b.)
-There are 7 extreme pathways. The only reaction that produces urea is associated with v_3, which corresponds to column 3 of the P matrix. You can see that 2 out of the 7 produce Urea.
-The reaction frequency is in red next to each of the 19 reactions below. Reaction frequency is computed by looking at matrix P and using the formula: (number of nonzero values for a reaction column) ÷ (total number of extreme pathways) for each column. The columns go from 1-19–v1 is column 1 and b14 is column 19.

v_1,ATP+L-citrulline+L-Aspartate,AMP+diphosphate+2-(Nomega-L-arginino)succinate,false" 0.286

"v_2,2-(Nomega-L-arginino)succinate,L-arginine+fumarate,false" 0.286

"v_3,L-arginine+H2O,Urea+L-ornithine,false" 0.286

"v_4,L-ornithine+carbamoylphosphate,L-citrulline+phosphate,false" 0.286

"v_5,2*L-arginine+3*NADPH+3*H+4*O2,2*L-citrulline+2*nitricoxide+3*NADP+4*H2O,true" 0.143

"B_1,∅,carbamoylphosphate,false" 0.286

"b_2,∅,L-Aspartate,false" 0.286

"B_3,fumarate,∅,false" 0.286

"b_4,Urea,∅,false" 0.286

"b_5,∅,H2O,true" 0.143

"b_6,phosphate,∅, true" 0.286

"b_7,diphosphate,∅, true" 0.286

"b_8,AMP,∅, false" 0.286

"b_9,∅, ATP,false" 0.286

"b_{10},NADPH,∅, false" 0.143

"b_{11},H,∅, false" 0.143

"b_{12},O2,∅, true" 0.143

"b_{13},∅, NADP,false" 0.143

"b_{14},∅, nitricoxide,false" 0.143

c.)

To rank the connectivities of metabolites and reactions, I looked at the numbers on the diagonal for each reaction/metabolite–the higher the number, the more reactions a particular metabolite is in/the more metabolites a specific reaction has. The more reactions a metabolite is in, the higher the rank. The more metabolites in a specific reaction, the higher the rank. That is how the rankings below were determined.

RCA:

```
julia> show(stdout, "text/plain", reaction_array)
19-element Vector{String}:
 "v₁,ATP+L-citrulline+L-Aspartate,AMP+diphosphate+2-(Nomega-L-arginino)succinate,false"
 "v₂,2-(Nomega-L-arginino)succinate,L-arginine+fumarate,false"
 "v₃,L-arginine+H2O,Urea+L-ornithine,false"
 "v₄,L-ornithine+carbamoylphosphate,L-citrulline+phosphate,false"
 "v₅,2*L-arginine+3*NADPH+3*H+4*O2,2*L-citrulline+2*nitricoxide+3*NADP+4*H2O,true"
 "b₁,Ø,carbamoylphosphate,false"
 "b₂,Ø,L-Aspartate,false"
 "b₃,fumarate,Ø,false"
 "b₄,Urea,Ø,false"
 "b₅,Ø,H2O,true"
 "b₆,phosphate,Ø, true"
 "b₇,diphosphate,Ø, true"
 "b₈,AMP,Ø, false"
 "b₉,Ø, ATP,false"
 "b₁₀,NADPH,Ø, false"
 "b₁₁,H,Ø, false"
 "b₁₂,O2,Ø, true"
 "b₁₃,Ø, NADP,false"
 "b₁₄,Ø, nitricoxide,false"
julia> show(stdout, "text/plain", RCA)
19×19 Matrix{Int64}:
 6  1  0  1  1  0  1  0  0  0  0  1  1  1  0  0  0  0  0
 1  3  1  0  1  0  0  1  0  0  0  0  0  0  0  0  0  0  0
 0  1  4  1  2  0  0  0  1  1  0  0  0  0  0  0  0  0  0
 1  0  1  4  1  1  0  0  0  0  1  0  0  0  0  0  0  0  0
 1  1  2  1  8  0  0  0  0  1  0  0  0  0  1  1  1  1  1
 0  0  0  1  0  1  0  0  0  0  0  0  0  0  0  0  0  0  0
 1  0  0  0  0  0  1  0  0  0  0  0  0  0  0  0  0  0  0
 0  1  0  0  0  0  0  1  0  0  0  0  0  0  0  0  0  0  0
 0  0  1  0  0  0  0  0  1  0  0  0  0  0  0  0  0  0  0
 0  0  1  0  1  0  0  0  0  1  0  0  0  0  0  0  0  0  0
 0  0  0  1  0  0  0  0  0  0  1  0  0  0  0  0  0  0  0
 1  0  0  0  0  0  0  0  0  0  0  1  0  0  0  0  0  0  0
 1  0  0  0  0  0  0  0  0  0  0  0  1  0  0  0  0  0  0
 1  0  0  0  0  0  0  0  0  0  0  0  0  1  0  0  0  0  0
 0  0  0  0  1  0  0  0  0  0  0  0  0  0  1  0  0  0  0
 0  0  0  0  1  0  0  0  0  0  0  0  0  0  0  1  0  0  0
 0  0  0  0  1  0  0  0  0  0  0  0  0  0  0  0  1  0  0
 0  0  0  0  1  0  0  0  0  0  0  0  0  0  0  0  0  1  0
 0  0  0  0  1  0  0  0  0  0  0  0  0  0  0  0  0  0  1
julia>
```

v5>v1>v3=v4>v2>b1=b2=b3=b4=b5=b6=b7=b8=b9=b10=b11=b12=b13=b14
MCA:

```
julia> show(stdout, "text/plain", species_array)
18-element Vector{String}:
 "2-(Nomega-L-arginino)succinate"
 "AMP"
 "ATP"
 "H"
 "H2O"
 "L-Aspartate"
 "L-arginine"
 "L-citrulline"
 "L-ornithine"
 "NADP"
 "NADPH"
 "O2"
 "Urea"
 "carbamoylphosphate"
 "diphosphate"
 "fumarate"
 "nitricoxide"
 "phosphate"
julia> show(stdout, "text/plain", MCA)
18×18 Matrix{Int64}:
 2  1  1  0  0  1  1  1  0  0  0  0  0  0  1  1  0  0
 1  2  1  0  0  1  0  1  0  0  0  0  0  0  1  0  0  0
 1  1  2  0  0  1  0  1  0  0  0  0  0  0  1  0  0  0
 0  0  0  2  1  0  1  1  0  1  1  1  0  0  0  0  1  0
 0  0  0  1  3  0  2  1  1  1  1  1  1  0  0  0  1  0
 1  1  1  0  0  2  0  1  0  0  0  0  0  0  1  0  0  0
 1  0  0  1  2  0  3  1  1  1  1  1  1  0  0  1  1  0
 1  1  1  1  1  1  1  3  1  1  1  1  0  1  1  0  1  1
 0  0  0  0  1  0  1  1  2  0  0  0  1  1  0  0  0  1
 0  0  0  1  1  0  1  1  0  2  1  1  0  0  0  0  1  0
 0  0  0  1  1  0  1  1  0  1  2  1  0  0  0  0  1  0
 0  0  0  1  1  0  1  1  0  1  1  2  0  0  0  0  1  0
 0  0  0  0  1  0  1  0  1  0  0  0  2  0  0  0  0  0
 0  0  0  0  0  0  0  1  1  0  0  0  0  2  0  0  0  1
 1  1  1  0  0  1  0  1  0  0  0  0  0  0  2  0  0  0
 1  0  0  0  0  0  1  0  0  0  0  0  0  0  0  2  0  0
 0  0  0  1  1  0  1  1  0  1  1  1  0  0  0  0  2  0
 0  0  0  0  0  0  0  1  1  0  0  0  0  1  0  0  0  2
julia>
```

"2-(Nomega-L-arginino)succinate"
"AMP"
"ATP"
"H"
"H2O"
"L-Aspartate"
"L-arginine"
"L-citrulline"
"L-ornithine"
"NADP"
"NADPH"

"O2"
"Urea"
"carbamoylphosphate"
"diphosphate"
"fumarate"
"nitricoxide"
"phosphate"

"H2O"= "L-arginine"= "L-citrulline">every other species (which all are equal in connectivity)

I do not see much of a correlation between extreme pathways and reaction connectivities. The reaction with the most connections (v5) is in the least number of extreme pathways (only 1). Unless that itself is a correlation and points towards that extreme pathway being the most likely of the bunch.