Polarized Beam Console Parsing for ICE with pbconsole

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1 pbconsole

"pbconsole" is software for parsing the ICE console text with added polarized beam annotations from the He3 installer personnel in order to produce "cellfiles". "cellfiles" are required for efficiency corrections of polarized beam data with the "pbcor" software. "pbconsole" is include in the "pbcor" distribution, as both programs use the same libraries for calculations.
ICE console text is stored in the same repository as the experiment data at ftp://ftp.ncnr.nist.gov/pub/ncnrdata/bt7. The log files look like *experiment_ start_ date.console.log.* "pbconsole" also requires the he3cell database information. If you are at NCNR "pbconsole" will get this information from the server at *erwin.ncnr.nist.gov.* If you do not have server access you can use the database in file form as he3Cells.txt or he3Cells.json which should be put into your data directory.

The "pbconsole" gui has multiple tabs. The first, "consol-text", tab holds the console text which can be loaded by reading the console.log file.. Look in the "File" menu for the text load choices. The common method is to "select data directory" which will look for the consol.log file. If you need to edit the console-text, for example to fix annotation mistakes, save it to a file (see the "File" menu), and then reload the edited file after restarting the "pbconsole" program.

The first tab of console text is parsed into an "he3-log" event log in the second tab. The "he3-log" tab is then parsed to an "he3-efficiencies" tab 3, and finally the "he3-efficiencies" tab is used to create "cellfiles" in tab 4. The "cellfile" is the input file for data corrections using the "pbcor" program. Write the cellfiles produced by "pbconsole" to disk using the command in the "File" menu or the "write-cellfiles" button in the top menubar.

Cellfile names look like *experimentID_ MonDay_ Year_ Mode,* where mode is either "V" or "Q". These two modes of data should always be corrected separately which is why two different cellfiles are always produced. If tranport efficiency depends on sample environment (temperature or magnetic field) then multiple cellfiles may be written for different ranges of sample environment values. This will append to the cellfile names "_TdashedListOfTemperaturesRanes" or

"_BdashedListOfBfldRanges" or both in case the efficiency depends on both environment types.

Note that cellfile names using exptID and startDate with Month and Day will be unique for a given *console.log*. If the same log is reparsed, any pre-existing cellfiles will be overwritten with the prescribed names without warning.

Check the error message tab to make sure nothing serious has gone wrong, and get help in fixing any problems with consol annotation.The polarized beam ICE console annotated text consists of alternating "transmission measurment" blocks and "user data blocks" or "polarized beam blocks". "transmission blocks" are introduced by transmission annotated commands listed below, and "user polarized-beam data blocks" are introduced by "flipping-ratio" annotations (or the pb both command).

2 annotation

All polarized beam annotations are introduced by typing at the ICE console (or editing later):

```
pb cmd [args]
```

ICE will not recognize "pb" as a valid ICE command and print an error message which can be ignored.

The basic annotations are:

transmission block annotations

```
pb m
pb a analyzerCellName
pb p polarizerCellName
```

polarized-beam data block annotations

```
pb fr
pb frscan
pb frend
pb both
```

It is important to annotate the he3cell state before any counting is done in that state. I you forget this annotation, please add a comment to the console to notify that the anotation is missing or in the wrong place. You can use

```
pb com any test...
```

to make comments

3 transmission

"m", "a", and "p" define what he3-cell is in the neutron beam for transmission measurements where "m" stands for Empty. The "a" and "p" transmissions require a He3 cell name, since each particular He3 cell has its own opacity and geometry parameters. Each "m", "a", "p" command is followed by ICE counting commands in order to measure transmissions:

```
ct/t seconds
```

This ICE command produces counting results for all detectors in a block of text starting at "Counters:". The "pbp" parser will tally the counts for detectors of interest and report the count totals as m|a|p {utc totalCounts totalSeconds} [cellname] in the "he3-log" tab.
Transmissions are complete when a polarized-beam block annotation is found (pb fr etc but not pb beam), or when a "START SCAN" is found.
If none of this is available use "pb start" to start the polarized-beam block.
Detectors of interest can be defined using:

```
pb ct counterString1 [+ counterString2 + ...]
```

Use the full string that precedes the counter number in the "Counters:" block for each counterString, for example "SDC TOTAL:". This example string is the default on bt7 if no other specification is supplied. It is highly recommended that SDC counting mode is used for transmission measurments (and experiment data) on bt7 to minimize corrections for fast-neutron-background. In SDC mode the fast-neutron-background is about 1 count/minute in SDC TOTAL:.

In order to assure that counting takes place without deadtime (to produce accurate transmission measurements) keep the countting rate for any bt7 He3-detector-tube to below 8 kHz. For reproducability when opening and closing the beam as required for transmission measurments, make sure to use the OPEN collimation position for the INPILE collimator.

Another consideration is the specification of the instrument and sample geometry for the transmission measurements. This improves the accuracy of the determined transport efficiency. Beam size restrictions, sample height and mosaicity are the most important of these considerations as described in the *geometry* section.

Transmissions are measured for He3-cells that have just been used to take polarized beam data, and also for initial or freshly polarized replacement He3-cells. The fresh cell transmissions must always be performed after any decayed cell measurments,although in some cases an already used cell gets reused to continue the experiment and there is only one tranmission measurment for it. The reason for this is that the last transmissions for each cell position (polarizer and analyzer) are used to determine which cells are in the beam for following data.

A special case is "half-polarized-beam" where one of the cells is not used for the data. To indicate that data is to be taken in this manner use nocell for the cellName at the postion of the removed cell. For example, if the polarizer is to be removed for data,

```
pb p nocell
```

Any counting after this command is ignored and the transmission for either polarized beam state at this position (p or a) gets set to unity for "half-polarized-beam" data.

The transmission of the he3-polarizer can be tracked during an experiment, from the beam monitor-rate as a function of time when the monitor is after the He3-cell (as on bt7). This data if available is used to sanity check the measured transissions at cell installs.

4 flip ratios and polarized beam block

"pb fr" starts a flipping-ratio console session and starts a "user data block" in polarized-beam mode. This indicates full polarized-beam mode with both "p" and "a" He3 cells in the beam. Flipping-ratio is used to determine the transport efficiency for the polarized beam under the experiment conditions. After the "fr" command use the ICE scripts to set a non-spin-flip state and a spin-flip state and execute ICE count commands for both states. Repeat this by using scripts for the different polarization-modes used in the experiment (Vertical or Qmode). If the transport efficiency depends on the sample environment (e.g. temperature or magnetic field) you should take flipping ratios under the various environment conditions for which you want to analyze data. The software tracks the environement parameter settings in the console and may produce separate "cell-files" for each environment condition if in fact the efficiencey turns out to be different. The same is true for the polarization modes (Vertical or Qmode) where the transport efficiencies may not be the same in the two modes. You can measure both polarization-mode flipping ratios in a single "pb fr" block, but you must use separate "pb fr", "pb frend" blocks to measure the flipping-ration for different sample environment conditions.

The boundary between flipping-ratio measurements and data-taking can usually be found by looking for "START SCAN" in the console. To be sure of this boundary you can use "pb frend" when the flipping-ratio measurment ends. This is necessary when flipping-ratios are collected using scans (via pb frscan) which will contain "START SCAN".

Please note that flipping-ratios determine the polarized-beam transport efficiency, and the accuracy of this determination is mostly due to counting statistics while counting the low-count-rate flipped states. It is recommended to spend time counting these low-count-rates. For example, 10000 total counts produces 1 % standard accuracy.

If flipping-ratios are skipped (not advisable since they measure transport efficiency), type one of the commands:

```
pb both
pb start
```

This indicates that both He3 cells are in the beam ready for a data block.

If transmissions are finished without a following flip-ratio block or "START SCAN", it is important to terminate the transmission block with "pb both" or

"pb start" which will enter polarized-beam mode, thus terminating transmission mode.

A special case ensues when measuring flipping ratio at high fields, for example when using a superconducting magnet. The magnet must be at high field just to provide polarization transport. This may induce a magnetic moment on nuclear peaks. To avoid or minimize this induced moment effect on the flipping ratio, try to make the measurment at a high enough temperature that the induced moment is small.

5 sample environment (temperature and magnetic field)

Polarized beam transport can depend on the sample temperture and magnetic field. "pbconsole" tracks the sample environment so that if the efficiency changes by "transportEffCI" listed in "pbconsole configure" window, then a separate cellfile will be made for data taken under those conditions. The tolerances for temperature and magnetic field are listed in the same panel as "envTempTol" and "envBfldTol".

6 geometry (not supplied by ICE console or not ICE tracked)

commands:

```
pb beam arguments
pb ei value
pb ef value
```

The ICE console is NOT guaranteed to contain all essential information about the experiment. For example, if a new experiment starts and the focussing condition, or incident/final energy, or PG filter, or Velocity Selector, or back slit, doesn't need to be changed, then ICE will not record their values on the console. The incident energy is critical for measuring transmissions and flip-ratios, so if it is missing it needs to be entered by annotation on the console. Most of this information is however, in data files. "pbconsole" will look in the first data file created by ICE for this console.log to try and find these values. "pbconosle" will show a warning dialog if it cannot determine critical parameters.

The "pb beam arguments" annotation is used to record missing ICE paramters and beam geometry parameters (that affect divergences and neutron pathlengths through the he3-cells) that are not available from ICE commands. Knowing the beam geometry improves the accuracy of calculations of he3-polarization from transmissions, and transport efficiency from flipping ratios. BT7 polarized-beam data analysis works best if the he3-opacity is measured under pinhole conditions where the beam travels through the center of the he3-cell. The corrections are

smaller when the beam geometry approaches the pinhole condition. This approximate pinhole geometry is accomplished on BT7 by adding a small slit at the beam exit of the sample enclosure or using the backslits (just before the analyzer drum) when the sample height is small. The slit that mounts on the sample enclosure currently has square side of 1 cm. The pb beam arguments that set the pinhole condition can be 1, 1cm, xcm, open or full where the last two indicate that there is NO slit. To define the slit size use [slitsize]cm as the argument. The sample height is another geometry parameter that controls beam geometry (the sample width also has a small effect). To record the sample height use the argument sh[sampleheight(cm)] or sh=[sampleheight(cm)]. You can do the same for sample width using sw. The sample mosaic setting is important because it controls whether or not the incoming beam divergence and outgoing beam divergence are related by the elastic scattering condition, or uncorrelated due to powder sample or inelastic scattering. To indicate a powder or inelastic scatteirng set the mosaic to 999 using sm=999. Often this effective sample mosaic will be different for the transmission measurments and the data. To set the sample mosiac for transmission use smt=mosaicInMinutes, and to set the sample mosaic for data use smd=mosaicInMinutes. The parser will remember these values and set the mosaic when transmission and data blocks are used. The user can install front slits to define the beam size as well. To define these use fsh=x, fsw=x, fsL=x. If the computer controlled back slits are not set on the console use bsh=x, bsw=x. h and w are for height and width in cm (ICE scans this device in mm). fsL defines the front slit distance from the bt7 sample enclosure. The back slit has a standard position just in front of the bt7 analyzer drum (which has a standared position for polarized beam). If the focus condition is missing from the console add it with beam argument focusV=0/1 or focusH=0/1.

The available arguments for `pb beam:`

beam size

```
pb beam 1
pb beam [x]cm
pb beam open/full
```

focussing, pg filter, velocity-selector

```
pb beam focusV=[0/1]
pb beam focusH=[0/1]
pb beam vs=[0/1]
pb beam pg in
pb beam pg out
```

sample-height, width, mosaic, transission-mosaic, data-mosaic

```
pb beam sh=[cm]
pb beam sw=[cm]
pb beam sm=[arcmin]
pb beam smt=[arcmin]
pb beam smd=[arcmin]
```

front and back manual slits (back is normally computerized)

```
pb beam fsh=[cm]
```

`pb beam fsw=[cm]`
`pb beam fsL=[cm]`
`pb beam bsh=[cm]`
`pb beam bsw=[cm]`
horizontal collimations inpile, mono-to-sample, sample-to-analyzer
`pb beam hc0=[arcmin]`
`pb beam hcms=[arcmin]`
`pb beam hcsa=[arcmin]`