```
1  # 2011-09-13 Michael Silberbauer gvisAnnotatedTimeLine creates a Google annotated time line app
2  # 2011-10-24 Michael Silberbauer apply Deon van Zyl's SET ISOLATION command to access locked tables
3  # plotting microbiological data from the Department of Water Affairs Water Management System
4  # source("C:/data/program/R/NMMP_AnnotatedTimeLine.R")
5
6  # TODO (2012-03-07) : plot a PNG version for non-java browsing: might need separate script with E. coli and turbidity - could use annual boxplots?
7  # 2012-05-29 Michael Silberbauer NEMP_TimeLine.R ver 0.1 plots a PNG time-series graph for non-java browsing
8
9  require(RODBC)
10 require(RJSONIO)
11 require(googleVis)
12 require(ggplot2)
13 db<-"wmsdb"
14 mv<-"E.COLI"
15 channel<-odbcConnect(db)
16 db_unlock<-"set isolation dirty read"
17 sqlQuery(channel, db_unlock)
18
19 vars<-sqlQuery(channel,"select * from monitorng_variable")
20 varid<-subset(vars$mon_variable_id,grepl(mv,vars$mon_variable_abbr))
21 wdir<-"C:/tmp/nmmp/"
22 nmmpID<-135
23 q<-paste("SELECT UNIQUE mon_feature_id FROM programme_sample WHERE mon_program_id =",nmmpID) # 135=NMMP
24 sites<-sqlQuery(channel,q)
25 #featid<-102626
26 for (n in 1:nrow(sites)) {
27 #for (n in 1:4) {
28     featid<-sites$mon_feature_id[n]
29     qs<-paste("SELECT mon_feature_id, sample_begin_date, sample_begin_time, sample_begin_depth, ",
30               "sample_end_depth, result_num_value FROM released_result WHERE mon_variable_id = ",varid,
31               " AND mon_feature_id = ", featid,
32               sep="")
33     qs<-paste("SELECT mon_feature_id, sample_begin_date, ",
34               "result_num_value FROM released_result WHERE mon_variable_id = ",varid,
35               " AND mon_feature_id = ", featid,
36               sep="")
37     ecolis<-sqlQuery(channel, qs)
38     ecolis$sample_begin_date<-as.Date(ecolis$sample_begin_date,"%Y-%m-%d")
39     nrow(ecolis)
40     summary(ecolis)
41     ecoli<-ecolis[!duplicated(ecolis$sample_begin_date),]
42     nrow(ecoli)
43     if(nrow(ecoli)>0) {
44     ecoli["id"]<-"E. coli"
45     gl1<-ecoli[1:2,]
46     gl1$sample_begin_date[1]<-min(ecoli$sample_begin_date)
47     gl1$sample_begin_date[2]<-max(ecoli$sample_begin_date)
48     gl1$id<-"Lo_risk"
49     gl1$result_num_value<-10
50     gl2<-ecoli[1:2,]
51     gl2$sample_begin_date[1]<-min(ecoli$sample_begin_date)
52     gl2$sample_begin_date[2]<-max(ecoli$sample_begin_date)
53     gl2$id<-"Hi_risk_untreated"
54     gl2$result_num_value<-2000
55     gl3<-ecoli[1:2,]
56     gl3$sample_begin_date[1]<-min(ecoli$sample_begin_date)
57     gl3$sample_begin_date[2]<-max(ecoli$sample_begin_date)
58     gl3$id<-"Hi_risk_contact"
59     gl3$result_num_value<-4000
60     gl4<-ecoli[1:2,]
61     gl4$sample_begin_date[1]<-min(ecoli$sample_begin_date)
62     gl4$sample_begin_date[2]<-max(ecoli$sample_begin_date)
63     gl4$id<-"Hi_risk_irrig"
64     gl4$result_num_value<-20000
65     gl5<-ecoli[1:2,]
66     gl5$sample_begin_date[1]<-min(ecoli$sample_begin_date)
67     gl5$sample_begin_date[2]<-max(ecoli$sample_begin_date)
68     gl5$id<-"Hi_risk_lo_treatment"
69     gl5$result_num_value<-max(ecoli$result_num_value)
70
71     if (max(ecoli$result_num_value) < 10) {
72         E.coli<-rbind(gl1,ecoli)
73         clist<-"['#0000ff','#000000']"
74     }
75     if (max(ecoli$result_num_value) >= 10) {
76         E.coli<-rbind(gl1,gl2,ecoli)
77         clist<-"['#0000ff','#00ff00','#000000']"
78     }
79     if (max(ecoli$result_num_value) >= 2000) {
80         E.coli<-rbind(gl1,gl2,gl3,ecoli)
81         clist<-"['#0000ff','#00ff00','#ffdd00','#000000']"
82     }
83     if (max(ecoli$result_num_value) >= 4000) {
84         E.coli<-rbind(gl1,gl2,gl3,gl4,ecoli)
85         clist<-"['#0000ff','#00ff00','#ffdd00','#ff0000','#000000']"
86     }
87     if (max(ecoli$result_num_value) >= 20000) {
88         E.coli<-rbind(gl1,gl2,gl3,gl4,gl5,ecoli)
89         clist<-"['#0000ff','#00ff00','#ffdd00','#ff0000','#9932CC','#000000']"
90     }
91     print(paste(featid,nrow(ecoli),max(ecoli$result_num_value),clist))
92     a2<-gvisAnnotatedTimeLine(E.coli,datevar="sample_begin_date",date.format = "%Y-%m-%d",
93         numvar="result_num_value", idvar="id",
94         options=list(width=1024,height=400,dateFormat="yyyy MM dd",fill=10,displayExactValues=TRUE,
95         colors=clist),
```

```
96            chartid=paste("nmmp",featid,sep=""))
97        gvf<-paste("C:/tmp/nmmp/Chart_nmmp",featid,".html",sep="")
98        print(a2,file=gvf)
99        #plot(a2)
100       
101   }
102   }
```