I have problem..~

When I process the average in amber, I have an error message like this

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 -/- PTRAJ: a utility for processing trajectory files

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 \-/ Version: "AMBER 10.0 integrated" (2/15/2008)

 -/- Executable is: "/applic/applications/AMBER/64BIT/ESSL//amber10/exe/ptraj"

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 \-/ Residue labels:

 DA5 DG DC DG DC DT DG DC DG DC

 DT3 DA5 DG DC DG DC DA DG DC DG

 DC DT3 Na+ Na+ Na+ Na+ Na+ Na+ Na+ Na+

 Na+ Na+ Na+ Na+ Na+ Na+ Na+ Na+ Na+ Na+

 Na+ Na+ WAT WAT WAT WAT WAT WAT WAT WAT

 WAT WAT WAT WAT WAT WAT WAT WAT WAT WAT

 ...

 WAT WAT WAT WAT WAT

**WARNING in ptraj(): Could not open input file (trajin), exiting**

.

**My script file is**

gaiae /home01/x796jsh/amber/11mer> cat 11mer-average.script

#!/bin/csh

#@ job\_type = parallel

#@ notification = complete

#@ class = normal

#@ error = 11mer-average.err

#@ output = 11mer-average.out

#@ Network.MPI = csss,shared,US

#@ node = 1

#@ tasks\_per\_node = 5

#@ resources = ConsumableCpus(1) ConsumableMemory(1gb)

##@ requirements = ( Machine == {"nobel18"})

#@ wall\_clock\_limit =05:00:00

#@ queue

export MP\_SHARED\_MEMORY=yes

cd /gpfs2/x796jsh/

cp /home01/x796jsh/amber/11mer/11mer-average.script /gpfs2/x796jsh/.

cp /home01/x796jsh/amber/11mer/11mer-1-ions-solvate.prmtop /gpfs2/x796jsh/.

cp /home01/x796jsh/amber/11mer/mdynamic2.mdcrd /gpfs2/x796jsh/.

/applic/applications/AMBER/64BIT/ESSL//amber10/exe/ptraj 11mer-1-ions-solvate.prmtop << EOF trajin mdynamic2.mdcrd 2000 3000

average 11mer-average.rst restrt

EOF

cp /gpfs2/x796jsh/11mer-average.rst /home01/x796jsh/amber/11mer/.