

Filman: User Guide

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Filman is a command line for controlling the motors of the triple-axis spectrometer GPTAS. This is the manual for researchers who use GPTAS for neutron experiments. Maintenance procedures (encoder redefinition, motor limits, wavelength calibration, IOC restarts) are collected in the separate *GPTAS Filman/EPICS: Staff Operations Manual*.

In this handout, commands are shown in **RED** bold monospace. **Commands are case-insensitive** (SC and sc are the same). **Filenames are case-sensitive**.

What changed in summer 2026 (for returning users)

The control backend was replaced: the LabVIEW control PC and the PXI rack are **retired**. Motors and the counter are now served by two small IOC servers (EPICS). The Filman command line itself is unchanged, plus:

- New commands: **HD** (set the scan heading from one line, works in command files), **FS** (fly scan for alignment), **SR/CC/TR/TC/TK** (relative / centering scans), **NT** (adaptive counting).
- Some rarely used maintenance commands refuse direct entry and print a “restricted command” message — they are for the instrument staff.
- Dangerous inputs are rejected at entry: **MG** accepts only 0 or 2, and the counting presets **MS/MT/MC** require $|v| \geq 1$.
- A scan whose tail points violate a motor limit now **saves the measured points** (an old bug — “scan touching a limit is not saved” — was fixed).
- **CA** marks limit-violating points with “*”.
- **LI** and **GO** now use the **same** range syntax (comma = enumeration, “:” or “-” = range).
- Variables are **auto-saved after every completed scan**; each scan also writes a **.meta** sidecar file with the full machine state and the heading.
- “**@**” now stops the *counter* as well as the motors.

System commands

“**@**” command: Emergency stop

“**@**” command can stop a command that is currently running. If you have run the wrong command, or if the spectrometer is about to come into collision, or if you are in trouble, immediately put “**@**” repeatedly. After a while, the display will show “TRAX>”. Both the motors and the counter are stopped.

WARNING: “@” during a command file

While a *command file* (**#FILE**) is running, a single “@” aborts only the line currently executing — **the file CONTINUES with the next line**, which may be another BR or GO! To abort the whole file, **keep pressing “@” until the “TRAX>” prompt returns**: each additional “@” still pending when Filman fetches the next line of the file aborts the file itself.

Example: stop a wrong move

```
1 TRAX> mv a2 130
2 @@@@@@@@@@@@@@@@@@
3 TRAX>
```

In this case, someone tried to move the a2 angle to 130 deg., but 130 deg. is too high so that the spectrometer would collide with the wall. Then put “@” to stop the a2 motor.

“SV” command: SaVe the variables

“SV” saves the Filman variables to disk. Since 2026 the variables are **also saved automatically after every completed scan**, so routine “SV spam” is no longer necessary. Still use “SV” after editing many variables by hand, and before quitting. Note: “ZZ”-style exits do *not* save — only “SV” and “AB” do.

“AB” command: ABort Filman

When quitting Filman, type “AB” (this saves the variables, then exits). To restart Filman, type “**filman**” on the Linux terminal.

“QU” command: List current values of motor angles

When you want to know the value of the motor angles, type “QU”. Each axis is shown with its angle and its drive state: **DRVN** (drivable) or **FRZN** (frozen; a frozen motor refuses to move — release with “**DR XX**”, freeze with “**FR XX**”). The emergency-stop status is also shown; while the E-stop is active every move prints **EMERGENCY STOP ACTIVE** and is refused.

For rough sample alignment

“CO” command: COunt for a specified time or MON

“CO” counts once, for the preset given by the variable MC. For constant-MON measurement use “MC = XXX” (XXX positive); for constant-seconds use “MC = -XXX”. $|MC| \geq 1$ is required (MC = 0 or a fractional value is rejected at input).

Example: Count for constant monitor (MON)

```
1 TRAX> MC = 100    (set monitor count: 100k)
2 TRAX> CO
3 319 count (MC = 100)
```

Example: Count for constant seconds

```
1 TRAX> MC = -10    (counting time 10 sec; negative = seconds)
2 TRAX> CO
3 319 count
```

“MV” command: MoVe the motor

“MV” moves the selected motor. When you set the motor and angle, like **MV MMM AAA**, the selected motor *MMM* will move to the angle *AAA*. Several motors can be moved at once by separating them with commas, e.g. **MV a1 10,c1 5**. Blanks are ignored by the parser (at the terminal and in command files alike), so a space after the comma is harmless.

Caution: by design, “MV” does *not* check Filman’s software limits (so that the limits themselves can be inspected and crossed deliberately). The motor-controller hardware limits still protect the machine — but hardware limits do *not* prevent collisions with the sample environment (cryostat, shielding); **think before you type the target angle**. Scans (**SC**, **GO**, ...) *do* check the software limits.

The following table lists the main motors:

- #0 c1: ω for the monochromator. Only used during adjustment of the spectrometer.
- #1 a1: 2θ for the monochromator. Only used during adjustment of the spectrometer.
- #2 c2: ω for the sample
- #3 a2: 2θ for the sample.
- #4 c3: ω for the analyzer. Only used during adjustment of the spectrometer.
- #5 a3: 2θ for the analyzer. Only used during adjustment of the spectrometer.
- #6 rx: sample tilt *X* (goniometer). Used for tilt alignment.
- #8 ry: sample tilt *Y* (goniometer). Used for tilt alignment.

Example: Move the motor

```
1 TRAX> MV a2 60 (sample stage 2theta to 60 deg.)
2 TRAX> MV c2 100 (sample stage omega to 100 deg.)
3 TRAX> MV a1 10,c1 5 (Two motors at once)
```

“SC” command: SCan with selected axis

AX:5 displays the variables of the “SC” scan. AX is the axis to be scanned, SA is the Start Angle, DA is the step angle ($\Delta\theta$), FA is the Finish Angle, and MS is the counting preset (MON for positive, seconds for negative; $|\text{MS}| \geq 1$). The AX value is the *motor number* from the table above, so AX=2 scans C2 (sample ω) and AX=3 scans A2 (sample 2θ). For example, **AX=3, 10, 0.2, 50, -10** means that motor #3 (A2) will be scanned from 10 to 50 degrees in 0.2 degree steps, counting 10 seconds per point. After setting the variables, input “SC” to start scanning.

Example: Scan using SC command

```

1  TRAX> AX:5
2  AX    SA    DA    FA    MS
3  0     10    0.2   15    -10
4  TRAX> AX=3, 10, 0.5, 50, -10
5  TRAX> AX:5
6  AX    SA    DA    FA    MS
7  3     10    0.5   50    -10
8  TRAX> SC
9  SCAN MOTOR A2 ( 3)  NUMBER OF STEPS      81
10  .....
```

If a scan point violates a software limit, the point is reported (**limit error**) and the scan is stopped safely — the already measured points are saved.

“TH” command: THeta-2theta scan

For a theta-2theta scan two motors move together, so a separate variable set is used: “**S1:5**” shows S1, D1, F1, S3, and MT. S1 is the Start angle of 2θ , D1 the step of 2θ , F1 the Finish angle of 2θ , S3 the start angle of ω , and **MT the counting preset of the theta-2theta family** (positive: MON; negative: seconds; $|\text{MT}| \geq 1$).

Example: Scan using TH command

```

1  TRAX> S1:5
2  S1    D1    F1    S3    MT
3  15    0.2   19    54    -10
4  TRAX> S1=30, 0.2, 34, 101, -10
5  TRAX> S1:5
6  S1    D1    F1    S3    MT
7  30    0.2   34    101   -10
8  TRAX> TH
9  THETA-TWO-THETA SCAN
10  .....
```

In this case, A2 is scanned from 30 to 34 degrees in 0.2 degree steps, and C2 follows from 101 degrees in 0.1 degree steps.

“FS” command: Fly Scan (new in 2026)

“FS *XX=AAA*” sweeps motor *XX* to angle *AAA* *without stopping*, while the counter runs freely; the counts are binned against the moving angle and saved as a normal **.ngx** scan. This replaces “watching the analog rate meter while jogging C2”: you can hunt a Bragg peak from outside the reactor room and see the profile live on the web plotter.

- “FS C2=20” sweep C2 to 20° at the default 0.3 deg/s.
- “FS C2=20,0.1” sweep at 0.1 deg/s.
- “FS C2=20,0” keep the present motor speed (fast coarse hunt).

The separator before the speed **must be a comma** — a space is not a separator (blanks are stripped, so “FS C2=20 0.1” would compact to target 200.1; a comma with a space after it is fine). The speed is restored automatically at the end and on “@”. A requested speed *faster* than the present one is refused (FS is slow-down only). FS data are saved as the next **.ngx** sector (they do not appear in the **CD** legacy listing).

For fine sample alignment

Variables for the crystal alignment

Filman describes every position in the scattering plane by two coordinates (H, K) defined through two reference reciprocal-lattice vectors $\mathbf{A}$ and $\mathbf{B}$:

$$\mathbf{Q} = H \mathbf{A} + K \mathbf{B}, \quad |\mathbf{A}| = AS, \quad |\mathbf{B}| = BS, \quad \hat{\mathbf{A}} \cdot \hat{\mathbf{B}} = CG,$$

where AS and BS are in $\text{\AA}^{-1}$ and CG is the cosine of the angle between $\mathbf{A}$ and $\mathbf{B}$ (typically $\mathbf{A} = \mathbf{a}^*$, $\mathbf{B} = \mathbf{b}^*$, $CG = \cos \gamma^*$). KI and KF ($\text{\AA}^{-1}$) are the wavevectors of incident and scattered neutrons. TM and TA are the wavevector lengths used for monochromating and analyzing (no need to change KI, KF, TM, TA for almost all users).

$\mathbf{A}$ and $\mathbf{B}$ can be chosen freely for the plane you want to measure. Example — an (HHL) scattering plane: take $\mathbf{A} = \mathbf{G}_{110}$ and $\mathbf{B} = \mathbf{G}_{001}$, i.e. input $AS = |\mathbf{G}_{110}|$, $BS = |\mathbf{G}_{001}|$; then Filman's (H, K) corresponds to (H, H, K) in crystal indices.

Example: input parameters

```
1 TRAX> as=0.84453, bs=0.84453, cg=0.5
2 TRAX> ki = 2.663, kf = 2.663
3 TRAX> as:7
4 AS BS CG TM TA KI KF
5 0.84453 0.84453 0.5 1.87325 1.87325 2.663 2.663
6 .....
```

“**CABR**” “**BR**” command: calculate or move to the Bragg reflections

If the sample orientation and the lattice constants are known, the motor angles can be calculated or driven by “**CABR**” or “**BR**”. HB is the Bragg index along H (AS), KB along K (BS), and **MB** is the counting preset used by **BR** (positive: monitor counts; negative: seconds — the same convention as MC/MS). For example, to move to the (2,0) reflection, enter HB=2, KB=0 (or HB=2, 0) and input “**BR**”.

Example: move to a particular Bragg reflection

```
1 TRAX> hb = 3, 0, -1
2 TRAX> hb:3
3 HB KB MB
4 3 0 -1
5 TRAX> cabr
6 H = 3.000 K = 0.000 MONITOR = -1
7 C2 A2
8 CALCULATED 28.410 56.810
9 TRAX> br
10 H = 3.000 K = 0.000 MONITOR = -1
11 C2 A2
12 CALCULATED 28.410 56.810
13 2497 counts at 162.350 K
```

“NA” command: Update sample orientations and lattice constants

After the position of a Bragg reflection is optimized by “SC”, “TH”, the lattice constants (and the ω encoder) should be updated from the optimized 2θ (A2) angle. This is done by “NA”. After setting the C2 and A2 angles to the optimized positions, input the indices of the Bragg reflection as HB and KB, then input “NA”. The lattice constants (AS for $H \neq 0$, BS for $K \neq 0$) are re-derived from the present 2θ (A2) angle, and the ω (C2) encoder is reset to the value calculated for that reflection (the bisecting angle $\omega = 1/2 \times 2\theta$ when KB=0).

WARNING: NA rewrites the coordinate system

NA rewrites the lattice constants **and the C2 encoder**. Executed on a wrong reflection index or a spurious peak, it silently corrupts the whole coordinate system for everything that follows. Checklist:

- use **NA** only on a *verified* Bragg peak;
- re-check HB/KB immediately before typing **NA**;
- after **NA**, verify with an *independent* reflection (**CABR/BR** to another (H, K) and check the peak is where it should be).

Relative and centering scans (new in 2026)

Variants of “SC”/“TH” that save typing during alignment:

- “**SR**” axis scan with SA/FA *relative* to the current angle.
- “**CR**” axis scan + move to the peak center afterwards.
- “**CC**” relative axis scan + move to the peak center.
- “**TR**” theta-2theta scan, relative.
- “**TC**” theta-2theta scan + center.
- “**TK**” relative theta-2theta scan + center.

The “center” is the **intensity-weighted centroid (first moment)** of the scan — *not* a fit. It is reliable for a single symmetric peak; for split or asymmetric peaks inspect the scan yourself before trusting the centering. If no usable moment is found, the axis returns to the starting angle and says so — nothing is redefined silently.

Sample alignment flowchart

1. **Before beginning** Set initial conditions. (You can skip this part)
 - Confirm spectrometer and motor positions by typing **QU**.
 - Confirm the k_i (and k_f) are the values you will use.
 - Check neutron beam and detector status.
2. **Set Crystal Parameters** Set reciprocal lattice parameters.
 - Calculate and input **AS, BS, CG** based on crystal symmetry and lattice constants.
 - Example: **as = 1.9746, bs = 1.3963, cg = 0**.
 - Confirm the setting with **as:7**.
3. **Rough Alignment** Roughly align sample orientation.
 - Input the expected reflection (e.g. **HB=2, KB=0**).
 - Calculate the angles (**cabr**) and go there (**br**).
 - Hunt the peak with a fly scan, e.g. **FS C2=xx** — watch the live plot instead of the rate meter.
 - Perform rough scans using **SC** to identify the Bragg reflection.
 - Refine the tilt angles using SC (**ax = 6** or **8**).
4. **Fine Alignment** Precisely align Bragg reflections.
 - Conduct fine scans (**SC, TH** — or the centering variants **CR/TC**) around the peak.
 - Set optimized motor angles (**MV**) to the peak positions.
 - Update crystal orientation and lattice parameters with **NA**.
 - Confirm updated parameters.
5. **Complete Alignment** Final checks before measurement.
 - Recheck alignment by repeating fine alignment scans as needed.
 - Save the state with **SV** (scans also auto-save on completion).
 - Confirm readiness for main scans.

Main scans

How to set scans

After you finish the alignment, let's go to main scans! A main scan is defined by a numbered *scan set*. NS is the scan-set number (1 to 48), HS/KS the start position of H/K , ES the start energy transfer (meV), DE the energy step, NP the number of points, MN the counting preset per point (positive: monitor; negative: seconds), and DH/DK the steps of H/K . The points of a scan are generated as

$$H_i = HS + i DH, \quad K_i = KS + i DK, \quad E_i = ES + i DE, \quad i = 0, \dots, NP - 1.$$

The energy transfer follows the standard convention $E = E_i - E_f$: **positive** E = **neutron energy loss** = **excitation of the sample**. By default GPTAS runs in E_f -fixed mode (**IK** = -1, k_f held constant); to fix E_i instead, set **IK** = +1.

IMPORTANT: scan-set variables go on ONE line

The set selector is reset at every new input line. Therefore **all variables of a set must follow “NS= n ” on the same line**, chained with commas. A variable typed on the next line without “NS=” is *not* applied (“ERROR IN SETTING VALUE FOR MNEMONIC”). If one line is not enough, start the next line with “NS= n ,” again.

Check a scan set

```
1  TRAX> li1      (list the variables of scan 1)
2  NS  HS  KS  ES  DE  NP  MN  DH  DK
3  1   1   0   0   0  101 100 0.01 0
```

To edit the variables, either give all values in order, or name them — *on one line*. The two lines below are equivalent:

Example: edit scan variables

```
1  TRAX> NS=2, 1, 0, 0, 0.2, 21, 100, 0, 0
2  TRAX> NS=2, HS=1, KS=0, ES=0, DE=0.2, NP=21, MN=100, DH=0, DK=0
```

Both define scan 2 as a constant-**Q** energy scan at $\mathbf{Q} = (1, 0)$ from $E = 0$ to 4 meV in 0.2 meV steps (21 points), 100k monitor per point.

For a **constant-Q** (energy) scan: fix HS, KS and set DH = DK = 0; sweep energy with DE.

For a **constant-E** (Q) scan: fix ES and set DE = 0; sweep H , K with DH, DK.

Example: constant-E scan along (H 0) at 2 meV

```
1  TRAX> NS=3, 1, 0, 2, 0, 21, 100, 0.05, 0
2  TRAX> li3
3  NS  HS  KS  ES  DE  NP  MN  DH  DK
4  3   1   0   2   0  21  100 0.05 0
```

Tip: “MN=0” is the official way to *disable* a scan set without deleting it (the set is skipped at run time with “Monitor not set”); restore its MN to re-arm it.

“NT” variable: adaptive counting (new in 2026)

“**NT=n**” sets a target *detector* count per point. When $NT > 0$, each point is first counted with $0.2\times$ the preset (probe); if the target is already reached, the point ends there (1/5 of the time on strong peaks), otherwise a second count tops it up — never exceeding the nominal preset (MS/MT/MN), so weak points get exactly the statistics of the fixed mode. The monitor actually used is recorded per point in the last column of the `.ngx` file — **always normalize by counts/MON when analyzing**. “**NT=0**” (default) disables it; NT is *not* stored in the saved variables, so a restart never resumes in adaptive mode by surprise. Check the current value with “**LI**”. As a rule of thumb $\text{error} \approx 1/\sqrt{NT}$: $NT=4000 \rightarrow 1.6\%$, $NT=10000 \rightarrow 1\%$.

Autofocus (new in 2026)

GPTAS now has an **autofocus** system: when it is enabled, the monochromator focusing motors (H1–H5 horizontal, V0 vertical) are driven *automatically* to the optimum for the current k_i before each measurement, so scans that change the incident energy stay focused without any user action. The target positions are interpolated from a calibration library file maintained by the instrument staff.

- The current mode is shown by “**LI**”: off / V0 only / V0 + H1–H5 all.
- Outside the calibrated k_i range the blades are *held at the nearest calibration endpoint* (no extrapolation). If your scans go beyond the calibrated range, tell the staff so the calibration can be extended.
- **Users do not operate the focusing motors and do not edit the calibration file.** If you need the autofocus enabled, disabled, or recalibrated, **ask the instrument staff**.
- The autofocus state and the calibration used are recorded in the `.meta` sidecar of every scan, so the focus condition of any past measurement can be reconstructed later.

“LI” command: list the scan parameters

“**LI n**” lists the parameters of scan n . The selection syntax is the **same as GO**: a comma enumerates (“**LI 1,5**” = sets 1 and 5 only), “:” or “–” gives a consecutive range (“**LI 1:5**” = sets 1 through 5), and they can be mixed (“**LI 1:5,8**”). “**LII**” lists all registered scans, together with the general variables, the NT value, and the autofocus mode. (In Filman versions before Aug. 2026, LI treated every separator as a range — unified with GO since.)

“HD” command: set the scan heading (new in 2026, recommended)

“**HD any text you like**” sets the heading (title) that is written into the data files. Everything after “HD” on the line becomes the heading, spaces and “=” and “,” included. “**HD**” alone *shows* the current heading. Unlike the older “**LG**”, “**HD**” works **inside command files** because it takes the text from the same line. The heading is saved in the `.ngx` header of Q – E scans and, since 2026, in the `.meta` sidecar of *every* scan (`#title|` line). Limitations: HD must be the first command on its line, and a “;” inside the heading truncates it.

Example: set the heading

```
1 TRAX> HD MySample xtal2, (HHL), ki=2.65, 2K
2 heading: MySample xtal2, (HHL), ki=2.65, 2K
```

(“**LG**” still exists for interactive use: it behaves like “**GO**” but first asks the scan order and the heading on the terminal. Do not use LG inside command files — its Heading? prompt reads the keyboard, not the file.)

“**CA**” command: simulate the scan

“**CA** *n*” simulates scan *n* *without moving any motors*. The output lists the calculated motor angles at every point. **CA** checks kinematic accessibility (can the scattering triangle close?) and the Filman software limits — nothing more. It does *not* model physical collisions with the sample environment, the cryostat tail, or the shielding: inspect the calculated angles and the actual clearances yourself. Always use “**CA**” before “**GO**”. Since 2026, a point that violates a software limit is marked with “*” in the first column, and a legend line gives the count. A “*” row is *exactly* a point the real scan will skip.

Example: simulate scan 2 with two limit-violating points

```
1 TRAX> CA 2
2 Scan set 2
3 E C2 A2
4 0.0000 16.42 32.84
5 0.5000 17.92 35.83
6 * 1.0000 19.40 38.81
7 * 1.5000 20.84 41.69
8 * = internal limit: 2 point(s) will be SKIPPED by the scan
```

If the tail of a scan is skipped this way, the measured points are still saved (old versions silently discarded the whole scan — fixed in Aug. 2026).

“**GO**” command: execute the scan

“**GO** *n*” executes scan *n*:

- “**GO** *n*” execute scan *n*.
- “**GO** *m:n*” or “**GO** *m-n*” execute scans *m* through *n* sequentially.
- “**GO** *m, n*” execute scans *m* and *n* *only* (comma = enumeration).
- “**GO**” (no argument) re-use the previous scan order: *after an “@” abort* it resumes from the interrupted scan and point (the aborted point is re-measured); *after a normal completion* it runs the whole previous order again from the beginning.

You can mix the syntaxes, e.g. “**GO** 1:5, 8, 10:12”. **LI** uses the same syntax — what **LI** lists is exactly what **GO** will run.

Example: run scans 1 to 5

```
1  TRAX> GO 1:5
2  STARTING SCAN 1 ...
3  .....
```

If the scan must be aborted (collision, wrong setting, sample problem, etc.), press “**@**” repeatedly; the motors and the counter stop. Filman keeps the interrupted scan and point, so a subsequent “**GO**” (no argument) resumes from there. (Careful: after a scan order has *completed*, a bare “**GO**” repeats the whole order instead.)

Quick reference: main-scan workflow

1. **NS=...** define each scan set **on one line**
2. **LI** list and check the sets
3. **HD ...** set the heading
4. **CA** simulate: angles, “*” marks, clearances
5. **SV** save
6. **GO** run (watch the first point on 4gweb)

Abort = **@** (repeat until “TRAX>” if a command file is running).

Resume after abort = **GO** with no argument.

Temperature control with TEMCON

TEMCN is the external temperature controller used at GPTAS. Filman talks to it for setting, reading, and stabilizing the sample temperature during scans. The four most-used commands for general users are “**AC**”, “**DC**”, “**TE**”, and “**QT**”.

Three modes of temperature handling

- **T no read**: temperature is neither read nor controlled. “**TE**”, “**QT**” are disabled.
- **T read only**: temperature is monitored but not controlled. “**QT**” works; “**TE**” does not.
- **T control**: temperature is controlled, and counting only proceeds when $|T_{\text{obs}} - T_{\text{set}}| < \text{DTEMP}$. All commands work.

Switch between modes with “**AC**” (activate control) and “**DC**” (deactivate).

“**AC**” command: A**C**tivate temperature control

“**AC**” enters T control mode. Filman then asks interactively which TEMCON channels to use:

- **1**: use channel #1 only (typical case — one sensor + heater).
- **2**: use channel #2 only.
- **3**: use both channels (e.g. CTI cryostat with sample sensor + control sensor).

After channel selection, Filman shows the current values of the four stability parameters and prompts for new values:

- **DTEMP1**: tolerance for channel #1, $|T_{\text{obs}} - T_{\text{set}}| < \text{DTEMP1}$ (K).
- **DTEMP2**: tolerance for channel #2 (K).
- **WTIME**: waiting time after a setpoint change (seconds). Stability must hold for at least this long.
- **DLMON**: unit of monitor (or seconds) for stability check during counting. ~60 sec is reasonable.

To keep the current values, just type “**N**”.

Example: activate T control on channel #1

```

1  TRAX> AC
2  #1 T control (1), #2 T control (2),
3      #1 and #2 T control (3) ? [1/2/3] 1
4  #1 T control, #1 print
5  temperature control activated
6  DTEMP1, DTEMP2, WTIME(sec), DLMON =
7  1.000000 2.000000 30 60
8  input new values (no change -> N) > N

```

“DC” command: DeaCtivate temperature control

“DC” switches from T control mode to either **T read only** or **T no read** mode. Filman asks whether to keep reading the temperature.

Example: deactivate but keep monitoring

```
1  TRAX> DC
2  temperature control deactivated
3  temperature read ? [Y/N] Y
4  which device ? 0=system, 1=TEMCON#1, 2=TEMCON#2 [0/1/2] 1
5  T read mode (TEMCON#1)
```

“TE” command: set the target temperature

“TE *a, b*” changes the setpoint of TEMCON. The arguments depend on which channel is in use:

- “TE *a*” or “TE *a, 0*”: set channel #1 to *a* K.
- “TE *0, b*”: set channel #2 to *b* K.
- “TE *a, b*”: set both channels.

After the setpoint changes, Filman checks the stability condition every 10 seconds and prints **Y/N**. The command returns when stability has held for $\geq$ WTIME seconds. To exit early (without waiting for stability), press “@”.

Example: change setpoint to 5 K

```
1  TRAX> TE 5, 0
2  ... Y N N Y Y Y Y Y Y ...
3  stable, exit TE
```

“QT” command: read the current temperature

“QT*n*” prints the current temperature reading.

- QT0: system voltmeter. : not in use
- QT1: TEMCON channel #1.
- QT2: TEMCON channel #2.

Filman prints the current value T , the deviation $\Delta T = T - T_{\text{set}}$, the average T_{avg} , and the heater output V_{heater} (%).

Example: read TEMCON #1

```
1  TRAX> QT1
2  #1 T, DT, TAV = 5.0021 0.0021 5.0010
3  DTMAX, DTMIN, VOUT = 0.0050 -0.0040 35.2
```

Command files

For long sequences — temperature ramps, repeated alignment, overnight scan series — it is much safer and more reproducible to write the commands into a text file and let Filman execute them line by line. This is especially important because a single line in the Filman terminal is limited to 80 characters.

“#” command: read a command file

“**#FILENAME**” reads the file *FILENAME* from the directory in which Filman was launched, and executes the commands inside one line at a time. (Note: “#” is *not* a comment character — as the first character of a line it triggers this command-file read. For comments, use “**”** as described below.)

- Place the file in the directory where you started Filman.
- Use the extension **.SCN** (recommended convention).
- Specify the full filename including the extension after “#”.
- File names are **case sensitive**.

Example: run a command file

```
1  TRAX> #overnight.SCN
2  ... (commands in overnight.SCN are executed)
```

How to write a command file

A command file is a plain text file. Each line contains exactly one Filman command (the same syntax you would type in the terminal). Some rules:

- **One command per line.**
- **Comments:** a line that begins with “**”** (double quote) is ignored. Use it freely for notes.
- Multiple commands can be chained on one line with “**;**”, e.g. “**te 20,0; hb=1,0; br**”. (Useful only for short sequences.)
- Use “**HD**” for the heading — it works in files. (“**LG**” does not: its prompt reads the keyboard.)
- Test a new command file by simulating the heavy steps with “**CA**” or by running it once on a dummy scan first.

*Assumption in the example below: temperature control has been activated beforehand with **AC** (channel #1).*

Example: command file 'overnight.SCN'

```
" --- temperature ramp + Bragg check + main scan ---
HD MySample (HHL) ki=2.65 T-ramp series
te 20,0
hb=1,0
br
ax=2,18,0.1,20,-1
cr
go 1
te 30,0
br
go 2:5
te 50,0
go 1:5
sv
```

The example sets the heading, sets $T = 20$ K, moves to (1,0), does a quick ω scan with centering (“**cr**” moves to the peak centroid), runs scan 1, ramps to 30 K, re-checks the Bragg peak, runs scans 2–5, ramps to 50 K, runs scans 1–5, and saves.

Tips for command files

- Re-check the Bragg peak after large temperature changes (thermal contraction shifts the alignment).
- Save with “**sv**” at the end of any long sequence.
- **Remember the “@” warning:** one “@” aborts only the running line and the file *continues* with the next line. To abort the whole file, keep pressing “@” until the “TRAX>” prompt returns.

Viewing and analyzing the data

4gweb: live plots in the browser

4gweb is the web plotter of GPTAS: open it in a browser on the instrument network (the address is posted at the instrument; ask the staff).

- **Live view:** the scan currently running appears point by point (every scan — SC, TH, GO, and also FS fly scans — feeds the live file as it measures). This is the standard way to watch an alignment or an overnight scan from outside the reactor room.
- **Saved scans:** completed sector files can be displayed and *merged* (repeated identical scans are summed with proper monitor normalization — including the per-point monitor column written by the adaptive counting mode).
- Intensities should always be compared as **counts/MON**; the plotter does this for you, but keep it in mind when reading raw numbers.

ngx2spice: convert data for analysis

ngx2spice converts Filman `.ngx` files (with their `.meta` sidecars) into SPICE-format text files, so that the data can be analyzed with the same tools used at other triple-axis instruments.

<https://github.com/kinjo-tohoku/ngx2spice>

Single-file Python script, no installation: `python ngx2spice.py files....` It handles axis scans, θ - 2θ scans, and Q - E scans, and reconstructs the per-point motor angles from the `.meta` information. See the README on GitHub for usage and options.

scanplanner: plan your beamtime and generate `.scn` files

scanplanner is a browser tool that plans triple-axis scans in (Q, E) *before* you run them — its purpose is to eliminate “just GO and die on a motor limit” at the planning stage.

<https://github.com/kinjo-tohoku/scanplanner>

You enter the crystal (lattice constants and two orienting reflections), the spectrometer configuration (fixed k_i or k_f and its value; GPTAS defaults are preloaded), and the C2/A2 soft limits; the tool then shows the *reachable region*, marks every requested point green (reachable) or red (not), and finally **generates a ready-to-run `.scn` file** (single lines or (h, k) / Q - E maps, adaptive-counting NT supported; maps are auto-fitted to the reachable region). Copy the generated file to the Filman directory and run it with “**#FILENAME**”. **Resolution tools** are also provided (Cooper–Nathans): resolution ellipses, convolution of a model $S(Q, \omega)$ with the instrumental resolution for simulating a measurement, and resolution-convoluted fitting — see the repository README.

Data files

Every scan is saved as a numbered sector file `4g0NNNNN.ngx` plus a sidecar `4g0NNNNN.meta` containing the full machine state at save time (all variables, auxiliary motor angles, autofocus state, and the heading). The `.meta` exists because the live variables change over time — the sidecar is the trustworthy record of the conditions of a given scan. Keep both files together when copying data.