



D = {seg\_mean, rpmmm, scaled\_est, p\_exp\_val}

C = {CNV, SNP, E-Gene, E-Protein, miRNA, Clinical}

B = {DNA-Methylation}

M = {beta\_value, position}

F = {Expression-Exon}

E = {RPKM}

A = {chromosome, result, bcr\_patient\_barcode} G = {start, stop}

$$C-1 = \{ \{p \in \{D \cup A \cup G\} \vee \{p = \text{rdf:type} \wedge o \in C\} \} \wedge \{ \{S\text{-Join}(p, D \cup C) \vee P\text{-Join}(p, D \cup C) \} \vee \{ \{S\text{-Join}(p, M \cup B \cup E \cup F) \wedge !P\text{-Join}(p, M \cup B \cup E \cup F) \} \} \}$$

$$C-2 = \{ \{p \in \{E \cup A \cup G\} \vee \{p = \text{rdf:type} \wedge o \in F\} \} \wedge \{ \{S\text{-Join}(p, E \cup F) \vee P\text{-Join}(p, E \cup F) \} \vee \{ \{S\text{-Join}(p, M \cup B \cup D \cup C) \wedge !P\text{-Join}(p, M \cup B \cup D \cup C) \} \} \}$$

$$C-3 = \{ \{p \in \{M \cup A\} \vee \{p = \text{rdf:type} \wedge o \in B\} \} \wedge \{ \{S\text{-Join}(p, M \cup B) \vee P\text{-Join}(p, M \cup B) \} \vee \{ \{S\text{-Join}(p, E \cup F \cup D \cup C) \wedge !P\text{-Join}(p, E \cup F \cup D \cup C) \} \} \}$$