g_sas computes incorrect values with -nopbc

02/28/2014 05:33 AM - Teemu Murtola

**Status:** Closed  
**Priority:** Normal  
**Assignee:** Teemu Murtola  
**Category:** analysis tools  
**Target version:** 4.6.6  
**Affected version:** 4.0.?-4.6.5

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**Description**

g_sas computes incorrect surface areas if -nopbc is specified. The problem has been introduced some time in the 4.0.x series, probably between 4.0 and 4.0.3 (e2045413, merged to development version in 1437fac0). The cell size of the grid used to search for neighboring atoms is determined as the radius of the first atom instead of double the maximum radius as it should.

Additionally, the 4.0.x series g_sas always triggers the -nopbc option (ed04b50), irrespective of what is provided on the command line (and thus always produces the incorrect result).

This explains at least some of the results reported on gmx-users:  

**Associated revisions**

Revision a56228ac - 03/02/2014 02:49 AM - Teemu Murtola

Fix incorrect grid cell size in g_sas -nopbc

Fixes #1445

Change-Id: I798fc8fe96608633f26d9a3500f83b44af008

**History**

#1 - 02/28/2014 05:34 AM - Gerrit Code Review Bot

Gerrit received a related patchset '1' for Issue #1445  
Uploader: Teemu Murtola (teemu.murtola@gmail.com)  
Change-Id: I798fc8fe96608633f26d9a3500f83b44af008  
Gerrit URL: [https://gerrit.gromacs.org/3199](https://gerrit.gromacs.org/3199)

#2 - 02/28/2014 05:41 AM - Teemu Murtola

- Status changed from In Progress to Fix uploaded

#3 - 03/02/2014 03:00 AM - Teemu Murtola

- Status changed from Fix uploaded to Resolved
- % Done changed from 0 to 100

Applied in changeset a56228accb86dc04c7ef08f6bf7c518da43c218d.

#4 - 03/04/2014 04:57 AM - João M. Damas

Teemu Murtola wrote:
Conclusion on this issue: [https://mailman-1.sys.kth.se/pipermail/gromacs.org_gmx-users/2014-March/087665.html](https://mailman-1.sys.kth.se/pipermail/gromacs.org_gmx-users/2014-March/087665.html)

#5 - 04/03/2014 07:47 PM - Roland Schulz

- Status changed from Resolved to Closed