

# Architecture for PDX class

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Drug Id	drug name	compound .name	.
D1			
D2			
D3			

Drug

Model Id	Mol. profile id	.
M1	S1	
M2	S2	
M3	S2	

Model

	S1	S2	S3		x	y	z
G1					S1		
G2					S2		
G3					S3		
G4							

Molecular profile

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

meta						
Model Id	M1					
Drug Id	D2					
Time	Days					
..	..					
		data				
Time		0	2	3	.	
Dose		0.5	NA	0.5	.	
Response		NA	0.6	0.4	.	

meta				
Model Id	M2			
Drug Id	D2			
Time	Days			
Dose	microMol			
Response	Volume3			
Weight	gram			
..	..			
		data		
Time		0	15	
Dose		0.5	0.5	
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