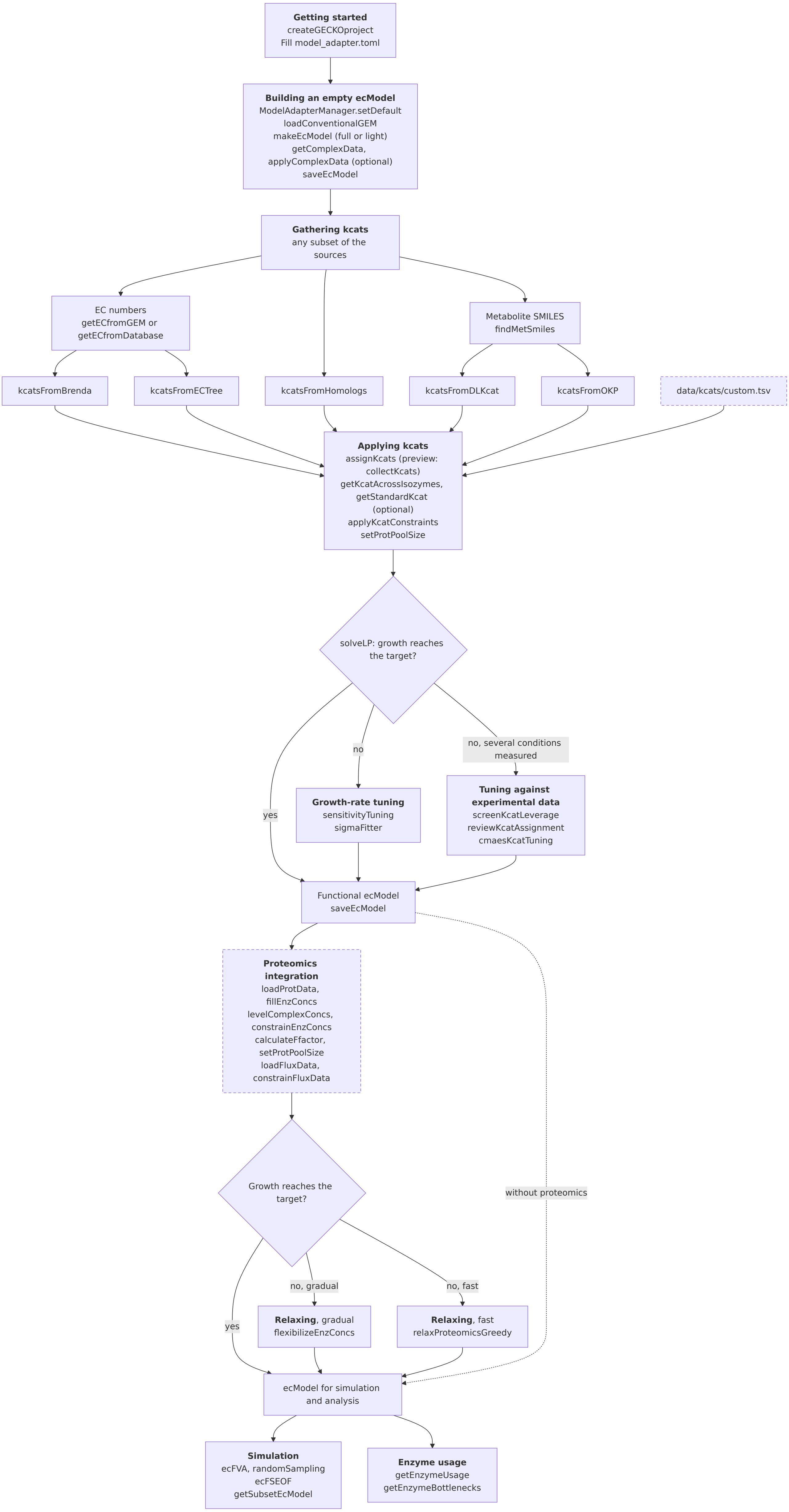

Getting started
createGECKOproject
Fill model_adapter.toml
Building an empty ecModel
ModelAdapterManager.setDefault
loadConventionalGEM
makeEcModel (full or light)
getComplexData,
applyComplexData (optional)
saveEcModel
Gathering kcats
any subset of the sources
EC numbers
getECfromGEM or
getECfromDatabase
Metabolite SMILES
findMetSmiles
kcatsFromBrenda
kcatsFromECTree
kcatsFromHomologs
kcatsFromDLKcat
kcatsFromOKP
data/kcats/custom.tsv
Applying kcats
assignKcats (preview:
collectKcats)
getKcatAcrossIsozymes,
getStandardKcat
(optional)
applyKcatConstraints
setProtPoolSize
solveLP: growth reaches the target?
yes
no
no, several conditions measured
Growth-rate tuning
sensitivityTuning
sigmaFitter
Tuning against experimental data
screenKcatLeverage
reviewKcatAssignment
cmaesKcatTuning
Functional ecModel
saveEcModel
Proteomics integration
loadProtData,
fillEnzConcs
levelComplexConcs,
constrainEnzConcs
calculateFfactor,
setProtPoolSize
loadFluxData,
constrainFluxData
Growth reaches the target?
yes
no, gradual
no, fast
without proteomics
Relaxing, gradual
flexibilizeEnzConcs
Relaxing, fast
relaxProteomicsGreedy
ecModel for simulation and analysis
Simulation
ecFVA, randomSampling
ecFSEOF
getSubsetEcModel
Enzyme usage
getEnzymeUsage
getEnzymeBottlenecks