```
parameter_file = "default_parameters.txt"

expression_params = {("negativehill_transcription", "k"):2.8}
```

Parameters default for rapid model building and can be programmatically set via dictionaries or custom parameter files.

```
lacI = Species(name= "lacI", material_type = "protein")
tetR = Species(name = "tetR", material_type = "protein")
cl = Species(name = "cl", material_type = "protein")

pLac = RepressablePromotor(name = "pLac", transcript = "tetR", repressor = lacI)
pTet = RepressablePromotor(name = "pTet", transcript = "cl", repressor = tetR)
pCl = RepressablePromotor(name = "pCl", transcript = "lacI", repressor = cl)

placI_tetR = DNAassembly(name = "lacI_tetR", promoter = pLac, rbs = "BCD8", protein = tetR)
ptetR_cl = DNAassembly(name = "tetR_cl", promoter = pTet, rbs = "BCD8", protein = cl)
pcl_lacI = DNAassembly(name = "cl_lacI", promoter = pCl, rbs = "BCD8", protein = lacI)
```

Modular Components are combined together to produce diverse biochemical circuits.

```
RepressilatorExp = ExpressionDilutionMixture(name = "expression",
           components = [placI_tetR, ptetR_cl, pcl_lacI],
           parameter_file = parameter_file, #can use multiple parameter sources
           parameters = expression_params)  #custom parameters take precedent
RepressilatorExpCRN = RepressilatorTxTl.compile_crn()
```

Mixtures determine the context and level of detail used to model Components.

Expression CRN models gene expression (with leak) and dilution.

```
RepressilatorTxTl = SimpleTxTlDilutionMixture(name = "txtl",
           components = [placI_tetR, ptetR_cl, pcl_lacI],
           parameter_file = parameter_file)
RepressilatorTxTlCRN = RepressilatorTxTl.compile_crn()
```

Transcription-Translation CRN models transcription (with leak), translation, and dilution.

```
RepressilatorEcoli = TxTlDilutionMixture(name = "e coli",
           components = [placI_tetR, ptetR_cl, pcl_lacI],
           parameter_file = parameter_file)
RepressilatorEcoliCRN = RepressilatorTxTl.compile_crn()
```

E. coli CRN models transcription via RNA-Polymerase, translation via ribosomes, mRNA-degradation via endo-nucleases, background cellular loading, and dilution.