# General Plan

1. ~~Get all BioCoder code updated and into MFSimSSA framework, so that we can compile it without removing functionality~~
   1. ~~Biocoder Folder (probably just copy over everything….may need to remove some MCFlow stuff and web stuff)~~
      1. ~~Remove VirtualLoC IO initializations:~~
         1. ~~initializeIO from assayProtocol.h/cpp~~
         2. ~~initializeIO from BioCoder.h/cpp~~
   2. ~~Conditional Folder (copy all contents (cfg/conditional\_group/expression) into Models folder)~~
   3. ~~Structs.h (Conditional struct, etc.)~~
   4. ~~Enums.h (ExOperandType, DagStatus, OperationType, etc.)~~
   5. Dag.cc/h (TransferIn/Out support)
      1. ~~Cool stuff~~
      2. ~~ConditionalGroup stuff, DagStatus & ReInitAssay~~
         1. ctsLeftToPrcoess may not be used
         2. May need to revisit ReInitAssay as some instance variables have changed
      3. Added AddTrans…() methods and all transferrIn/transferOut stuff
      4. ~~Copied over Fault tolerance split stuff~~
   6. AssayNode.cc/h
      1. ~~Temperature~~
      2. ~~Added System as friend class~~ – May want to undo later
   7. ~~Include system.h/cc just to eliminate compiler errors~~
      1. ~~Commented out all VirtualLoC stuff –~~ **~~FILE IS ALL SHREDED UP JUST TO COMPILE~~**
2. ~~Copy over testing methods~~
   1. ~~biocode\_test.cc/h (Copy over Conditional methods(CONDITIONAL\_TEST, CONDITIONAL\_WITH\_TRANSFER\_DROPS\_TEST, SIMPLE\_CONDITIONAL\_WITH\_TRANSFER\_DROPS\_TEST, CONDITIONAL\_B2\_InVitroDiag, B3\_Protein\_FaultTolerant, B3\_GenerateFtLevelCase\_RMS, B3\_GenerateFtLevelCase\_Det, ); most methods just have extra dynamic virtual LoC code that was already properly removed and still unusable to me know)~~
   2. ~~test.cc/h (Has some nice methods that show explicit creation of CFG….may want to copy some code, but most of this is done in the biocode\_test.cc file, just not directly)~~
      1. ~~Moved into demo.cc/h~~
   3. ~~Main.cc (Leftover code for BiocodeTest::Conditional… commands)~~
3. ~~Patch BioSystem.TranslateCFG() so that it returns a CFG, which we should be able to output (using CFG’s output method) and visualize to make sure BioCoder is generating valid CFGs~~
   1. ~~Moved several methods from System to CFG, where they really belong~~
      1. ~~ConstructAndValidateCFG(), convertFTSplits(), separateFTSplitParents(), recursiveSeparate()~~
      2. ~~The System class is not currently being used anywhere…~~
   2. ~~Removed all references to System class in BioSystem and worked directly with CFGs~~
      1. ~~Changed “~~*~~void BioSystem::TransformCFG()~~*~~”~~~~to “~~*~~CFG \*BioSystem::GetDmfbExecutableCFG()~~*~~”~~
   3. ~~Updated all Conditional methods in BiocodeTest and Demo to return a CFG \* that is ready to be processed by microfluidic system; all methods generate output CFG and contained DAGs~~
4. Examine System.h/cc and pull out relevant code for processing CFGs
   1. System.h/cc (probably just portions; need CFG processing portions)
      1. Convert BioSystem.TranslateCFG() into a method that returns a CFG
5. Add functionality to Scheduler/Placer to schedule/place transfer-in/out nodes
   1. Does router need additional attention or not?
   2. pe\_le\_binder.cc/h (Copy TransferIn/Out stuff into grissom\_left\_edge\_binder.cc/h)
   3. pe\_mls\_scheduler.cc/h & pe\_path\_scheduler.cc (Copy TransferIn/Out stuff into list\_scheduler.cc & path\_scheduler.cc)
6. DAG modification
   1. Pull apart DAGs to remove first routing stage OR
   2. Create small DAGs that consist only of routing stages
7. Loose Ends
   1. Add support for cooling (search for heating) everywhere

## ~~Files to COPY from dynamic framework~~

* ~~System.h/cc (probably just portions; need CFG processing portions)~~
  + ~~Convert BioSystem.TranslateCFG() into a method that returns a CFG~~
* ~~Biocoder Folder (probably just copy over everything….may need to remove some MCFlow stuff and web stuff)~~
* ~~Conditional Folder (copy all contents (cfg/conditional\_group/expression) into Models folder)~~

## ~~Files to MODIFY from dynamic framework~~

* ~~Structs.h (Conditional struct, etc.)~~
* ~~Enums.h (ExOperandType, DagStatus, OperationType, etc.)~~
* ~~Dag.cc/h (TransferIn/Out support)~~
* ~~Main.cc (Leftover code for BiocodeTest::Conditional… commands)~~
* ~~pe\_le\_binder.cc/h (Copy TransferIn/Out stuff into grissom\_left\_edge\_binder.cc/h)~~
* ~~pe\_mls\_scheduler.cc/h & pe\_path\_scheduler.cc (Copy TransferIn/Out stuff into list\_scheduler.cc & path\_scheduler.cc)~~
* ~~biocode\_test.cc/h (Copy over Conditional methods(CONDITIONAL\_TEST, CONDITIONAL\_WITH\_TRANSFER\_DROPS\_TEST, SIMPLE\_CONDITIONAL\_WITH\_TRANSFER\_DROPS\_TEST, CONDITIONAL\_B2\_InVitroDiag, B3\_Protein\_FaultTolerant, B3\_GenerateFtLevelCase\_RMS, B3\_GenerateFtLevelCase\_Det, ); most methods just have extra dynamic virtual LoC code that was already properly removed and still unusable to me know)~~
* ~~test.cc/h (Has some nice methods that show explicit creation of CFG….may want to copy some code, but most of this is done in the biocode\_test.cc file, just not directly)~~