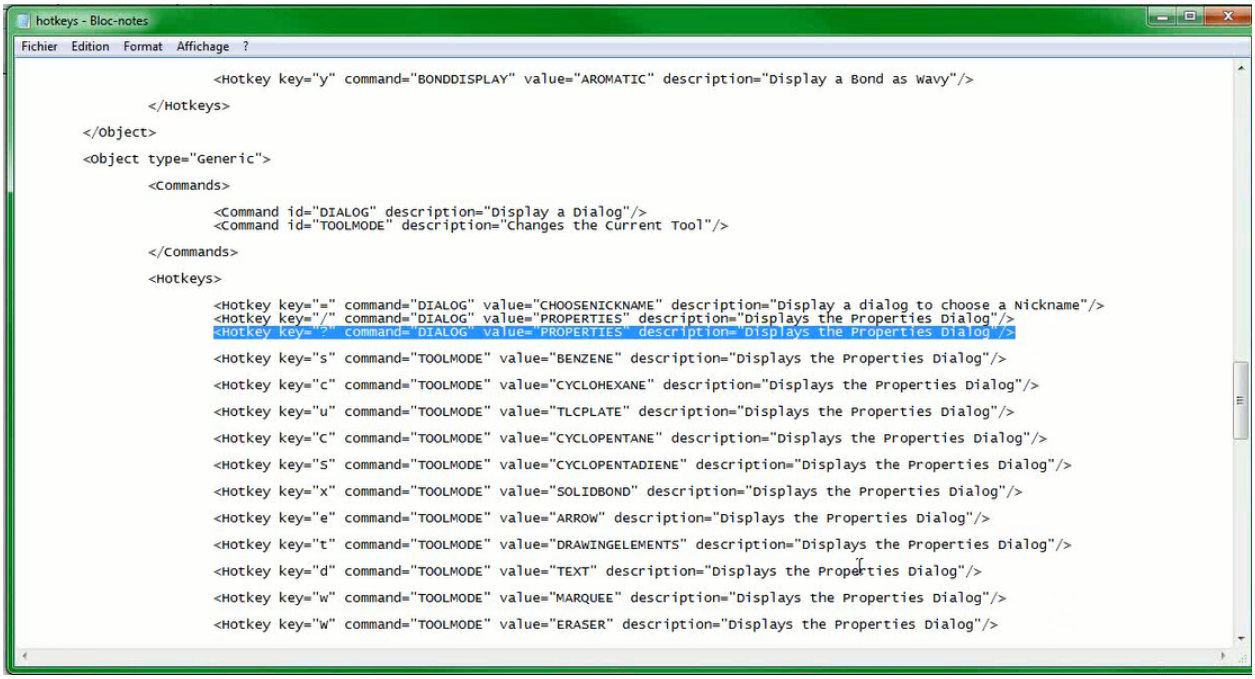
The webinar I used to learn all of these things has been put on the group computer in the conference room if you want to watch it. Not all of it is relevant, but overall it has been a total game changer. It's so much easier and faster to make nice looking ChemDraws.

Setting Hotkeys in ChemDraw The single most important thing I learned!

File --> Preferences --> Directories --> find the one that says ChemDraw Items
Find that on your computer by following the path shown
Open hotkeys XML document in a text editor

First section is for when you hover over an atom
Second section is when you hover over a bond
Third section is Generic (see below) and will only have the first three lines shown below.
Copy a line and paste to next line. Change "DIALOG" to "TOOLMODE" and the value to the hover label of whichever tool you want to add the hotkey. Change the hotkey value to whatever you want.

Note: if two tools have the same hotkey, only the first one in the list will actually work. Capital and lower case letters for the hotkeys matter. Structure Perspective or Chains wouldn't become hotkeys for me.



0 for sprout

building polycyclic rings with 5,6,7,8

Generic structures: [NH, O, S], $(CH_2)_{1-3}$, variable connection points (highlight the points, then Structure --> Add variable attachment), R1 query tools

Structure --> expand generic structure to have ChemDraw draw all possible combinations

Nicknames: '.' for attachment point. select whole structure Structure --> Define nickname. Caps sensitive, but then you can add that group to anything without having to draw it again. Just type in the nickname, then Structure --> Expand Label

Hotkeys in Chemdraw, see Setting hotkeys in ChemDraw (above)

Excel to ChemOffice spreadsheet. Save ChemDraw as MDL SDFile .sdf
Import into ChemOffice. Can calc MW, add values to create a database for querying later.

If fixed length bonds, press and hold alt to stretch

ctrl while dragging to copy, ctrl + shift while dragging to copy only in horizontal and vertical planes

ctrl + j for join

double click arrow to select the whole reaction

Structure --> clean up reaction (ctrl + shift + x)