

## Methods Supplement II: R code for exposure derivation

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#~~~~~ Pattern matching in free text of old MBR~~~~~#
# Find patterns that indicate usage of a drug
#~~ IRON ~~~#
# fuzzy matching
ironmatches <- NULL
patterns <- c("NIFEREX", "HEMOFER", "BLUTSAFT", "DUROFERON", "JÄRN", "JÄRNTILLSKOTT",
"JÄRNTABL", "FERRONOL", "ERCOFER", "FE TABL", "GLOBIFER", "FE 100 MG",
"VENOFER", "FERRO", "HEMIRON")
for (i in patterns){
temp <- agrep(i, drugs$drugs)
ironmatches[[i]] <- as.character(drugs$drugs[temp])
}
# exact matching
patterns <- c("FE", "IRON", "FE KOMB FOLACID", "FE M FOLACIN", "FE, FOLACIN",
"IRON-FOLLIC PLU", "FE & VITAMINER", "FE-SAFT",
"VITAMINER +FE", "VIT/MINERAL/FE", "FE-VITAMINER",
"FE & ACO VITAMINER", "FE + VITAMINER", "FE MED VITAMINER",
"FE OCH C-VITAMINER", "FE VITAMINER", "VITAMINER/FE", "FLYTANDE FE",
"T. FE", "FE+", "FLYT FE")
ironmatches[["EXACT"]] <- patterns
# exact matching for specific part
patterns <- c("JÄRN")
for (i in patterns){
temp <- grep(i, drugs$drugs)
ironmatches[[i]] <- c(ironmatches[[i]], as.character(drugs$drugs[temp]))
}
# manual cleaning of incorrect matches
incorrect <- c(# from JÄRN #
"PUMPAKÄRNE-EXTRAKT", "SE JORNAL ANTECKNING", "PUMPAKÄRNE-EXTRAKT",
# from FE TABL #
"DEXOFEN TABL", "TRANDATE TABLETT 100", "TRIOBE TABLETT", "ALVEDON FORTE TABLET",
"POSTAFEN TABL", "POSTAFEN TABL", "LUGNANDE TABL.", "TRANDATE TABLETT 200", "ALVEDON FORTE TABL 1",
"BLTR HÖJANDE TABL", "DEXOFEN TABL 50", "DEXOFEN TABL 50 MG", "DEXOFEN TABL.", "DEXOFEN TABLETT",
"DEXOFEN TABLETT 100", "DIANE TABLETT 2 MG/", "FOLSYRE TABL", "POSTAFEN TABL 25",
"POSTAFEN TABL.V", "ILLAMÄNDE TABL", "ILLAMÄNENDE TABL", "ILLAMÄNDE TABL I T",
"POSTAFEN TABL 25 MG",
# from FE 100 MG #
"TRANDATE 100 MG", "DEXOFEN 100 MG", "ZOLOFT 100 MG", "DOLOXENE 100 MG", "T TRANDATE 100 MG",
"T. TRANDATE 100 MG", "T.DEXOFEN 100 MG", "T.TRANDATE 100 MG", "TRANDATE 100 MG",
"T TRANDATE 100 MG", "T .TRANDATE 100 MG", "T.SOLOFT 100 MG", "TANDATE 100 MG", "TRANDATE 100 MG",
# from FERRO #
"BETAFERON", "CAFERGOT", "INJ BETAFERON", "TOCOFEROL", "BETAFERONINJ", "BEFERON", "BERROCCA BRUS",
"CEFERGOT", "CHOLECALCIFEROL", "ERRONL", "FERRHYD", "FEROMYN S", "FERRACODIL",
"EFEROX", "ERGOKALCIFEROL", "ERGOKALCIFEROL APL", "FERMONEST", "FEROMFOL", "FEROMOL", "FEROMOL 15 ML",
"T BERROCCA", "SERRODETTE", "SERROVENT DISKUS", "OMEPRAZOL ERRO", "PROGESTERRON VAG",
"INJ. INTERFERON", "INTERFERON", "FERRATI",
# from HEMIRON #
"REMIRON", "REMIRON 15 MG", "T REMIRON", "T.REMIRON-S")
for (i in 1:length(ironmatches)) {
ironmatches[[i]] <- setdiff(ironmatches[[i]], incorrect)
}
#~~~ FOLIC ACID ~~~#
folicmatches <- NULL
# fuzzy matching
patterns <- c("FOLSYRA", "FOLACIN", "FEMIBION", "HEMOPLETT", "TRIOBE", "FOLIC",
"FERRONOL", "HEMOFER PLUS", "BIOFOLIN")
for (i in patterns){
temp <- agrep(i, drugs$drugs)
folicmatches[[i]] <- as.character(drugs$drugs[temp])
}
# exact matching
patterns <- c("HEMOFER +", "HEMOFER+", "HEMOPLUS",
"T.HEMOFER+", "T HEMOFER +", "HEMOFER MED FOL", "T HEMOFER M FOL",
"HEMOFER M FOLS", "T HEMOFER FOLS", "HEMOFER+FOL", "T.HEMOFER M FOL",
"THEMOFER+", ".HEMOFER+", "HEMOFER M. FOLS", "T HEMOFER MED F",
"HEMOFER M FOL", "HAEMOFER +", "HEMOFER+BVIT", "TABL HEMOFER MED FOL",
"THEMOFER M FOL", "THEMOFER M. FOL", "VITAMINER + FOL",
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"T VITAMINERAL M. FOL", "VITAMINER MED F", "VITAMINER/ FOLS",
"HÄMO-FER+")
folicmatches[["EXACT"]] <- patterns
# exact matching for specific part
patterns <- c("FOLS", "FOLAC", "FEMIBIO", "FOLIC")
for (i in patterns){
temp <- grep(i, drugs$drugs)
folicmatches[[i]] <- c(folicmatches[[i]], as.character(drugs$drugs[temp]))
}
# manual cleaning of incorrect matches
incorrect <- c(# from TRIOBE#
"TRIOMEGA", "TRIONETTA", "T TRIOMEGA", "T TRIONETTA", "TRIONETTA 28", "TRIODERON", "TRIOMEGA F KVINNA",
"TRIOMEGALL",
# from FOLIC#
"KYOLIC", "DIFLICAN", "DUFLICAN", "PROCYANIDOLIC", "SOLICO", "SYMFONIC", "T METABOLIC PRE", "T KOLICIN",
"KRYOLIC (VITLÖK)", "FOLIO",
# from HEMOFER PLUS#
"HEMOFER BLUTSAFT")
for (i in 1:length(folicmatches)) {
folicmatches[[i]] <- setdiff(folicmatches[[i]], incorrect)
}
#~~~ MULTIVITAMIN ~~~#
# fuzzy matching
mvmatches <- NULL
patterns <- c("MITT VAL KVINNA", "MULTIVITAMIN", "MITT VAL",
"VITAMIN KVINNA", "MAMMAVITAL", "KVINNA VITAMIN", "VITAMAX", "KVINNA",
"APOTEKET KVINNA", "MULTIPLEX", "ENOMDAN", "BEROCCA", "GRAVITAMIN",
"MULTI KVINNA", "MIVITOTAL", "KVINNA VITAL", "VIT FÖR GRAVIDA", "MULTIVIT GRAVID",
"PREGNACARE", "MULTIVIT", "KVINNA GRAVID",
"ACO KVINNA", "ACO FAMIL", "ACO FERTIL", "ACO MULT", "ACO GRAV",
"KVINNAMITVAL", "VITAMIN FÖR GRAVIDA")
for (i in patterns){
temp <- agrep(i, drugs$drugs)
mvmatches[[i]] <- as.character(drugs$drugs[temp])
}
# fuzzy matching with lower tolerance
patterns <- c("ACO VITAMIN")
for (i in patterns){
temp <- agrep(i, drugs$drugs, max.distance=0.001)
mvmatches[[i]] <- as.character(drugs$drugs[temp])
}
# exact matching
patterns <- c("MATERNA")
mvmatches[["EXACT"]] <- patterns
# exact matching for specific part
patterns <- c("VITAMINERAL", "VITAPLEX", "ACO Q")
for (i in patterns){
temp <- grep(i, drugs$drugs)
mvmatches[[i]] <- c(mvmatches[[i]], as.character(drugs$drugs[temp]))
}
# manual cleaning of incorrect matches
incorrect <- c(# from MULTIPLEX#
"MULTIPLEX OMEGA", "MULTIPLEX OMEGA3", "MULTIPLEX C", "MULTIPLEX C-VITAMIN",
"OMEGA 3 MULTIPLEX", "OMEGA3 MULTIPLEX",
# from ACO VITAMIN #
"FOLSYRA O VITAMIN", "FOLSYRA O VITAMINER")
for (i in 1:length(mvmatches)) {
mvmatches[[i]] <- setdiff(mvmatches[[i]], incorrect)
}

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