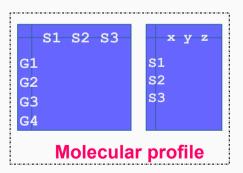
Architecture for PDX class

By Arvind Mer

Model Id	Mol. profile id	
M1	S1	
M2	S2	
мз	S2	



meta						
Model Id	M1					
Drug Id	D1					
Time	Days					
Dose	microMol	d	ata			
Response	Volume3		ala			
Weight	gram	Time	0	4	8	
IC50	0.6	Dose	0.5	NA	0.5	•
AUC	0.8	Response	0.9	0.6	0.4	
		Weight	100	NA	50	

meta	3					
Model Id	M1	da	ata			
Drug Id	D2	Time	0	2	3	
Time	Days	Dose	0.5	NA	0.5	
• •		Response	NA	0.6	0.4	

meta	meta				
Model Id	M2				
Drug Id	D2				
Time	Days	data			
Dose	microMol	Time	0	15	
Response	Volume3	Dose	0.5	0.5	
Weight	gram	Response	0.9	0.6	
		Weight	100	NA	

Experiments

Architecture for PDX class

Molecular profile: List of Biobase objects containing RNASeq, micro-array data etc.

Model :

- Information about each model used in experiments
- "Model Id" and "Molecular Profile Id" are required
- "Model Id" will be used in experiments
- "Molecular Profile Id" will be used to map model to molecular profile
- Multiple models can have same "Molecular Profile Id"

Drug:

- Information about all the drugs used in experiments
- "Drug Id" is required
- "Drug Id" will be used in experiments
- Experiments: This is list of objects from class "PDX_Experiments"
 - Class "PDX_Experiments" will have 2 slots
 - meta :
 - This will hold all the necessary meta information
 - "Model Id" and "Drug Id" is required
 - Other variables can be unit of experiment time (days, weeks etc.), AUC etc.

Data :

- This will hold all the experimental data
- Will have variable such as time, dose and response etc.
- The variable can be NA