```bash
#!/bin/bash

# This script preps for the next model run

pathBase="/home/ukurien/projects/def-yaumanko/ukurien/ED50"

echo Press 1 for simulation with monodisperse
echo Press 2 for bi disperse
read varChoice

if [ $varChoice -eq 1 ]
then
        # Gathering info on data to be prepped
        echo Enter the smallest droplet size for which the simulation was run
        read dropSizeLB
        echo Enter the largest drop size for which the simulation was run
        read dropSizeUB
        echo Enter the increments through which the droplet size was changed
        read dropSizeInc

        echo Please specify gomic flags used
        read gomicFlag


        if [ $gomicFlag -eq 0 ]
        then
                # Initiating loop to cycle throug paths
                for (( dropSize=$dropSizeLB; dropSize<=$dropSizeUB;dropSize=$dropSiz
e+$dropSizeInc))
                do
                        # Cloning model and output files to new directory
                        # ----------------------------------------------
                        pathModel="Rr$dropSize$dropSize"
                        echo $pathModel
                        pathOrigin="$pathBase/$pathModel/gomic0"
                        pathDestination="$pathBase/$pathModel/gomic1"

                        echo Creating gomic1
                        mkdir -p $pathDestination
                        echo

                        echo Cloning gomic0 to gomic1
                        cp -r $pathOrigin/* $pathDestination/
                        echo

                        # Naming restart files
                        # --------------------
                        cd $pathDestination/
                        echo Renaming turbulent restart file,in gomic1, from Zk4.out
.ncf to Zk.in.ncf
                        mv Zk4.out.ncf Zk.in.ncf
                        echo

                        # Modifying model flags for next run
                        # ----------------------------------
                        echo Changing value of gomic flag from 0 to 1, in gomic1
                        sed -i 's/gomic= 0/gomic= 1/g' param.inc
                        echo
                done


        elif [ $gomicFlag -eq 1 ]
        then
                #Initiating loop to cycle through paths
                for (( dropSize=$dropSizeLB; dropSize<=$dropSizeUB;dropSize=$dropSiz
e+$dropSizeInc))
                do

                        # Cloning model and output files to new directories
                        # -------------------------------------------------
                        pathModel="Rr$dropSize$dropSize"
                        pathOrigin=$pathBase/$pathModel/gomic1
                        pathDestination1=$pathBase/$pathModel/gomic2ihydro0
```

```
pathDestination2=$pathBase/$pathModel/gomic2ihydro1

echo Creating gomic2ihydro0
mkdir -p $pathDestination1
echo

echo Creating gomic2ihydro1
mkdir -p $pathDestination2
echo

echo Cloning gomic1 to gomic2ihydro0
cp -r $pathOrigin/* $pathDestination1/
echo

echo Cloning gomic1 to gomic2ihydro1
cp -r $pathOrigin/* $pathDestination2/
echo


# Shifting into gomic2ihydro0 folder
#----------------------------------
cd $pathDestination1

# Naming restart files
# --------------------
echo Naming droplet distribution and turbulent restart files
  in gomic2ihydro0

rm Zk.in.ncf
mv Zk4.out.ncf Zk.in.ncf
mv drop4.out.ncf drop.in.ncf
echo

# Modifying model flags for next run
# ---------------------------------
echo Changing flags gomic and ihydro from 1 and 0 to 2 and 1
, respectively

sed -i 's/gomic= 1/gomic= 2/g' param.inc
sed -i 's/ihydro  = 0/ihydro  = 0/g' main.F90
echo

# Shifting into gomic2ihydro1 folder
# ---------------------------------
cd $pathDestination2

# Naming restart files
# --------------------
echo Naming droplet distribution and turbulent restart files
  in gomic2ihydro1

rm Zk.in.ncf
mv Zk4.out.ncf Zk.in.ncf
mv drop4.out.ncf drop.in.ncf
echo

# Modifying model flags for next run
# ---------------------------------
echo Changing flags gomic and ihydro from 1 and 0 to 2 and 1
, respectively

sed -i 's/gomic= 1/gomic= 2/g' param.inc
sed -i 's/ihydro  = 0/ihydro  = 1/g' main.F90
echo
            done
        fi
elif [ $varChoice -eq 2 ]
then
        echo Code for this part has not been written as yet.
fi
```