1. $\boldsymbol{A} = \begin{pmatrix} 5 & 3 & 1 \\ 3 & 2 & 1 \\ 1 & 1 & 1 \end{pmatrix}$

   a. $\boldsymbol{b}_0 = \begin{pmatrix} 1 \\ 2 \\ 3 \end{pmatrix}, \widehat{\boldsymbol{b}}_0 = \begin{pmatrix} \frac{1}{\sqrt{14}} \\ \frac{2}{\sqrt{14}} \\ \frac{3}{\sqrt{14}} \end{pmatrix}$

   b. $\boldsymbol{b}_1 = \boldsymbol{A}\boldsymbol{b}_0 = \begin{pmatrix} 3.7417 \\ 2.6726 \\ 1.6036 \end{pmatrix}, \widehat{\boldsymbol{b}}_1 = \begin{pmatrix} 0.7683 \\ 0.5488 \\ 0.3293 \end{pmatrix}$

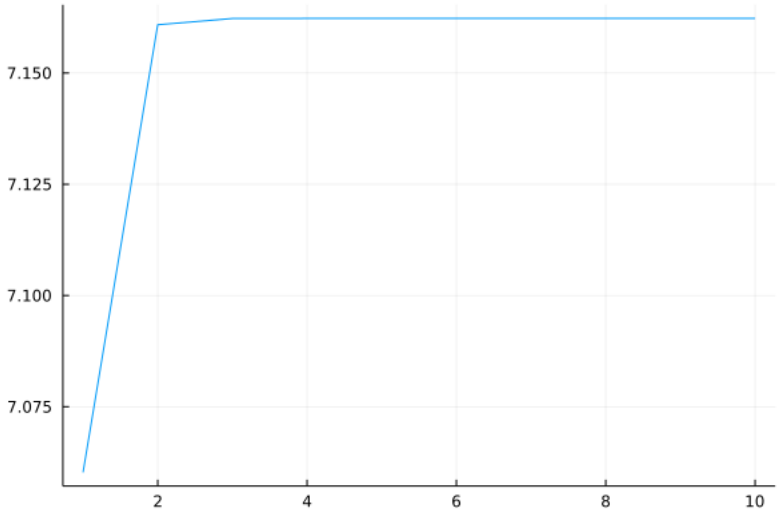
   c. $\lambda_{max} = 7.0602$

   d.

Iter.	1	2	3	4	5	6	7	8	9	10
$\widehat{\boldsymbol{b}}_{\#}$	$\begin{pmatrix} 0.7683 \\ 0.5488 \\ 0.3293 \end{pmatrix}$	$\begin{pmatrix} 0.8188 \\ 0.5253 \\ 0.2317 \end{pmatrix}$	$\begin{pmatrix} 0.8240 \\ 0.5220 \\ 0.2200 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5217 \\ 0.2187 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5216 \\ 0.2185 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5216 \\ 0.2185 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5216 \\ 0.2185 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5216 \\ 0.2185 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5216 \\ 0.2185 \end{pmatrix}$	$\begin{pmatrix} 0.8247 \\ 0.5216 \\ 0.2185 \end{pmatrix}$
λ_{max}	7.0602	7.1609	7.1623	7.1623	7.1623	7.1623	7.1623	7.1623	7.1623	7.1623

   e. Eigenvalue max = 7.1623, so yes.

   f.



      i. About 3 iterations for a value accurate within 4 decimal places.

   g. The ratio between the max eigenvalue and second largest eigenvalue was rather large (7.1623/0.8377) resulting in a high rate of convergence.

2. Centrality

a.
$$\begin{pmatrix} Protein & PI3K & RAS & PKC & PLC & PIP3 & PIP2 \\ PI3K & 0 & 1 & 0 & 0 & 1 & 1 \\ RAS & 1 & 0 & 1 & 0 & 0 & 0 \\ PKC & 0 & 1 & 0 & 1 & 0 & 1 \\ PLC & 0 & 0 & 1 & 0 & 1 & 1 \\ PIP3 & 1 & 0 & 0 & 1 & 0 & 1 \\ PIP2 & 1 & 0 & 1 & 1 & 1 & 0 \end{pmatrix}$$

b. Leading eigenvector is: $\begin{pmatrix} -0.3851 \\ -0.2473 \\ -0.3851 \\ -0.4294 \\ -0.4294 \\ -0.5230 \end{pmatrix}, \lambda = 3.1149$

c. Most central is PIP2, least central is RAS, and this matches up directly to the number of connections each protein has. PIP2 has the most (4) and RAS has the least (2). The protein with the largest number of direct connections is not always the most central node. Centrality is also determined by the centrality of the nodes it is connected to.