

new and improved

The chado *genetics* module

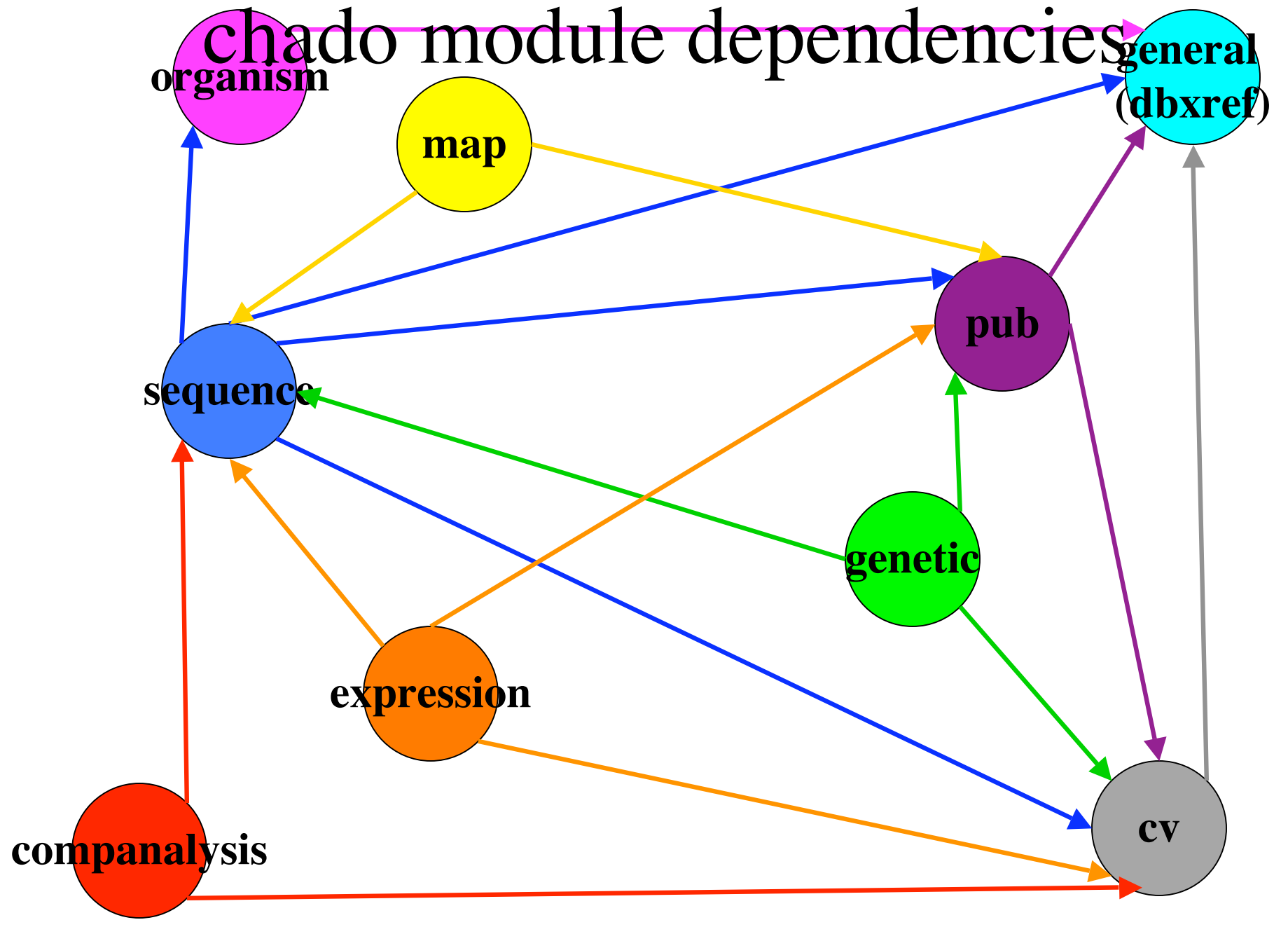
GMOD Meeting

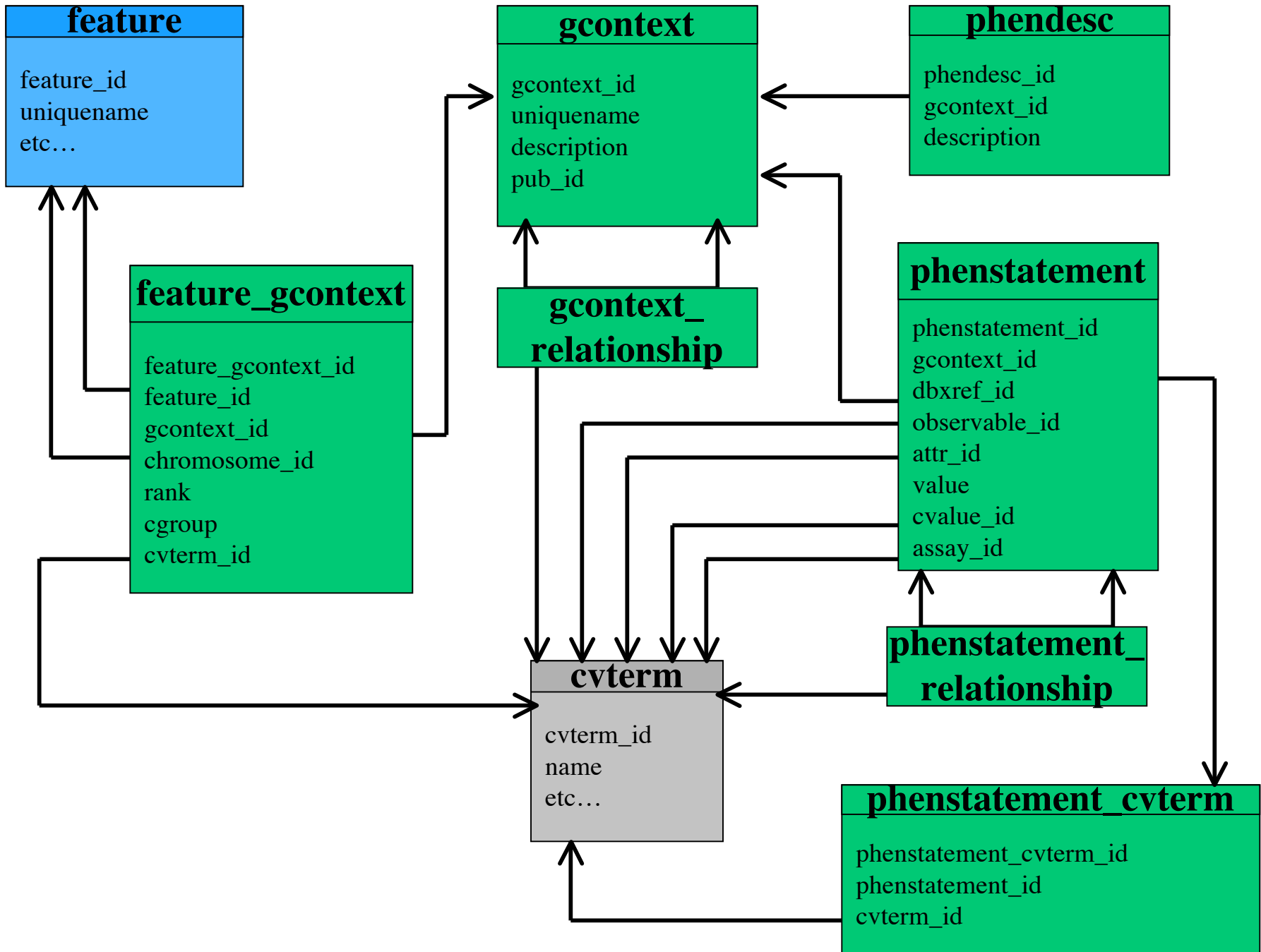
4/26/2004

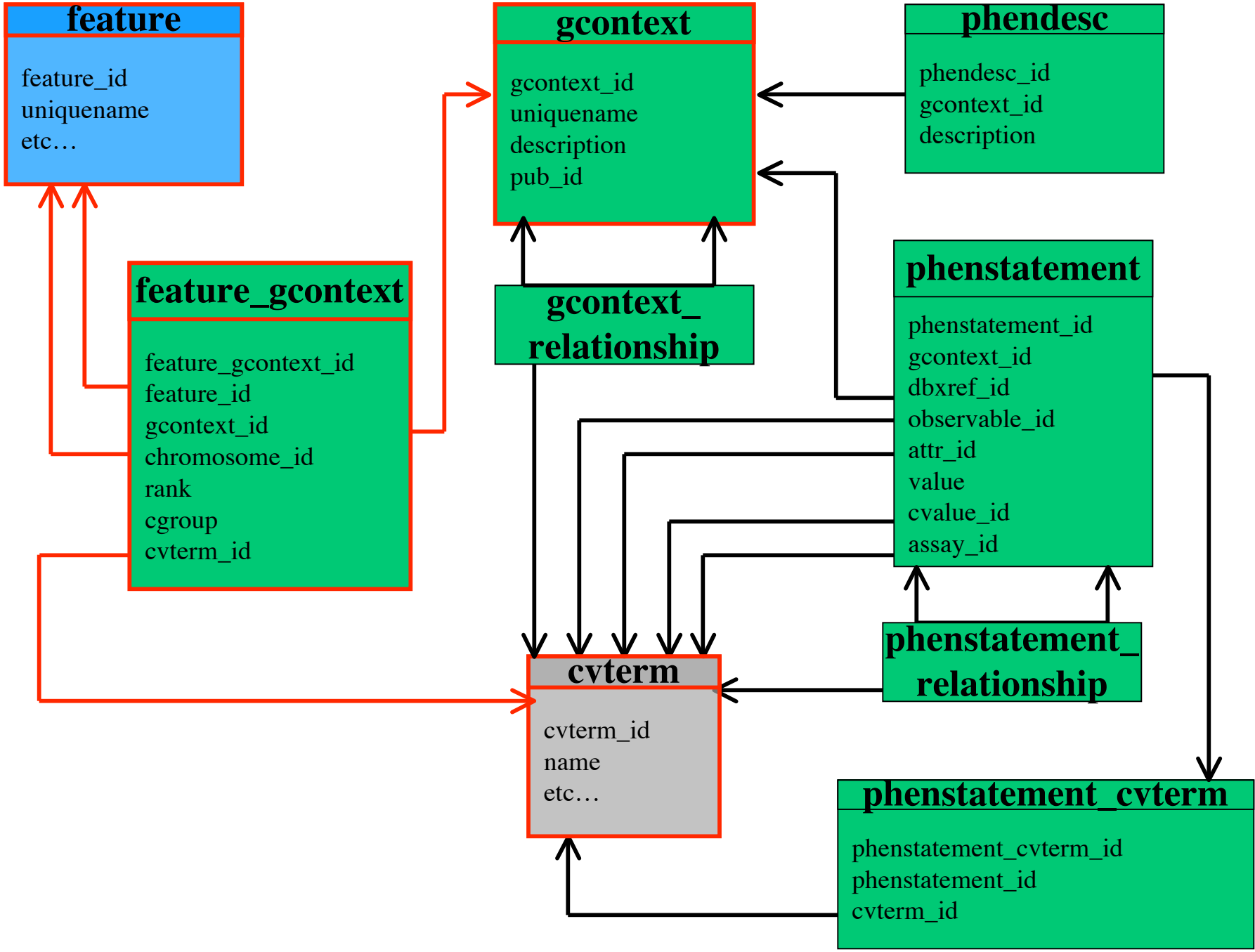
Cambridge, MA

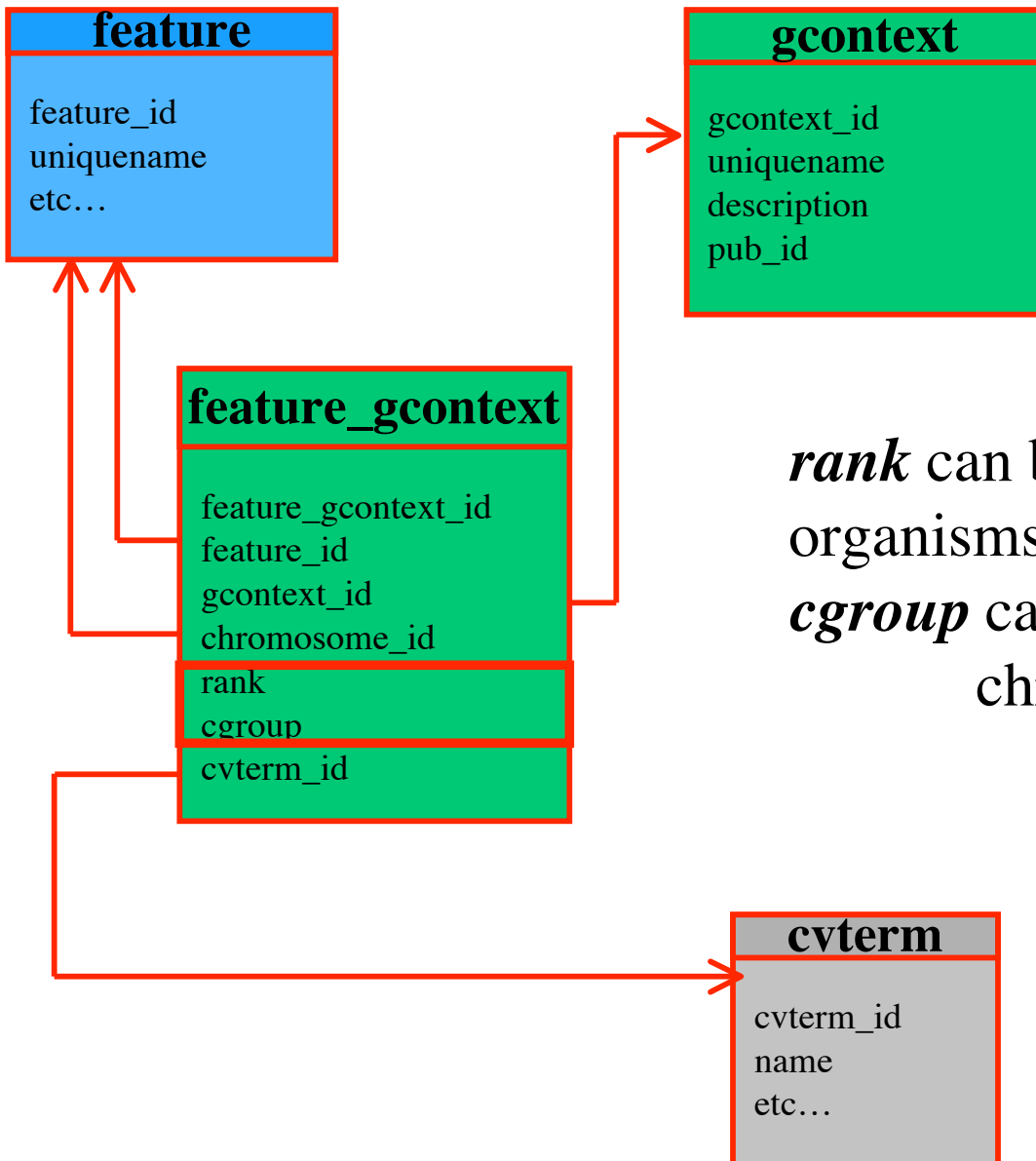
David Emmert
FlyBase - Harvard
emmert@morgan.harvard.edu

chado module dependencies



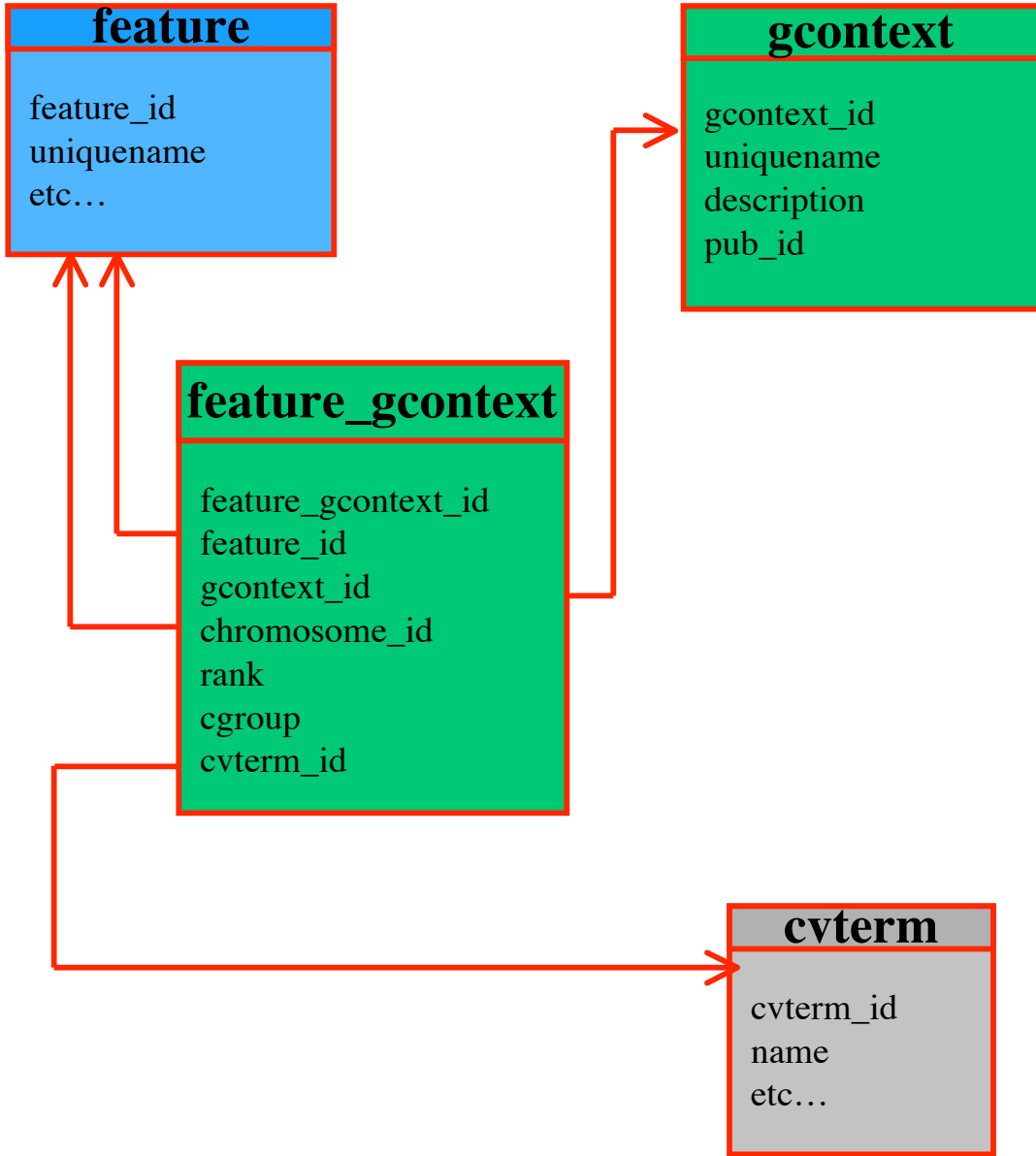






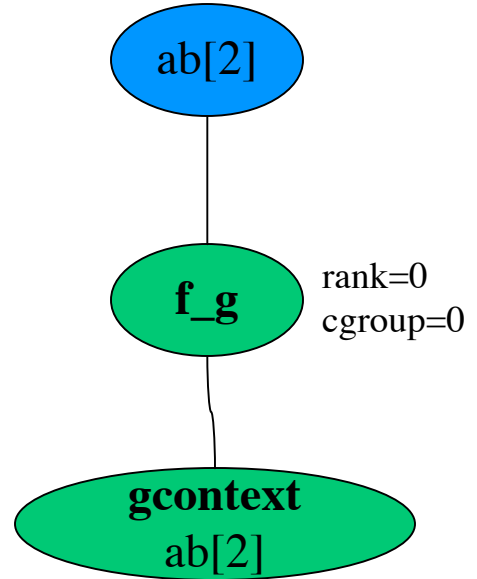
rank can be used for n-ploid organisms.

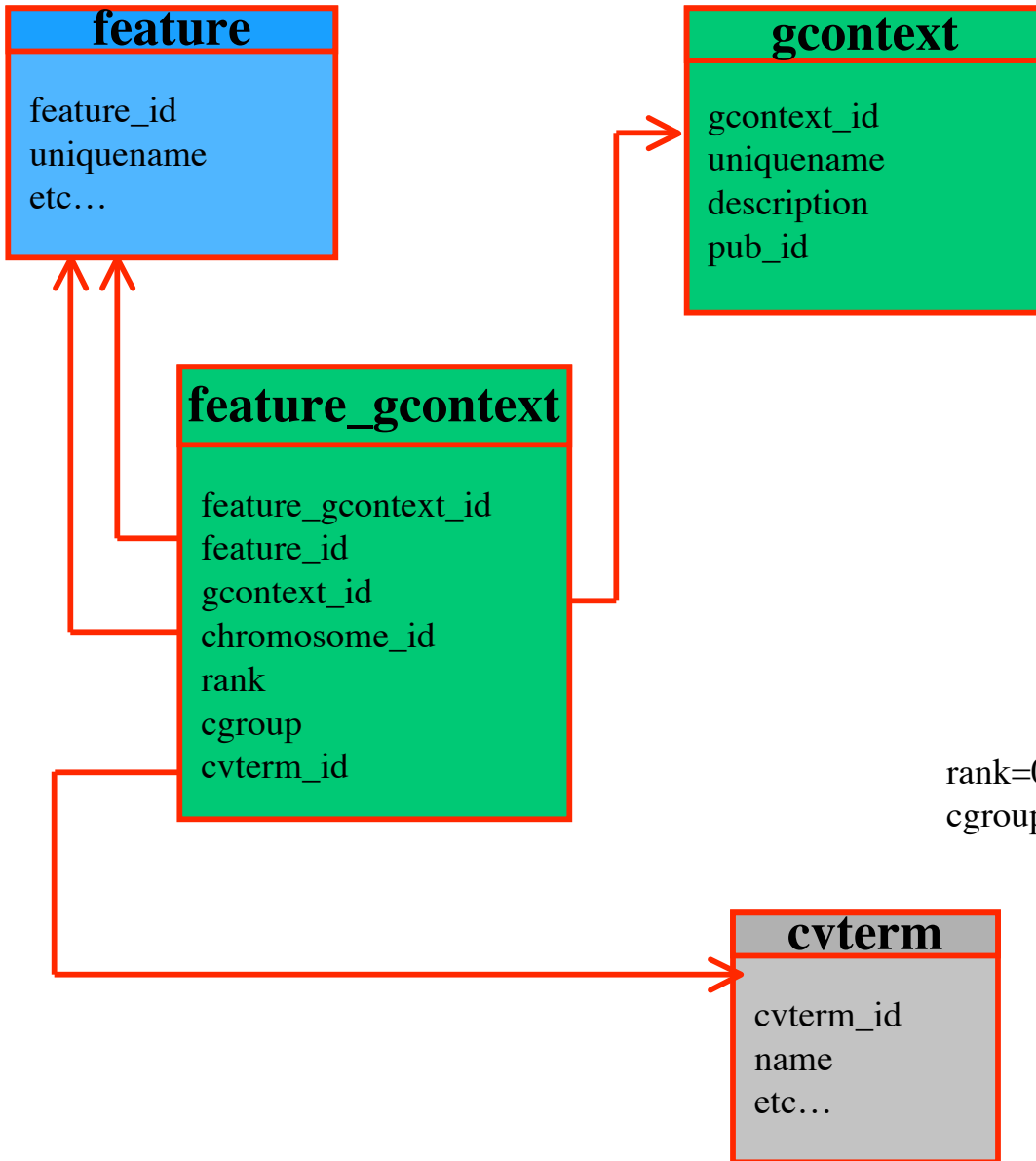
cgroup can be used for distinguishing chromosomal groups



Partial Genotype
(aka: allele)

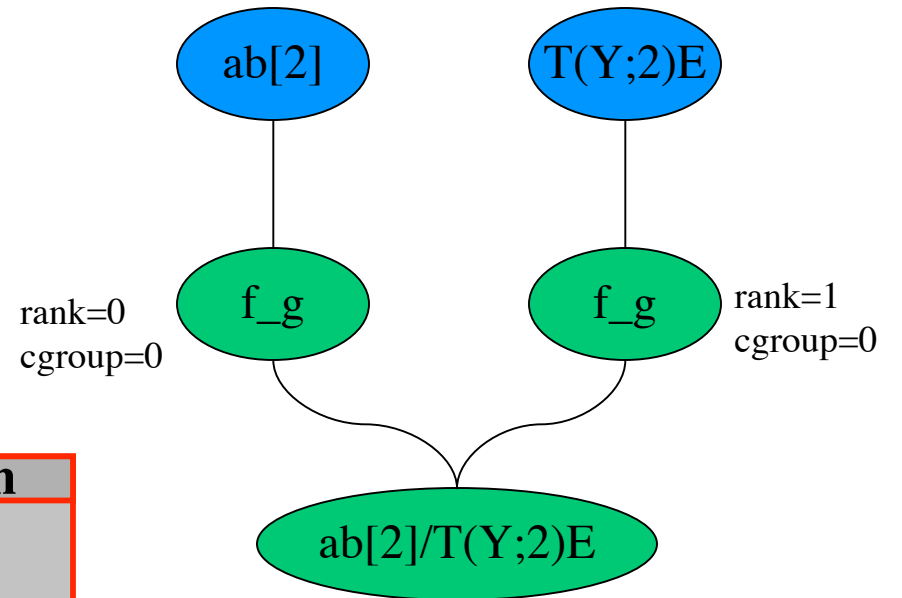
ab[2]

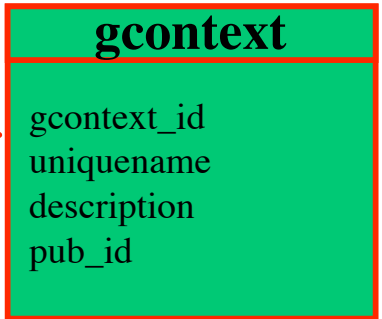
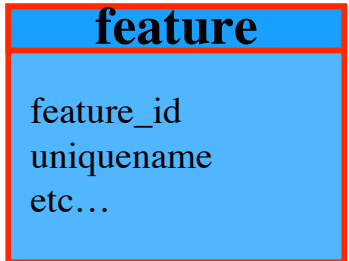




Simple Stock Genotype

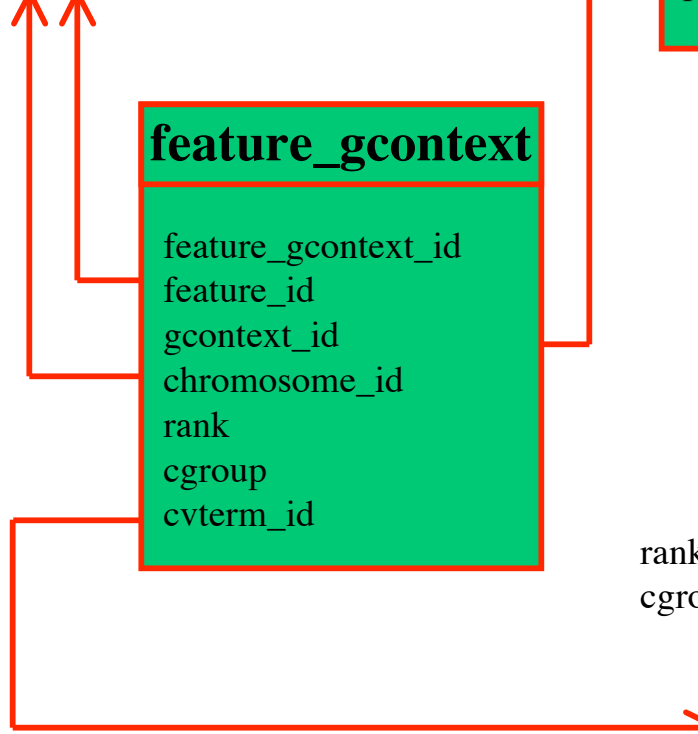
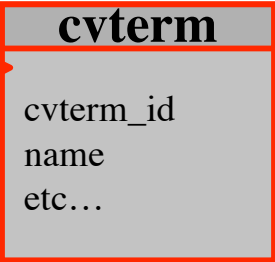
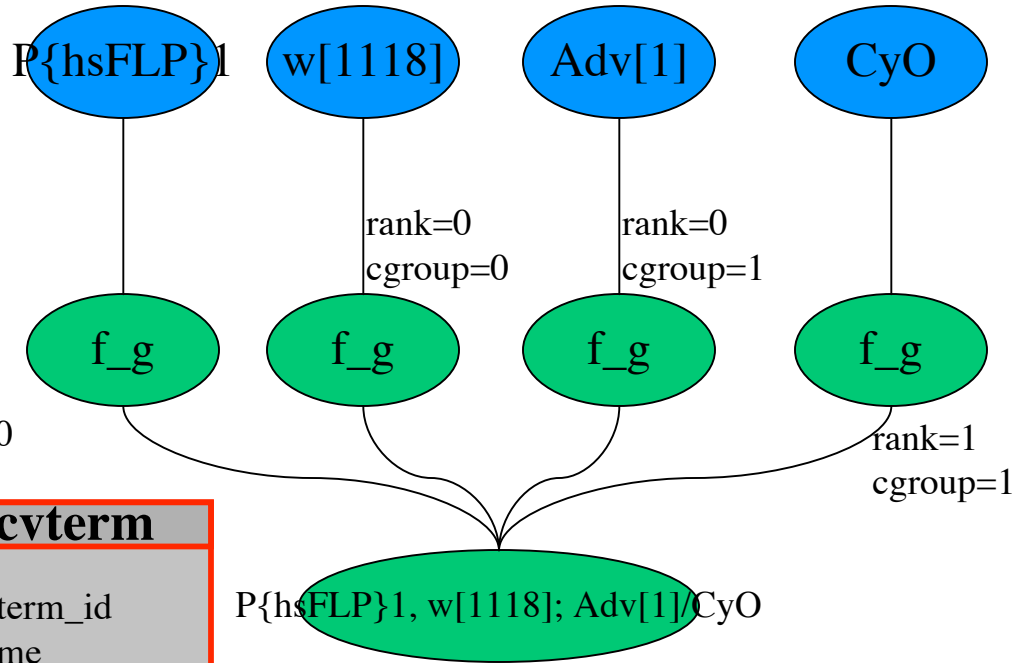
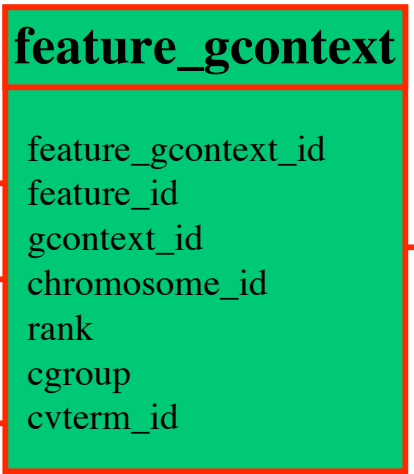
ab[2]/T(Y;2)E

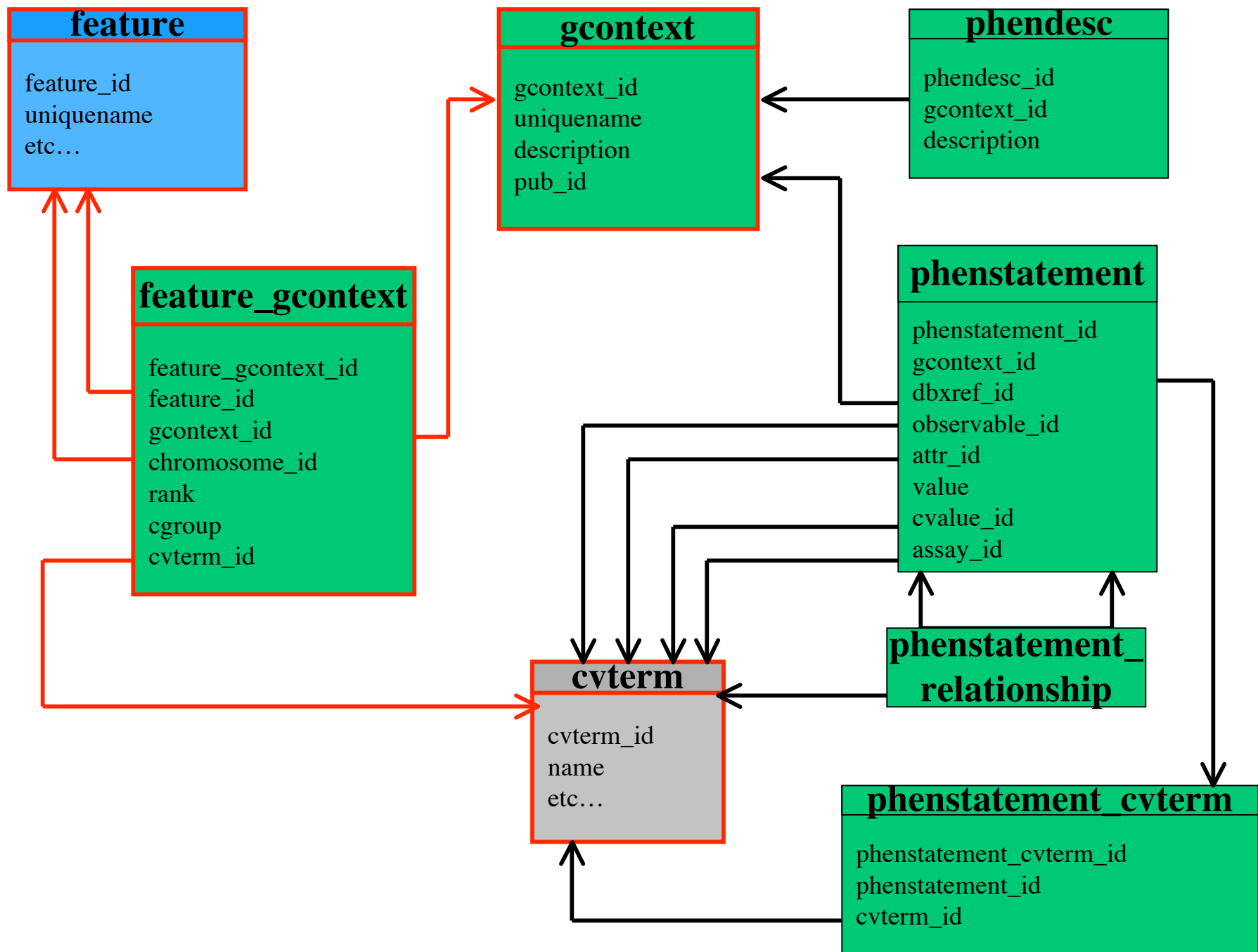


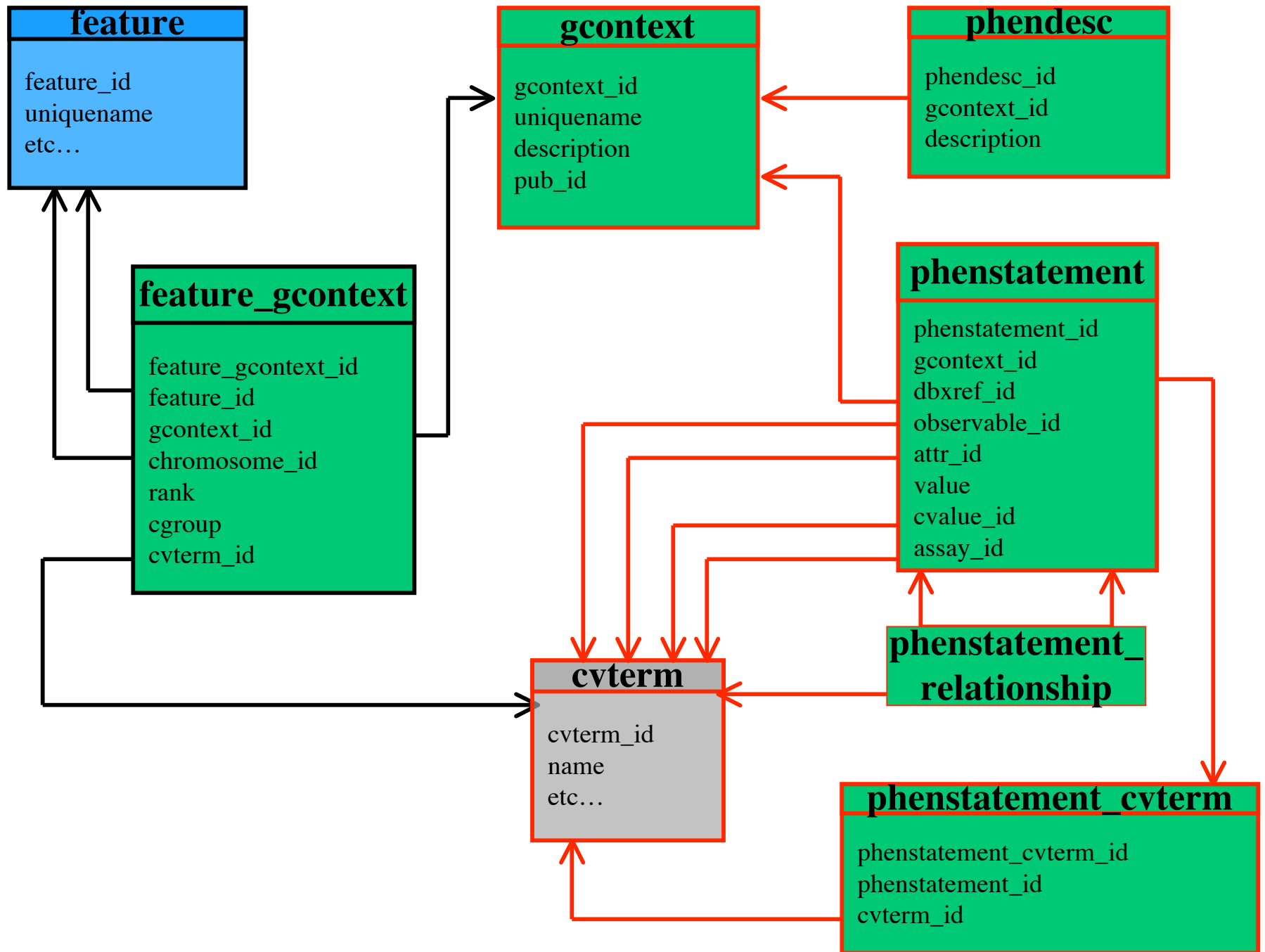


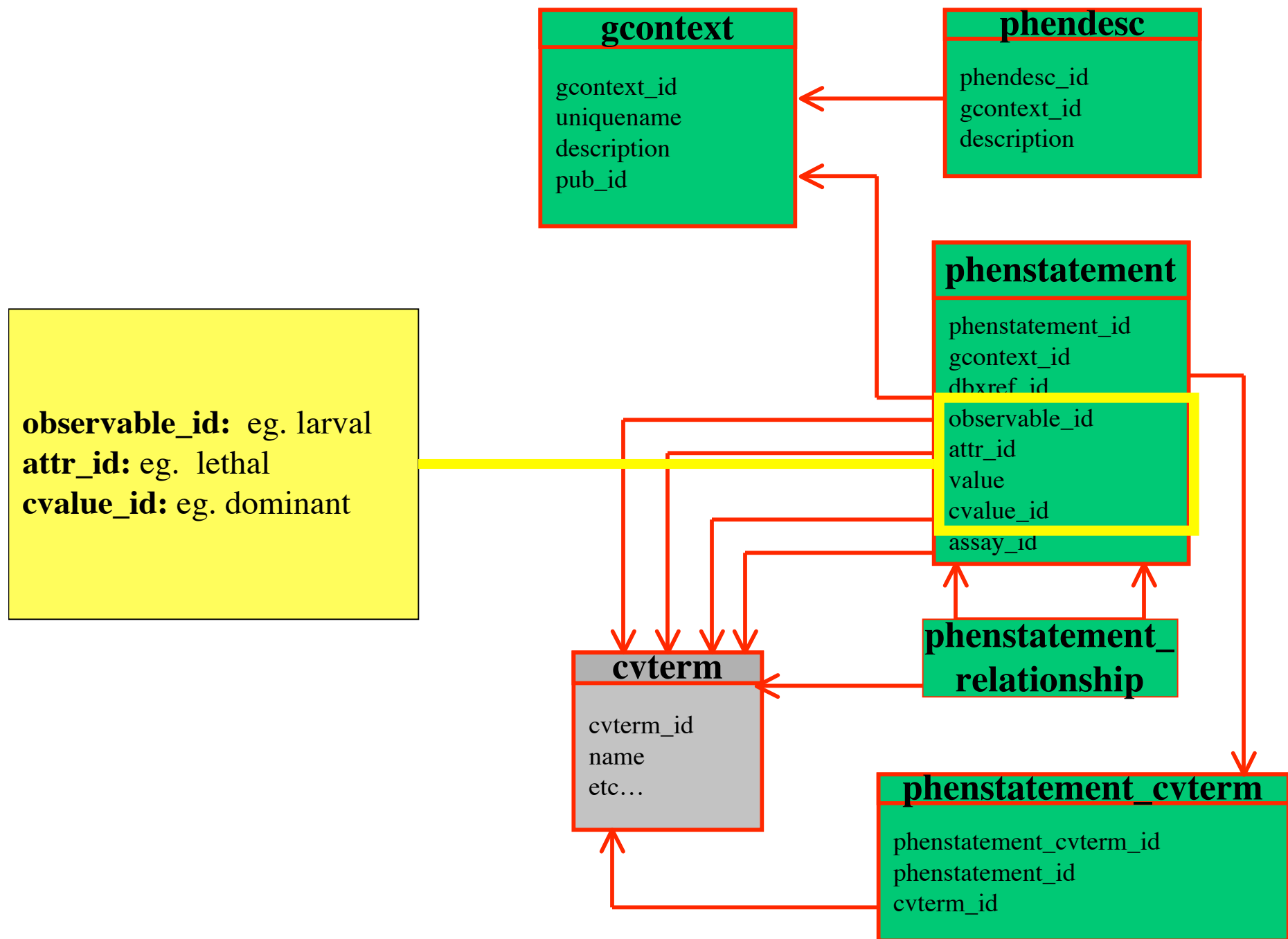
Stock Genotype I:

P{hsFLP}1, w[1118]; Adv[1]/CyO



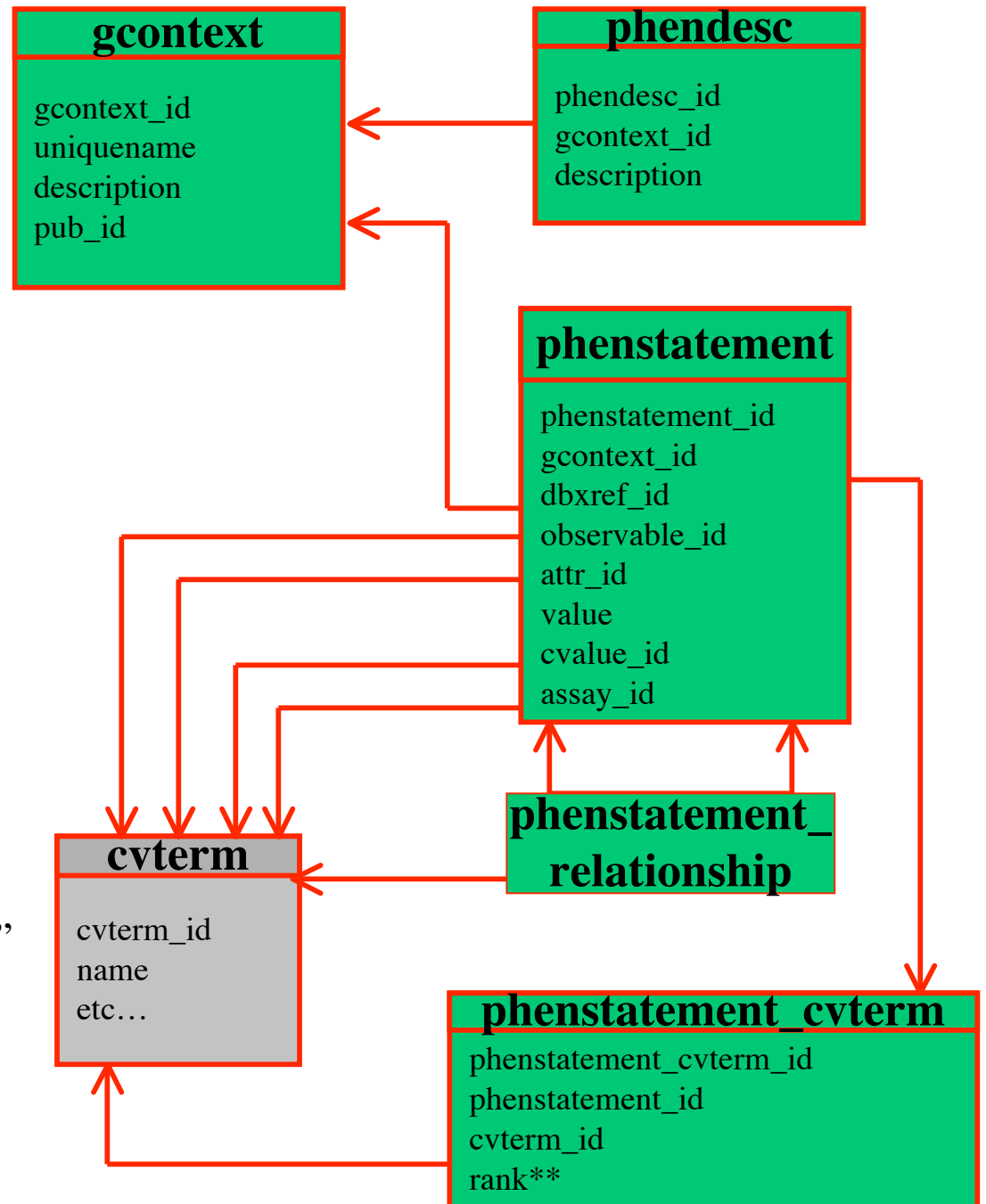
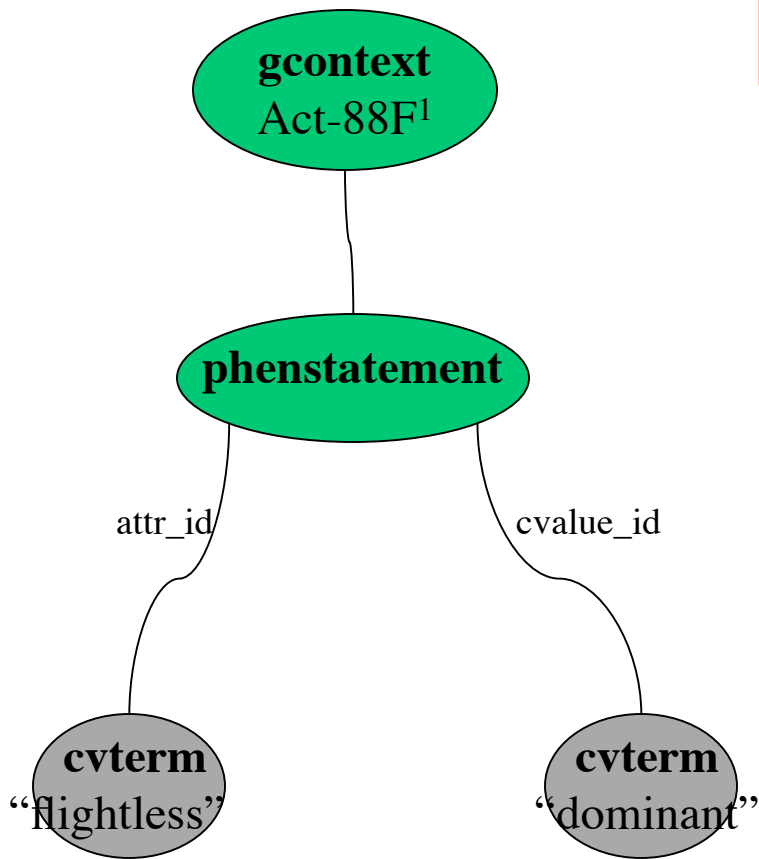






Allele phenotype Act-88F¹

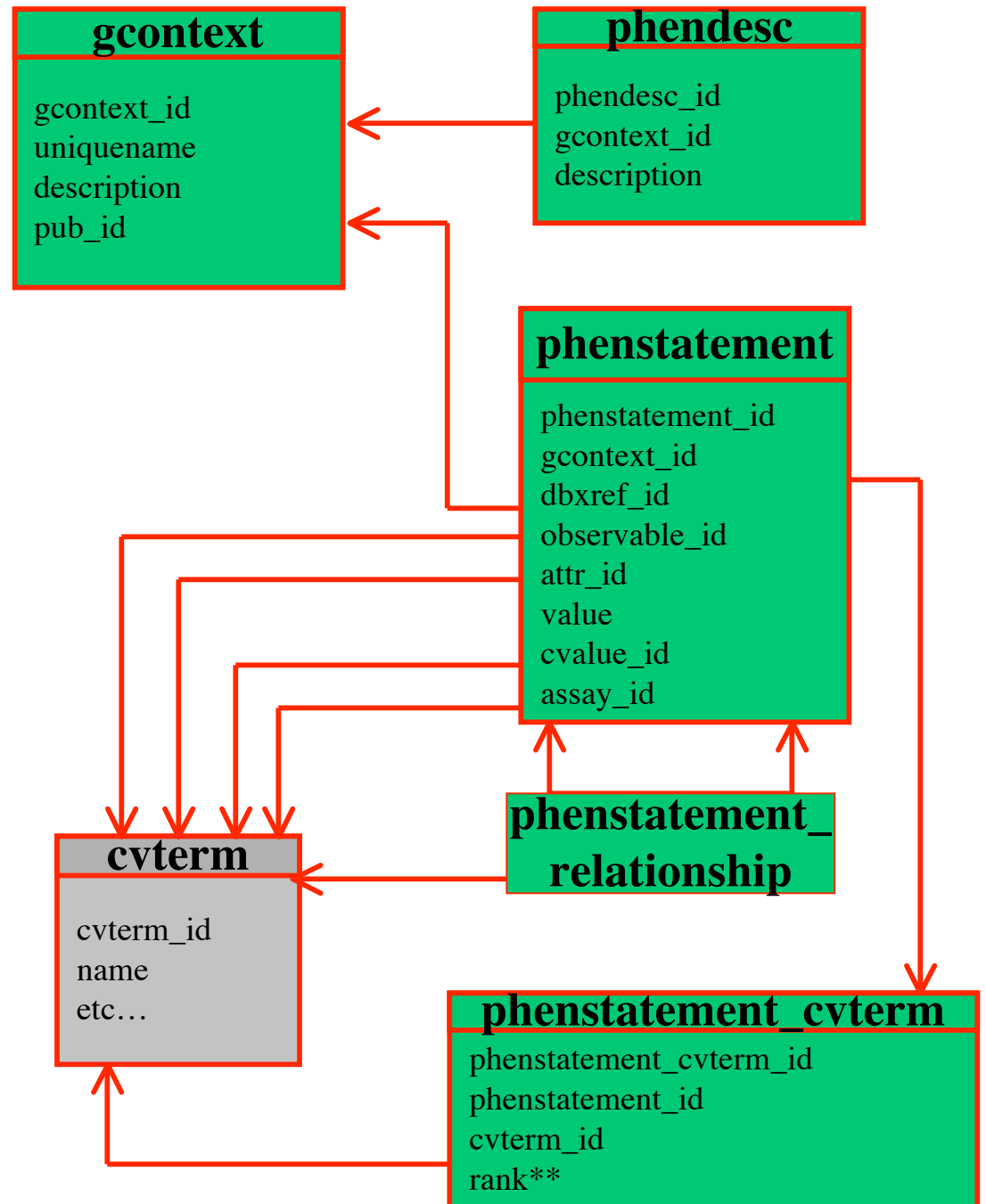
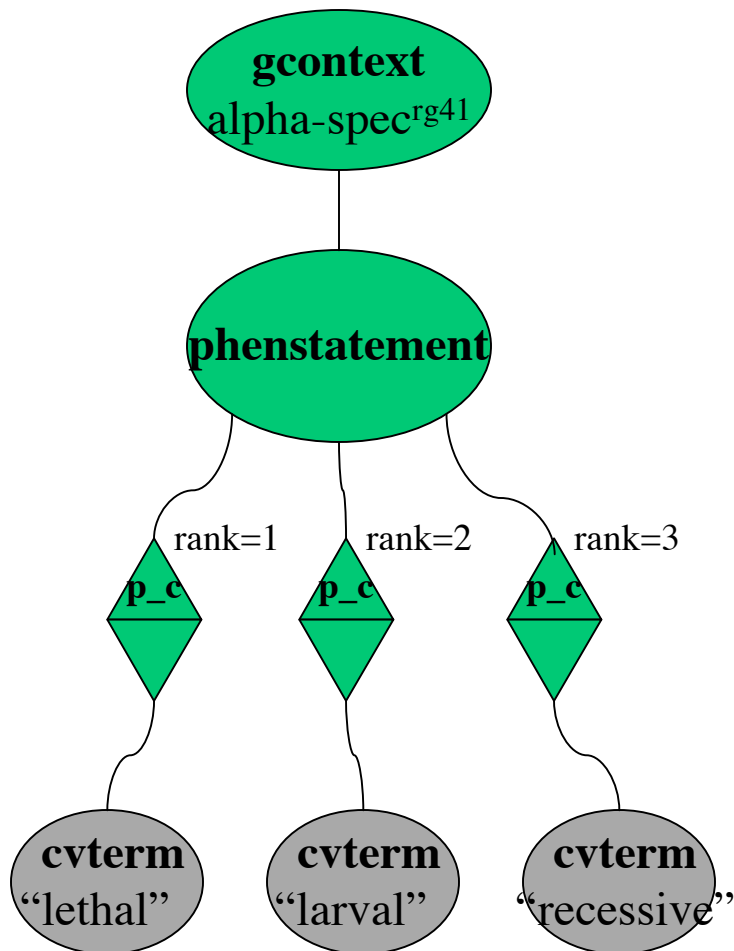
Phenotypic class:
flightless | dominant



Allele phenotype $\alpha\text{-spec}^{\text{rg41}}$

Phenotypic class:

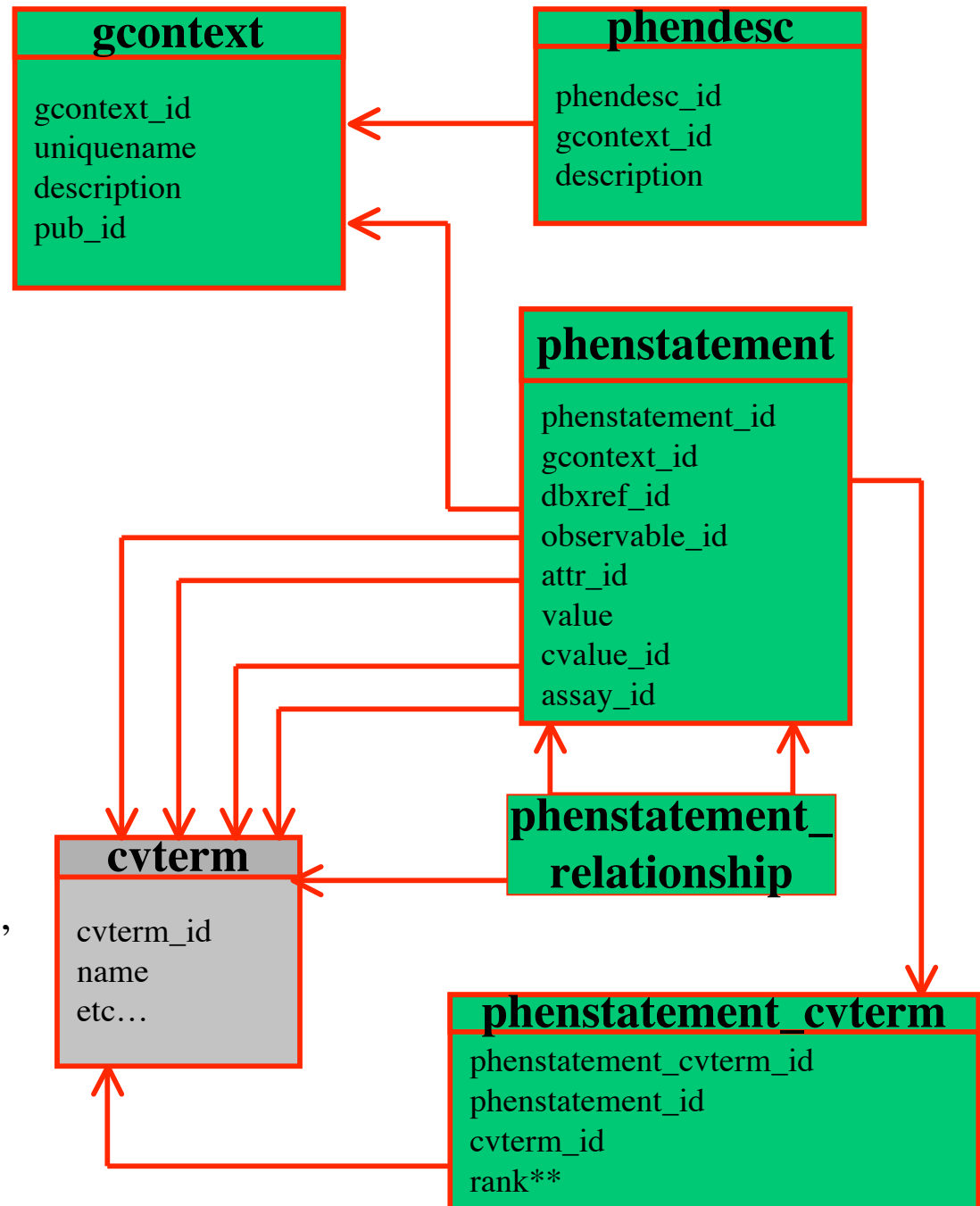
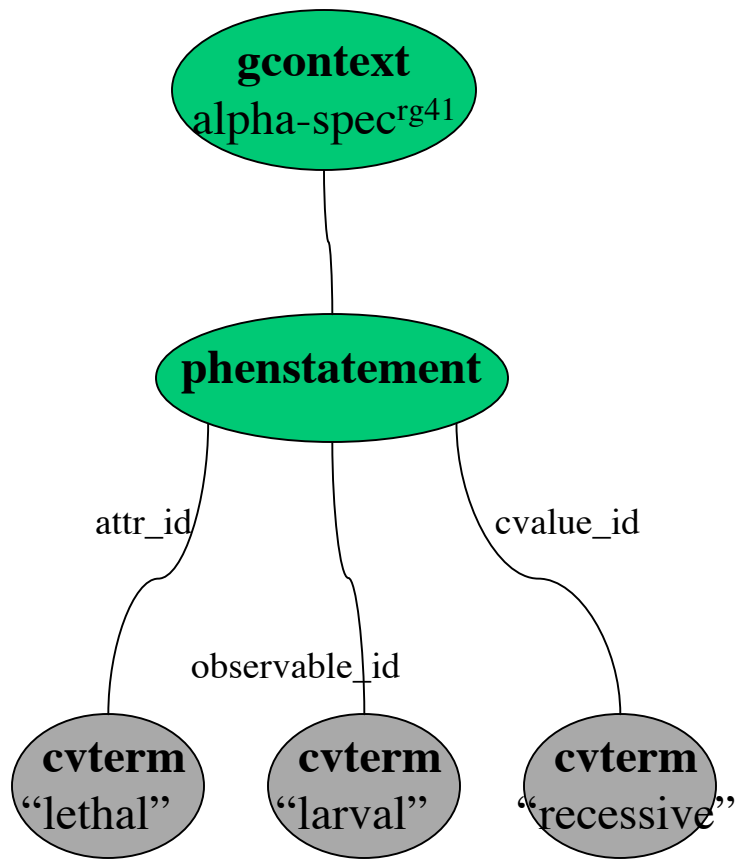
lethal | larval | recessive



Allele phenotype α -spec^{rg41}

Phenotypic class:

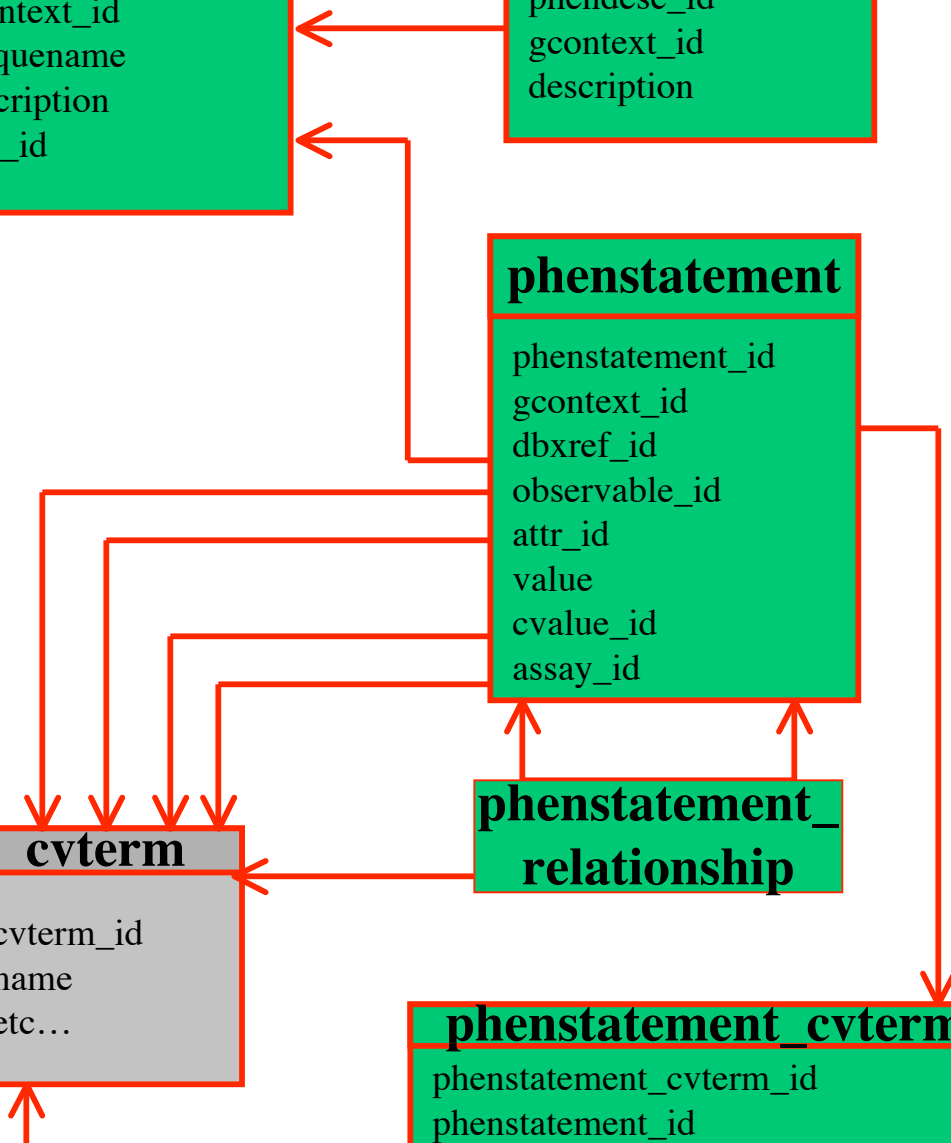
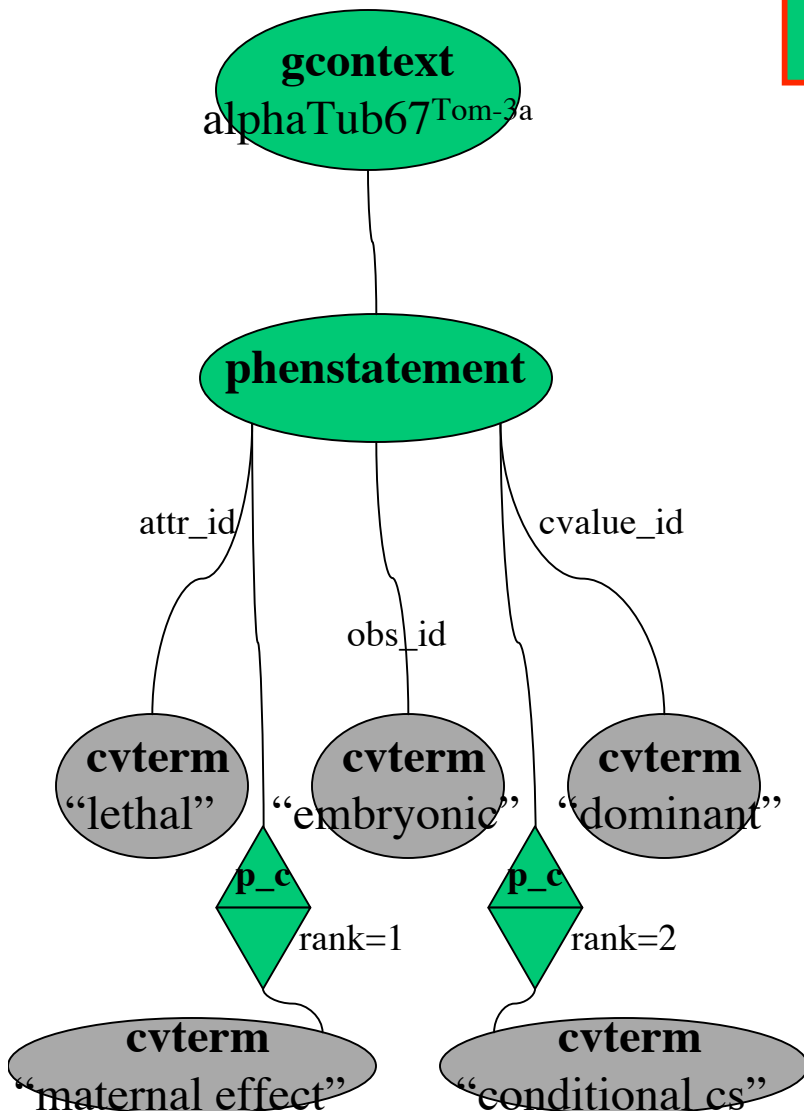
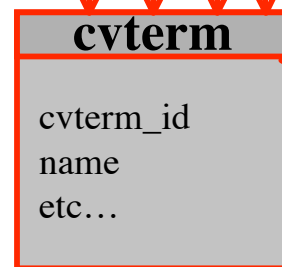
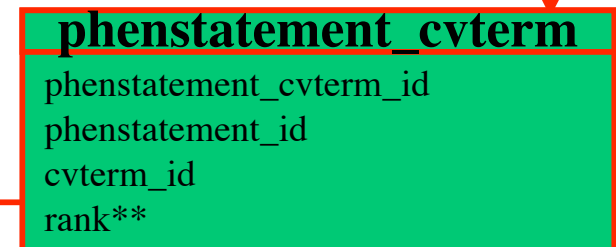
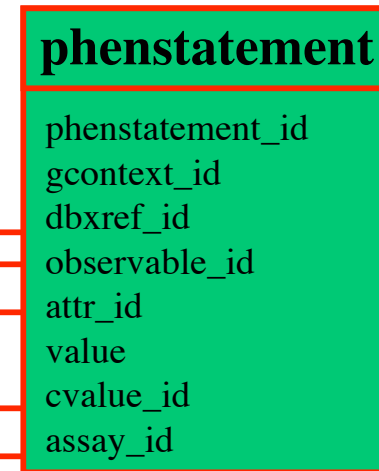
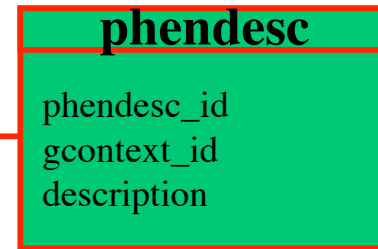
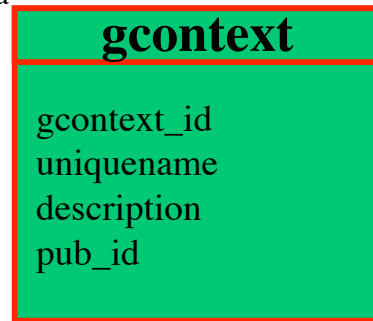
lethal | larval | recessive



Allele phenotype α Tub67^{Tom-3a}

Phenotypic class:

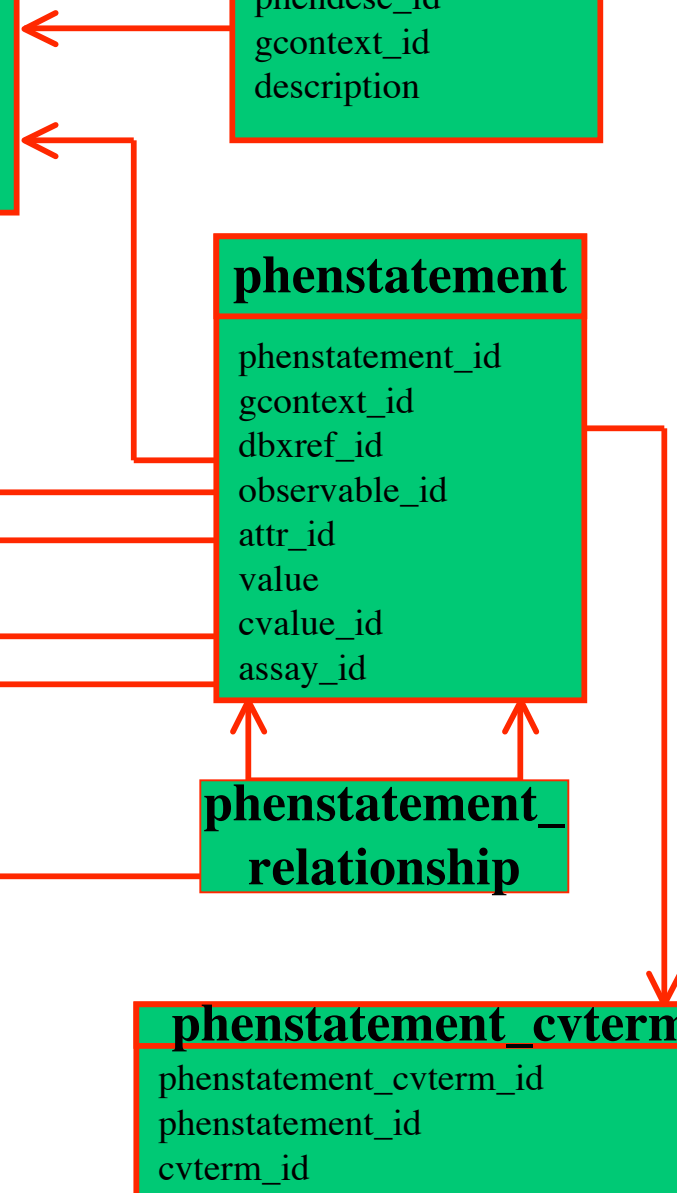
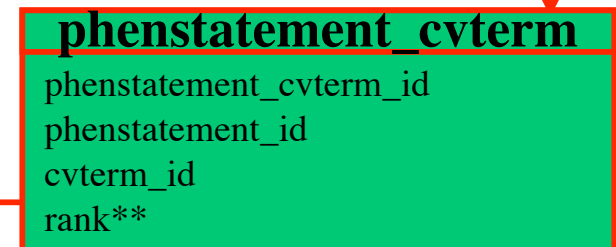
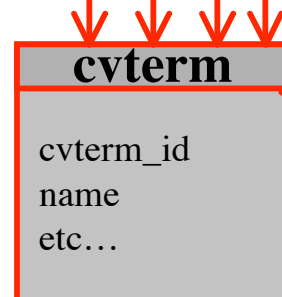
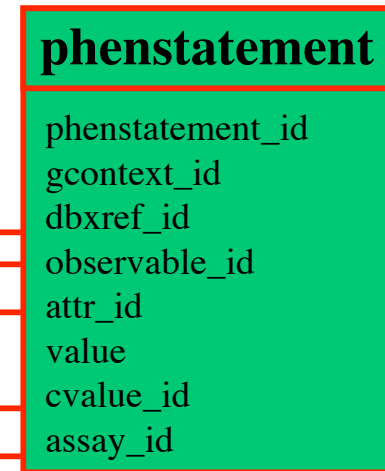
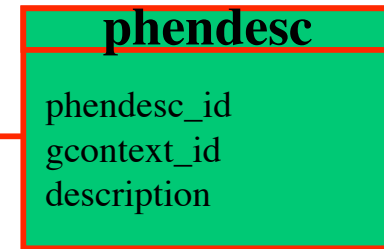
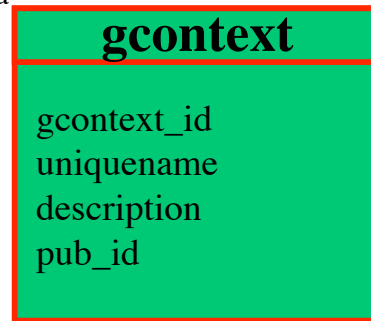
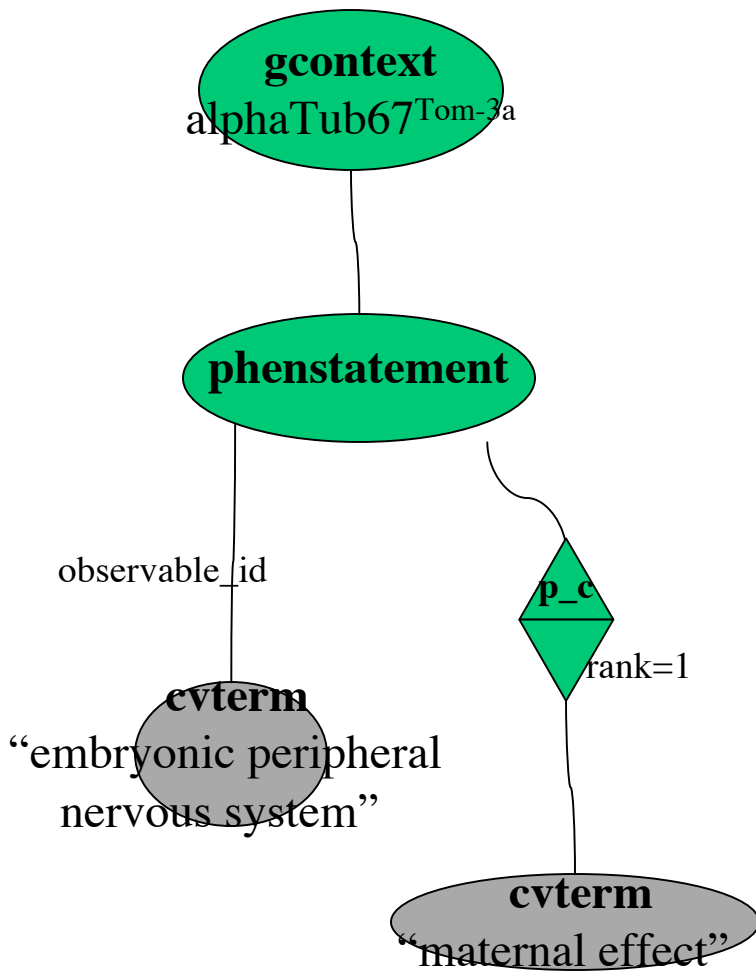
lethal | embryonic | dominant |
maternal effect | conditional cs



Allele phenotype α Tub67^{Tom-3a}

Phenotypic manifest in:

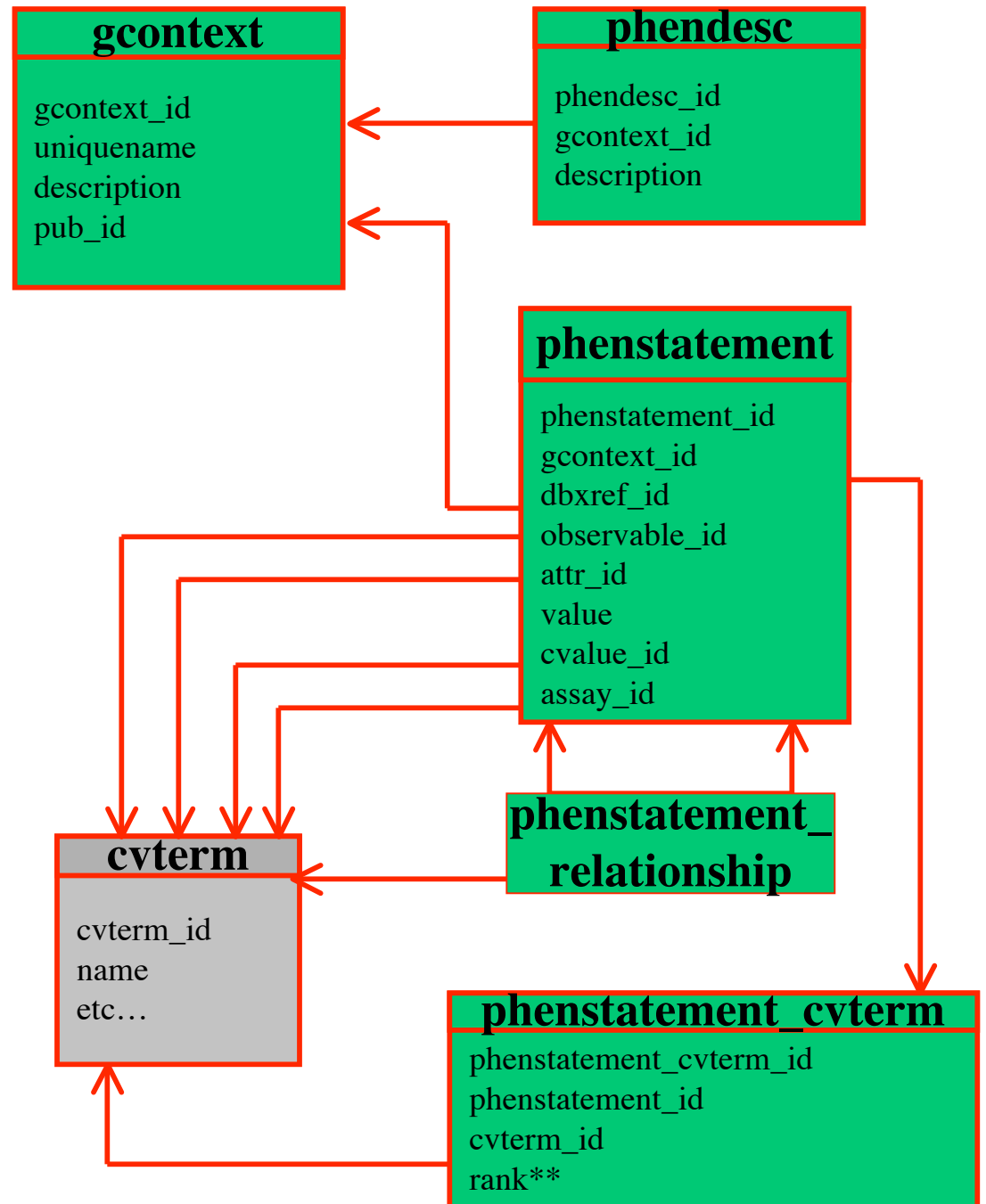
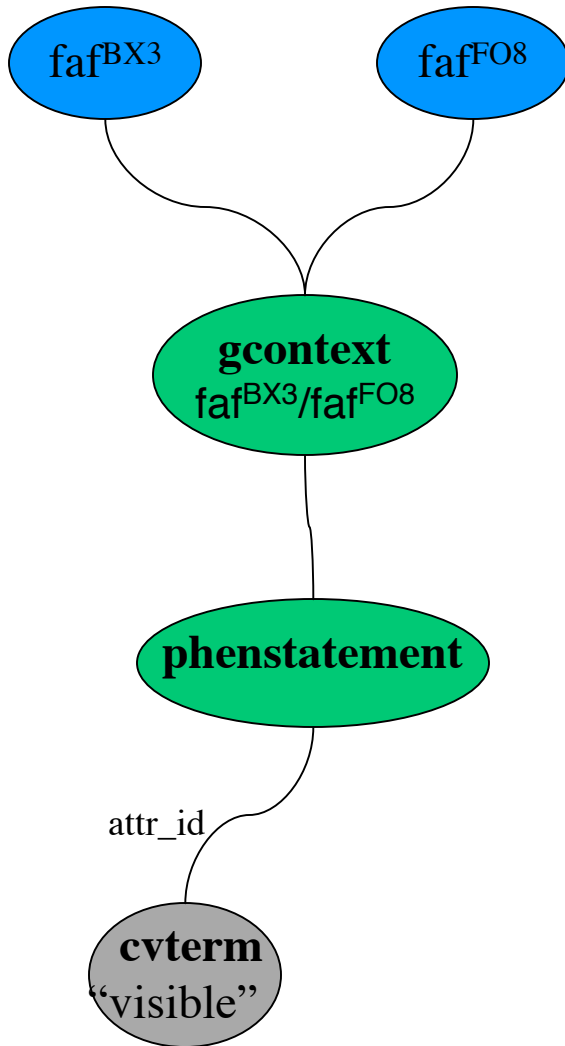
embryonic peripheral nervous system |
maternal effect

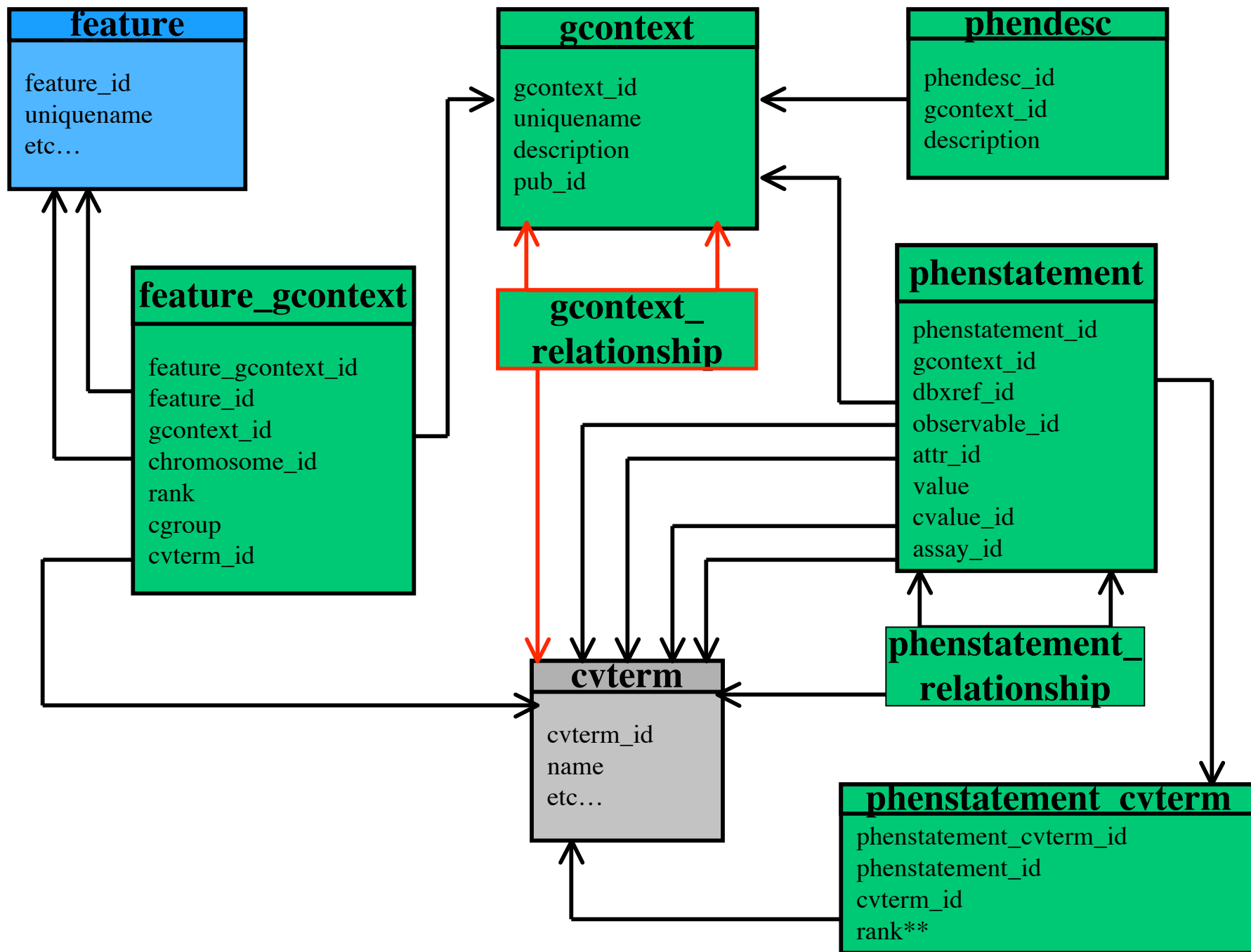


Transheterozygous phenotype:

faf^{BX3}/faf^{FO8}

Phenotypic class: visible

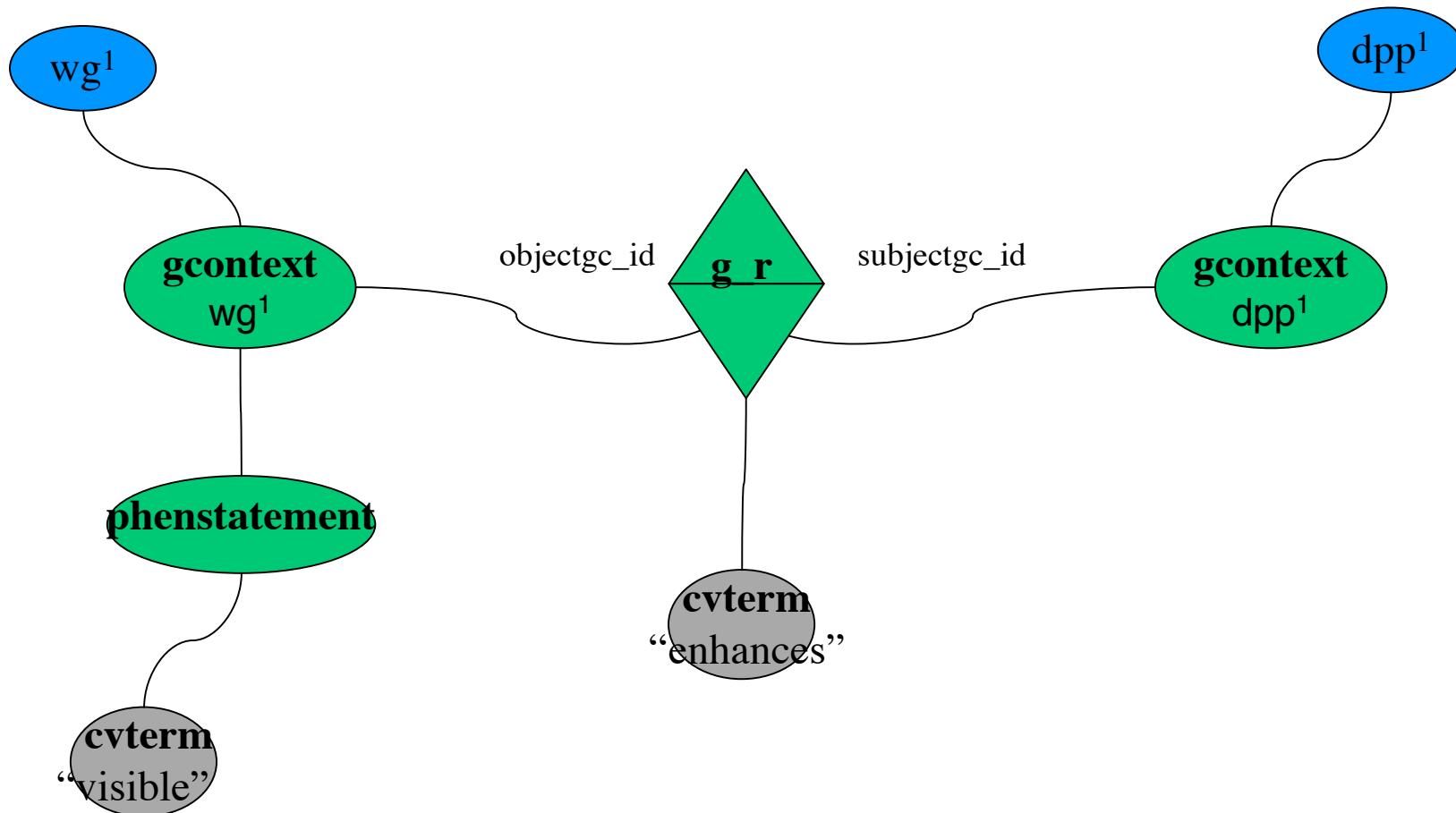




Genetic Interactions

“wg¹ has a wing phenotype that is enhanced by dpp¹”

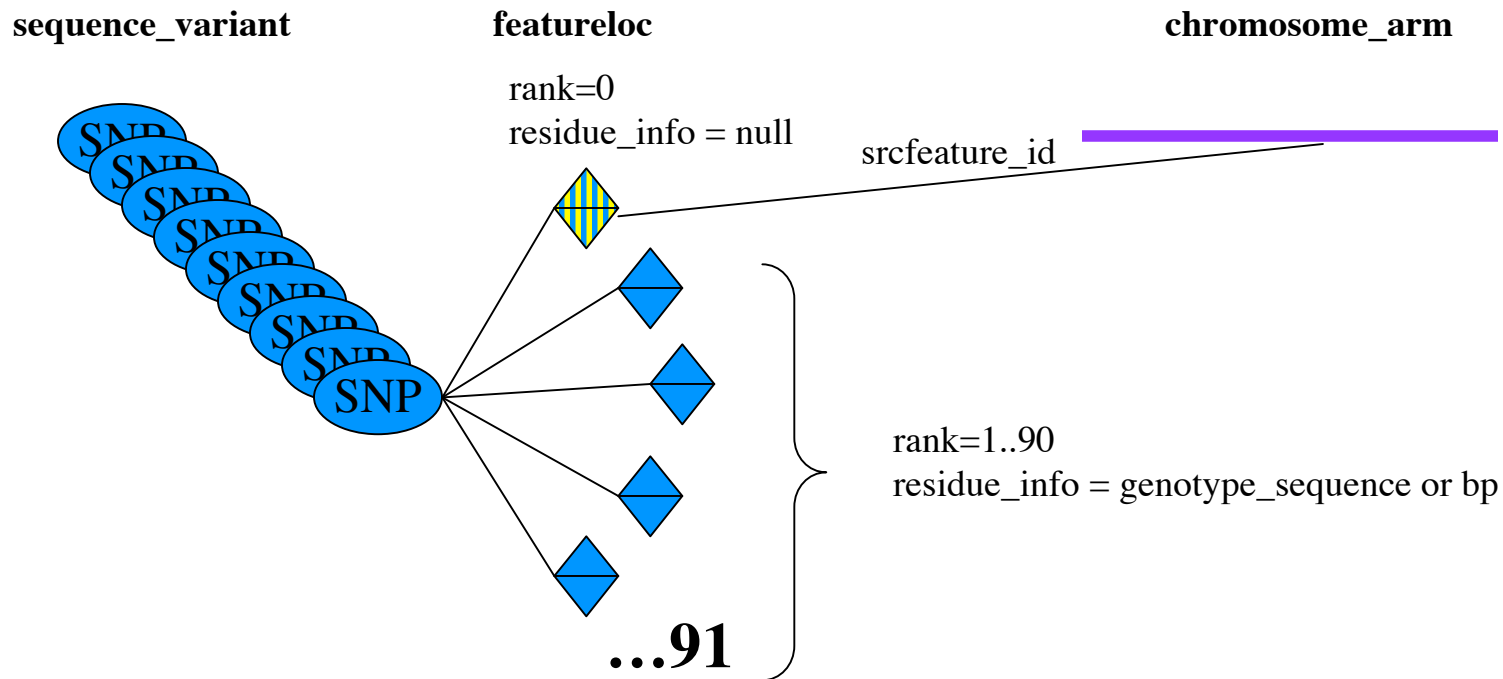
FlyBase Curation for wg¹: **visible, enhanceable { dpp[1] }**



Representing hapmap genotype data in chado

(Chris Mungall and Mummi Thorisson)

- Several hundred thousand human SNPs (dbSNP rs#).
- 90x samples (Coriell cell lines).
- genotypes for each of the 90 samples at a given SNP site.



Acknowledgements

- **genetic module design team**
 - Chris Mungall (BDGP - Berkeley)
 - Pinglei Zhou (FlyBase - Harvard)
 - Aubrey de Grey (FlyBase - Cambridge)
 - Bill Gelbart (PI, FlyBase)
 - Stan Letovsky (FlyBase - Harvard)
 - FlyBase Curators at Cambridge and Harvard
- **GMOD**
 - Scott, Lincoln, Everybody who's helped / commented