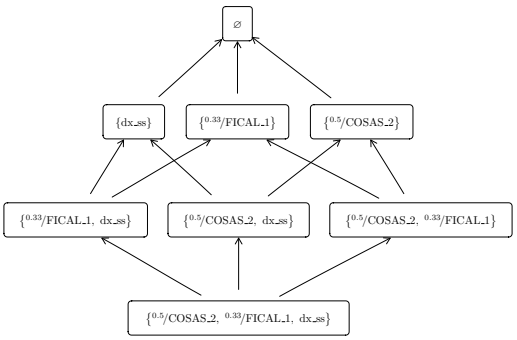

Figure 4: Hasse diagram for a sublattice of the `cobre32` formal context.

an individual) and returns the degree of the diagnosis attributes using the implications extracted from the formal context as an inference engine.

Next, we use the NEXTCLOSURE algorithm to extract implications and compute the set of concepts, using `fc$find_implications()`.

The concept lattice is quite big (14706 concepts); therefore, it cannot be plotted here for space and readability reasons. For this reason, we only plot a sublattice of small size in Figure 4.

There is an aggregate of 985 implications extracted. Let us compute the average cardinality of the LHS and the RHS of the extracted rules:

```
> colMeans(fc$implications$size())
     LHS      RHS
2.417597 1.954146
```

Note that our paradigm can deal with non-unit implications, that is, where there is more than one attribute in the RHS of the implication. This feature is an extension of what is usual in other paradigms, for example, in transactional databases.

We can use the *simplification logic* to remove redundancies and reduce the LHS and RHS size of the implications. The reason to do this is to decrease the computational cost of computing closures:

```
> fc$implications$apply_rules(rules = c('simplification', 'rsimplification'))
> colMeans(fc$implications$size())
     LHS      RHS
1.998308 1.557191
```

We can see that the average cardinality of the LHS has been reduced from 2.418 to 1.998 and that the one of the RHS, from 1.954 to 1.557.

With the simplified implication set, we can build a recommender system by simply wrapping the `recommend()` method inside a function:

```
> diagnose <- function(S) {
+
+   fc$implications$recommend(S = S,
+                             attribute_filter =
+                               c('dx_ss', 'dx_other'))
+
+ }
```

This function can be applied to `"Set"`s that have the same attributes as those of the formal context. The `attribute_filter` argument specifies which attributes are of interest, in our case, the diagnosis attributes.

Let us generate some sets of attributes and get the recommendation (diagnosis) for each one:

```
> S1 <- Set$new(attributes = fc$attributes,
+               COSAS_1 = 1/2, COSAS_2 = 1, COSAS_3 = 1/2,
+               COSAS_4 = 1/6, COSAS_5 = 1/2, COSAS_6 = 1)
> diagnose(S1)
   dx_ss dx_other
       1        0
```