**Description**

Is it possible restoring the feature in g_rmsf where the program prompts for different group, one for fitting and a second group for rmsf calculation?

**History**

- **#1 - 11/12/2012 05:36 PM - Roland Schulz**
  - Category set to analysis tools

- **#2 - 06/25/2014 02:58 PM - Erik Lindahl**
  - Status changed from New to Rejected

I'm somewhat reluctantly rejecting this, but that is mainly based on the fact that I don't see how it should be used.

The reason for removing it is that we want the tool to calculate fluctuations in a group, but if the fitting between frames is not based in this group but something completely different you are rather calculating something like an RMS of the group based on a different fit. That is a very valid task, but we have the g_rms tool for that :-)

IIRC correctly, we removed the option from g_rmsf since the output labels and everything would be wrong - such a result no longer represents a fluctuation in the molecule.

Now, if somebody can provide me with a clear-cut usage case and why it is valid, we can open it again ;)}