



'g2f' Package

An R Package to Find and Fill Gaps for genome-scale metabolic networks

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Language: R

Stable: CRAN

Development: gibbslab/g2f

License: GPL-2

Binaries: Windows - Linux - Mac

```

h2o[r] + dheas[r] => h[r] + dhea[r] + so4[r]
                                uri[e] <=> uri[c]
na1[e] + uri[e] => na1[c] + uri[c]
atp[c] + pi[m] => pi[c] + atp[m]
na1[e] + gchola[e] => na1[c] + gchola[c]
...

```

RXNLIST

```

getReference()
DOWNLOAD
STOICHIOMETRIC REACTIONS
FROM THE KEGG DATABASE

```



REFERENCE



GENOME SCALE METABOLIC NETWORK

```

additionCost()
CALCULATE ADDITION COST

```

```

cost =  $\frac{n(\text{metabolites}(\text{newReaction}) \notin \text{metabolites}(\text{reactionList}))}{n(\text{metabolites}(\text{newReaction}))}$ 

```



gapFill()
FIND AND FILL GAPS

```

original = n(orphanMetabolites)
do{
  if(orphanMetabolite ∈ metabolites(newReactions)){
    gapFill: | cost ≤ limit → reaction ∪ newReactions
              | cost ≥ limit → reaction
  }
  filled = n(orphans(reaction ∪ newReactions) ∈ orphanMetabolites)
}
while ( original ≤ filled )

```



```

blockedReactions()
IDENTIFY REACTIONS
NEVER ACTIVATED

```