

GROMACS - Bug #2511

Editconf mead generated pqr file didn't follow pqr spec

05/22/2018 04:09 PM - zhiyi wu

Status: Closed	
Priority: High	
Assignee:	
Category:	
Target version: 2018.2	
Affected version - extra info:	Difficulty: uncategorized
Affected version: 2018	

Description

When using editconf to generate pqr files.

```
gmx editconf -f enmin.tpr -mead system.pqr
```

The generated pqr file didn't follow the pqr file format specification (<https://apbs-pdb2pqr.readthedocs.io/en/latest/formats/pqr.html>), where:

1. The pqr shouldn't contain atom type at the end of the line
2. There should always be a space separating the columns.

Here is a sample of pqr file.

```
REMARK The B-factors in this file hold atomic radii
REMARK The occupancy in this file hold atomic charges
TITLE system
REMARK THIS IS A SIMULATION BOX
CRYST1 35.060 34.040 38.990 90.00 90.00 90.00 P 1 1
MODEL 1
ATOM 1 N MET A 1 81.952 52.151 32.219 0.16 1.62 N
ATOM 7335 N MET B 1 30.317 32.933 28.543 0.16 1.62 N
ATOM 7855 N POPEE 474 9.856 33.258 32.940 -0.29 1.65 N
ATOM 10605 N POPEa 496 37.380 63.975 30.931 -0.29 1.65 N
ATOM 13855 N POPE0 522 90.878 72.350 68.454 -0.29 1.65 N
ATOM 15105 N POPE 532 16.405 8.140 68.984 -0.29 1.65 N
TER
ENDMDL
```

As is shown in the snapshot provided, if the residue name has a length of 4 characters (POPE), there will be no space between residue name and chain id (POPE a) instead of (POPEa).

Associated revisions

Revision b0f4bf1d - 06/06/2018 10:24 AM - Paul Bauer

Fix PQR file output

PQR files from editconf were always written as fixed format PDB files with just the field information added. As pointed out in the linked redmine, this can violate the PQR file standard if the field lengths are too long, even though the file would still be a valid PDB.

This adds a slightly different form of the writeout that has a flexible, PQR conform format.

Fixes #2511

Change-Id: I626380b642a0214970753da289e9c969ce411ea7

History

#1 - 05/22/2018 05:09 PM - Gerrit Code Review Bot

Gerrit received a related patchset '1' for Issue [#2511](#).
Uploader: Paul Bauer (paul.bauer.q@gmail.com)
Change-Id: gromacs~release-2018~l626380b642a0214970753da289e9c969ce411ea7
Gerrit URL: <https://gerrit.gromacs.org/7929>

#2 - 05/22/2018 05:11 PM - Mark Abraham

Can you please share the .tpr file, so we can perhaps agree on how the output should look if/when we fix editconf?

#3 - 05/22/2018 05:15 PM - Mark Abraham

- Status changed from New to Fix uploaded

#4 - 05/22/2018 05:23 PM - zhiyi wu

- File enmin.tpr added

Mark Abraham wrote:

Can you please share the .tpr file, so we can perhaps agree on how the output should look if/when we fix editconf?

Here is a sample tpr file contain two POPE molecules.
If "gmX editconf -f enmin.tpr -mead system.pqr" was run, the output pqr file will be

```
REMARK   The B-factors in this file hold atomic radii
REMARK   The occupancy in this file hold atomic charges
TITLE    GkApcT YneM POPE POPG in water
REMARK   THIS IS A SIMULATION BOX
CRYST1  109.329  90.329  91.654  90.00  90.00  90.00 P 1      1
MODEL   1
ATOM    1  N  POPEA  1   14.430  46.000  29.240 -0.29  1.65      N
...
ATOM   250  H16Z POPEB  2   100.140  5.340  54.660  0.02  1.10      H
TER
ENDMDL
```

The suggested output which adheres to the pqr spec will be:

```
REMARK   The B-factors in this file hold atomic radii
REMARK   The occupancy in this file hold atomic charges
TITLE    GkApcT YneM POPE POPG in water
REMARK   THIS IS A SIMULATION BOX
CRYST1  109.329  90.329  91.654  90.00  90.00  90.00 P 1      1
MODEL   1
ATOM    1  N  POPE A  1   14.430  46.000  29.240 -0.29  1.65
...
ATOM   250  H16Z POPE B  2   100.140  5.340  54.660  0.02  1.10
TER
ENDMDL
```

#5 - 06/06/2018 10:30 AM - Paul Bauer

- Status changed from Fix uploaded to Resolved

Applied in changeset [b0f4bf1d0a83e6bf095d3e557d3a160fe9fac8fc](#).

#6 - 06/07/2018 01:48 AM - Mark Abraham

- Status changed from Resolved to Closed

- Target version set to 2018.2

Files

enmin.tpr	46.1 KB	05/22/2018	zhiyi wu
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