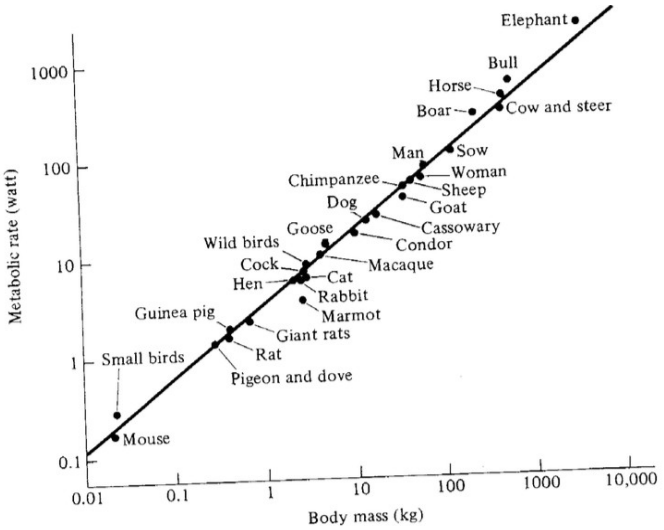
Aging, Lifespan & Metabolism

- Ageing and lifespan regulated by metabolism
- Free radical theory provides potential mechanism that links metabolism to aging
- Ageing due to accumulation of free radical damage over time
- Free radical formed as the by-product of oxidative phosphorylation
- Damage DNA by attacking sugar-phosphate backbone or the base or via lipid peroxidates

Metabolic Rate

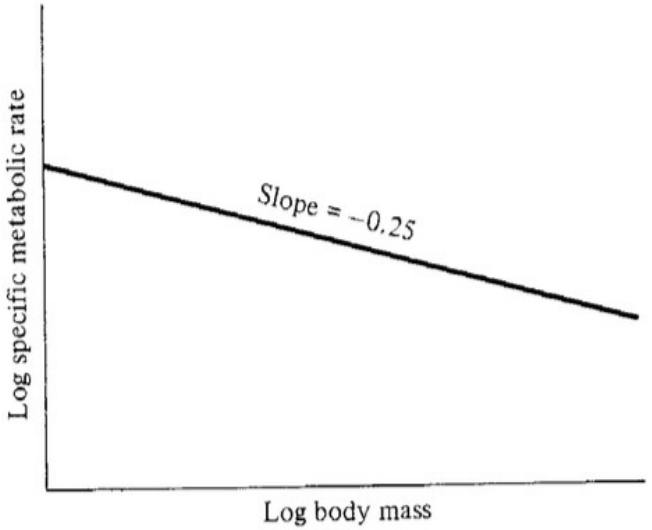
- The total use or turnover of chemical energy
- Increases as body mass\size increases
- Not appropriate for inter-species study of metabolism
- Adaptive features affect metabolic rate



Specific Metabolic Rate

- Metabolic rate per unit mass
- Obtained by dividing metabolic rate by body mass
- More appropriate for inter-species metabolic study
- Decreases as the as the body size\mass increases
- Indicate, per unit body mass metabolism is higher in small than in large animals
- Studies show that a gram of tissue on average expand same amount of energy before it dies regardless the organism

Figure 6.3. The specific metabolic rate (P^*_{met}, the metabolic rate per unit body mass, M_b) decreases with increasing body size, the regression line having a slope of -0.25.



Base of Project

- Ageing and longevity depend on free radical and metabolism
- If ageing and longevity depend on free radical, they depend on oxidative phosphorylation and thus to mitochondrial proteins
- If ageing and longevity depend on metabolism, they depend on metabolic proteins
- If ageing and longevity depend on metabolism, they can be correlated with metabolic rate and thus to specific metabolic rate among different species
- If ageing and longevity can be correlated with specific metabolic rate they can be correlated with body mass\size of organism

Ageing and longevity depends on metabolic and mitochondrial protein, and can be correlated with the body mass\size of the organism

Objective

The object of the research is to perform a correlation study of proteins involved in both mitochondria and metabolism with respect to the size of the organism

Tools & Resources Used

- Virtual BioLinux Machine
- Tools & API :

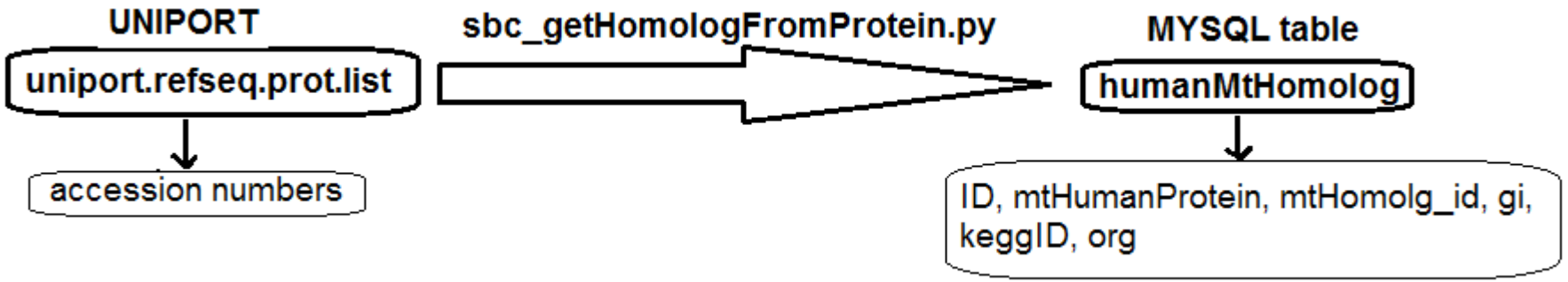
  python(biopython), KEGG REST API, mysql
- Database :

  uniport, NCBI homologene, KEGG

Approach

- List of Human mitochondrial proteins were obtained from Uniport. Filename: uniprot.refseq.prot.list (Provided by Ishwor)
- Python program “sbc_getHomologFromProtein.py” developed to obtain the respective homologous proteins, their gi number, keggID and the organism, of proteins in “uniprot.refseq.prot.list” and inserted in the table “humanMtHomolog”

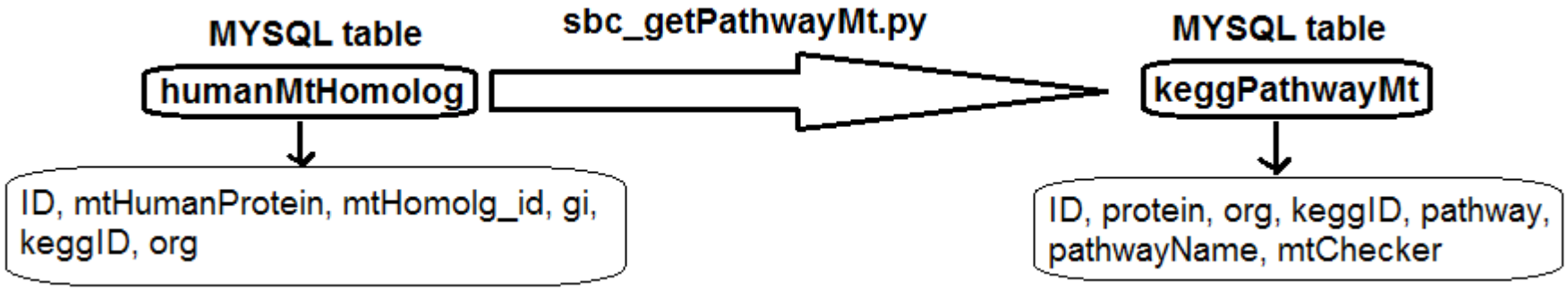
KEGG REST module slightly modified to allow organism independent gi conversion to keggID



Approach

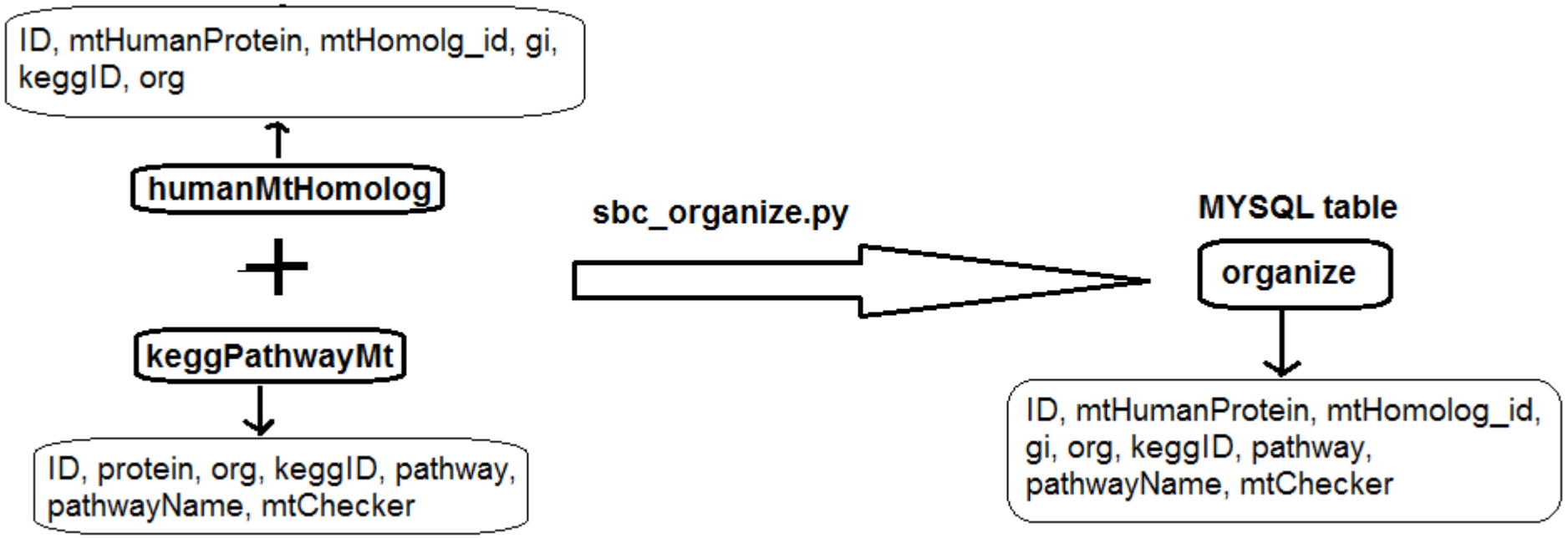
- Program “sbc_getPathwayMt.py” was developed to obtain the pathways ID, pathway name, and mitochondrial reference lines of the proteins in table “humanMtHomolog” and inserted in table “keggPathwayMt”

Hypothesis: If the protein is involved in a particular pathway then it can be said that it is involved in the particular process



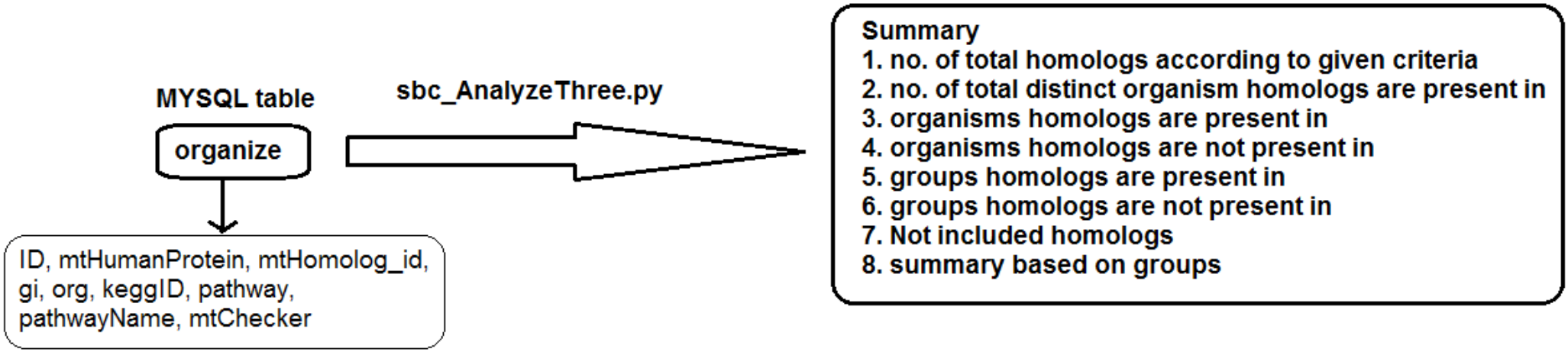
Approach

- Program “sbc_orgrnize.py” develop to combine data from table “humanMtHomolog” and “keggPathwayMt” to a single table called “organize” to make queries simpler



Approach

- Program “sbc_AnalyzeThree.py” develop to analyze the data from the “organize” table based on pathways entered by the user.
- Divides 21 organisms into a group of 11
- “sbc_AnalyzeThree.py” gives the summary of the set of homologs in terms of organisms the homologs are present in and not present in, groups the homologs are present in and not present in, not included homologs, and summary based on groups.



Groups

- **Size of organism decreases as group number increases**
- **Specific metabolic rate increases as group number increases**

Group1 = bta

Group2 = has, ptr

Group3 = mcc

Group4 = cfa

Group5 = gga

Group6 = mmu, rno

Group7 = xtr

Group8 = dre

Group9 = aga, dme

Group10 = spo, mgr, ncr, kla, ago, sce

Group11 = ath, osa

Search

- “sbc_AnalyzeThree.py” used to obtain the analysis on the following pathways sets:

  1. metabolic pathways
  2. oxidative phosphorylation
  3. metabolic pathways and oxidative phosphorylation

Result: Metabolic pathways

Proteins involved in metabolism = 359

Group1: 231

Group2: 307

Group3: 114

Group4: 188

Group5: 163

Group6: 251

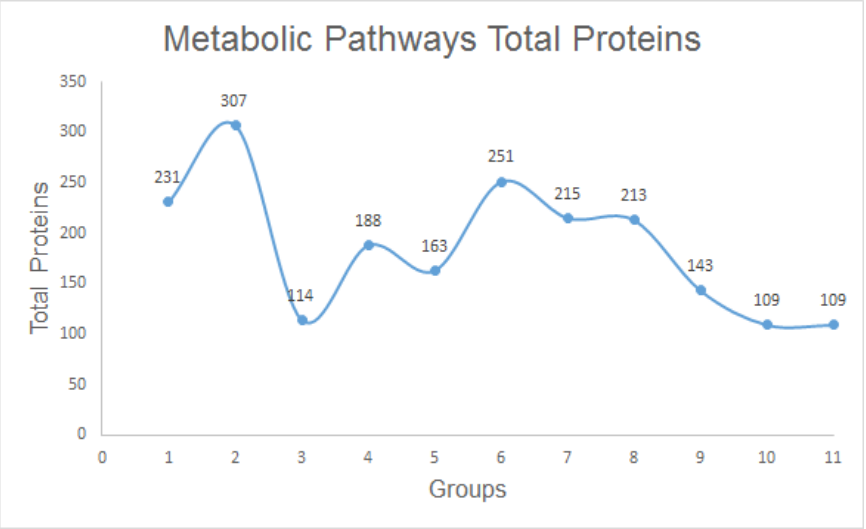
Group7: 215

Group8: 213

Group9: 143

Group10: 109

Group11: 109



Result: Oxidative phosphorylation

Proteins involved in oxidative phosphorylation = 113

Group1: 72 Group2: 102

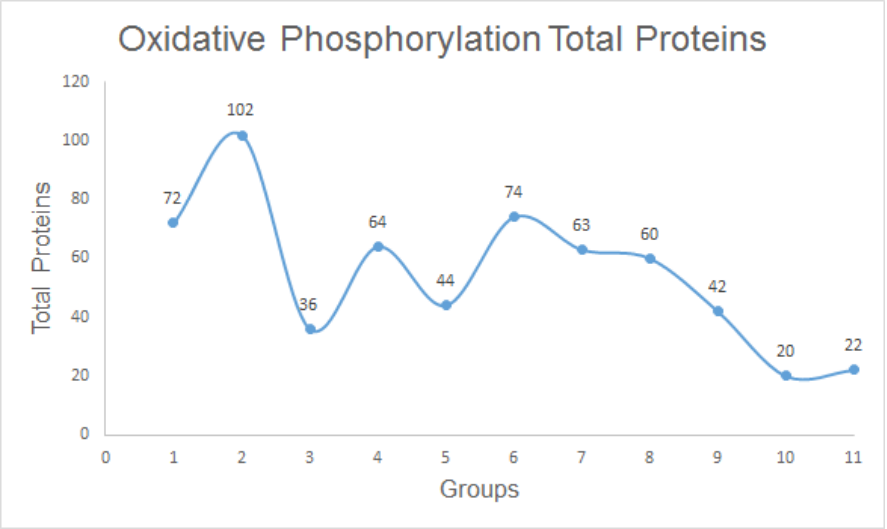
Group3: 36 Group4: 64

Group5: 44 Group6: 74

Group7: 63 Group8: 60

Group9: 42 Group10: 20

Group11: 22



Result: Metabolic and Oxidative Phosphorylation

Proteins involved in metabolism and oxidative phosphorylation= 108

Group1: 68 Group2: 98

Group3: 33 Group4: 61

Group5: 42 Group6: 70

Group7: 60 Group8: 57

Group9: 42 Group10: 20

Group11: 22