

Excluding Data in Sift

In biomechanics, some trials or trace may not be suitable for analysis. A missed marker, an incorrect force plate assignment, or an unexpected movement during a trial can all introduce noise into the results. Rather than deleting these trials outright, Sift allows users to flag them for exclusion, which keeps the analysis clean while preserving the original data.

Data cleaning is an ongoing process, and exclusions can be revisited at any time as new issues are identified.

How Exclusions Work

Excluding a trace removes it from analysis (and optionally, plots), but does not delete the underlying data. Exclusions can be undone at any time using Ctrl+Z or by right-clicking a workspace and selecting Re-Include Data, and excluded traces can be toggled back on to review them alongside valid data.

Sift supports three levels of exclusion:

- **Individual trace:** exclude a single signal cycle only
- **All traces at those frames:** exclude all queried signals during the same cycle
- **Entire trial:** exclude all data from the affected trial

Writing Exclusions Back to the Data

Once exclusions have been identified, they can be written back to the original workspace files. This is done by adding a “Bad” event, using one of the three methods:

- Only exclude individual traces: the narrowest option. An event like AnkleAngle_BAD is created during the bad cycle, and the group definition for AnkleAngle then excludes any sequences containing that event. has-motion So only that specific signal on that specific cycle is flagged.
- Exclude all traces for this side: a mid-level option. An event is created for all queried signals during the specified cycle, but only on the same side of the body (R/L). has-motion Useful if, say, a right-side marker dropout corrupts all right-side kinematics for that cycle.
- Exclude all traces regardless of side: the broadest option. An event is created for all queried signals during that cycle, regardless of side. has-motion Use this when the entire trial/cycle is compromised.

See the [excluded_traces](#) section of the Update CMZs Dialog.

It is also possible to tag entire trials that contain excluded data, making it easy to identify and filter problematic files downstream.

Plot Options

Two display options in the plot are available:

- **Hide Excluded Data:** removes excluded traces from the plot entirely.
- **Show Excluded Data:** keeps excluded traces visible in the plot while still omitting them from analysis.

Tutorials

- [Clean your Data](#)
 - A step-by-step walkthrough of using Sift to identify and exclude bad trials across a full dataset, using a ground reaction force quality check as an example.

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