2019–20 outbreak of novel coronavirus '2019-nCoV'

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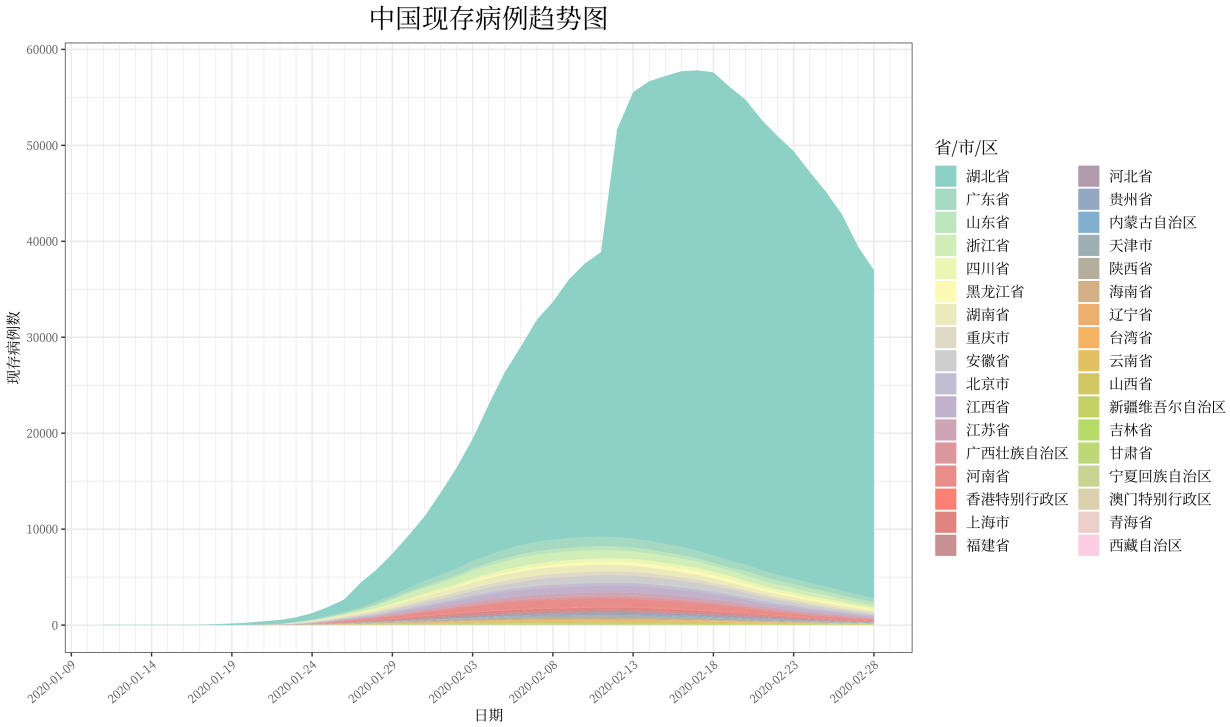
Source Code

```
library(tidyverse)
library(lubridate)
library(scales)
library(RColorBrewer)
library(maps)
library(mapdata)
library(maptools)

if('content' %in% dir()){setwd('content/special/data')}

source('ncov_commons.R')

# read data ----------------------------------------------------------------

read_ncov <- function(sheet, caseType, fn = 'wuhan.xlsx'){
  readxl::read_excel(fn, sheet = sheet) %>%
  replace(is.na(.), 0) %>%
  mutate(date = as_date(date)) %>%
  mutate_at(-1, cumsum) %>%
  gather(location, !!caseType, -1) %>%
  mutate(location=as_factor(location))
}
```

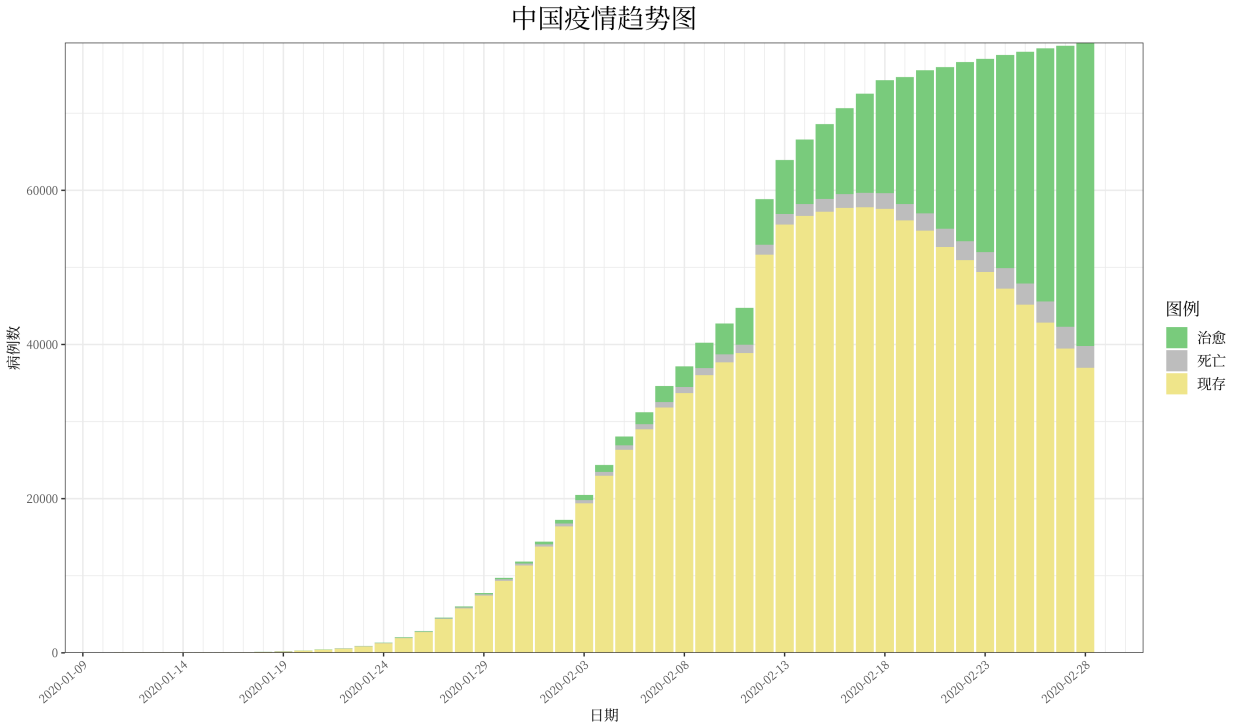
```r
calc_ncov_params <- function(df){
  mutate(df,
         current = all-death-cure,
         deathRate = death/all,
         cureRate = cure/all)
}

ncov <- read_ncov('incidence-wiki', 'all') %>%
  left_join(read_ncov('death-wiki', 'death')) %>%
  left_join(read_ncov('cure-wiki', 'cure')) %>%
  calc_ncov_params()

ncovByHubei <-
  bind_rows(
    ncov %>% # hubei
      filter(location==' ') %>%
      select(-location) %>%
      add_column(type=' '),
    ncov %>% # non-hubei
      filter(location!=' ') %>%
      group_by(date) %>%
      summarise(all = sum(all, na.rm = TRUE),
                death = sum(death, na.rm = TRUE),
                cure = sum(cure, na.rm = TRUE)) %>%
      calc_ncov_params() %>%
      add_column(type=' ')
    )


typeColorPairs = c(cure='palegreen3', death='grey', current='khaki')

hubeiContrastColor = c( ="orangered2",   ='seagreen3')

{ # death and cure rates
ncov %>%
  ggplot(aes(date, deathRate))+
  geom_line(aes(group=location, alpha=log(current)))+
  geom_line(data = ncovByHubei, aes(color=type), size=1.1)+
  scale_alpha_continuous(guide=FALSE)+
  scale_y_continuous(limits = c(0,0.15), minor_breaks = seq(0, 0.15, 0.01), labels = scales::percent)+
  theme_default+
  dateScale+
  labs(title='    ', x=' ',y='  ',
       color = ' ',
       caption = '  /   / /           ')+
  scale_color_manual(values=hubeiContrastColor)

ggsave('img/china_death_rate.png', width = 13, height = 8)

ncov %>%
  ggplot(aes(date, cureRate))+
  geom_line(aes(group=location, alpha=log(current)))+
  geom_line(data = ncovByHubei, aes(color=type), size=1.1)+
```

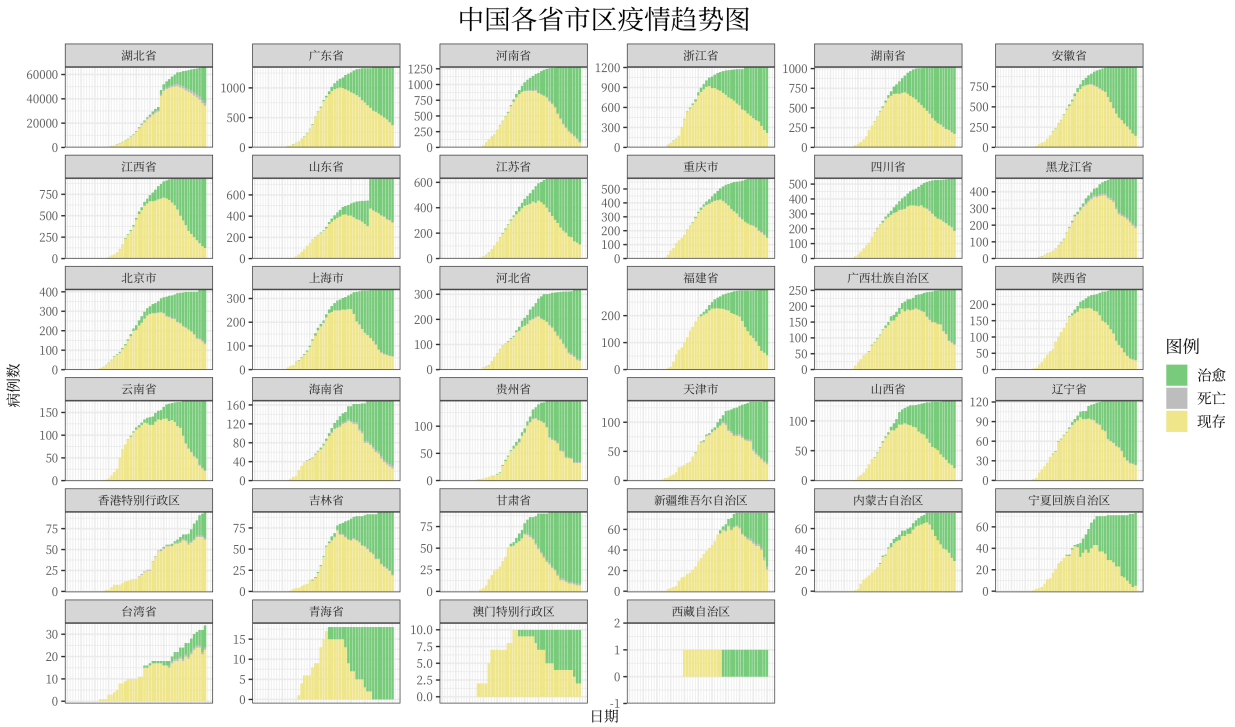
```
  scale_alpha_continuous(guide=FALSE)+
  scale_y_continuous(limits = c(0,0.9), breaks = seq(0,0.8,0.2), labels = scales::percent)+
  theme_default+
  dateScale+
  labs(title='    ', x=' ',y='  ',
       color = ' ',
       caption = '  /   / /           ')+
  scale_color_manual(values=hubeiContrastColor)

ggsave('img/china_cure_rate.png', width = 13, height = 8)
}

{ #
(p <- ncov %>%
  mutate(location = fct_reorder(location, -all, min)) %>%
  select(-all) %>%
  gather(type, cases, 3:5) %>%
  mutate(type=factor(type, levels=names(typeColorPairs)))%>%
  ggplot(aes(date, cases, fill=type))+
  geom_col()+
  scale_fill_manual(labels=c(' ',' ',' '), values = typeColorPairs)+
  labs(title = '    ', fill = ' ', x=' ', y='  ')+
  theme_date+
  dateScale+
  scale_y_continuous(expand = c(0, 1))
)

ggsave('img/china_cure_death_current_all.png', width = 13, height = 8)

p + facet_wrap(~location, scales = 'free_y')+
  theme(axis.ticks.x = element_blank(),
        axis.text.x = element_blank())+
  labs(title = '      ', fill = ' ')

ggsave('img/china_cure_death_current_facet.png', width = 13, height = 8)
}

{ #
ncov %>%
    ggplot(aes(date, current, fill=fct_reorder(location, -current, last)))+
    geom_area(position = position_stack())+
    dateScale+
    theme_date+
    fill_province+
    scale_y_continuous(breaks = seq(0, 70000, 10000))+
    labs(fill=' / / ', x = ' ', y='   ',
         title = '     ')
ggsave('img/china_current.png', width = 13, height = 8)
}

setwd('../../..')
```

2.1 Number of cases reported by the government

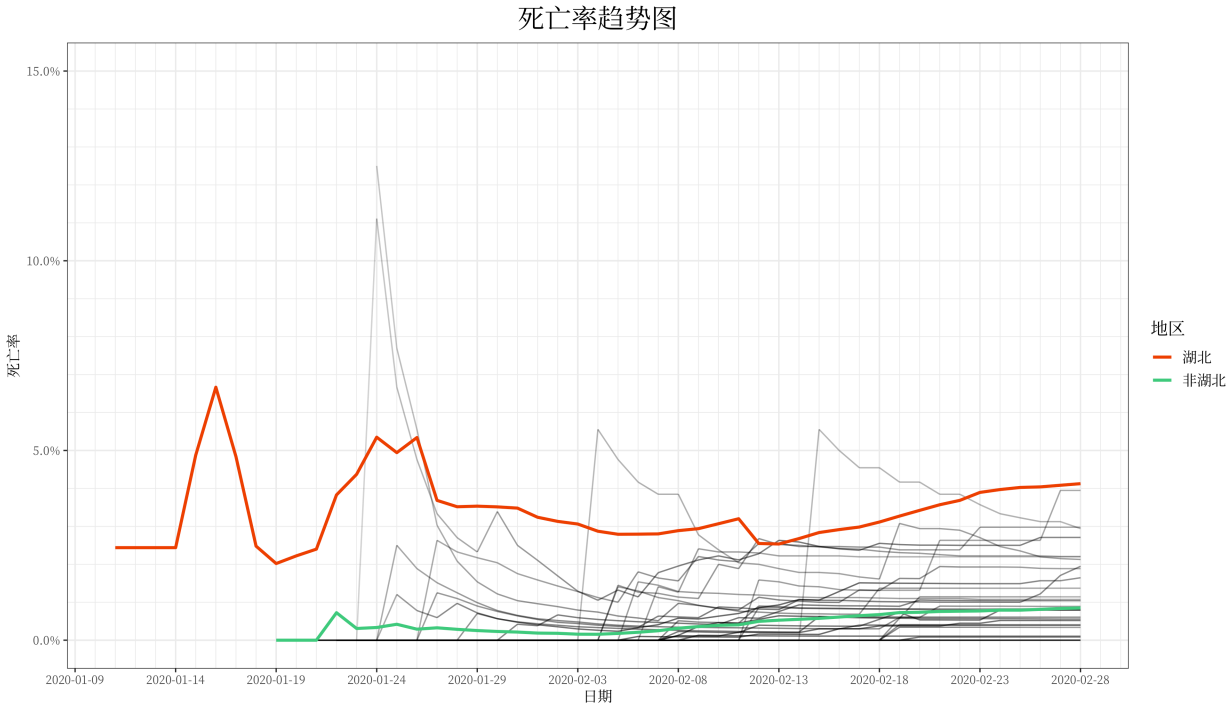


2.2 Incidence, Death and Cure Over Time

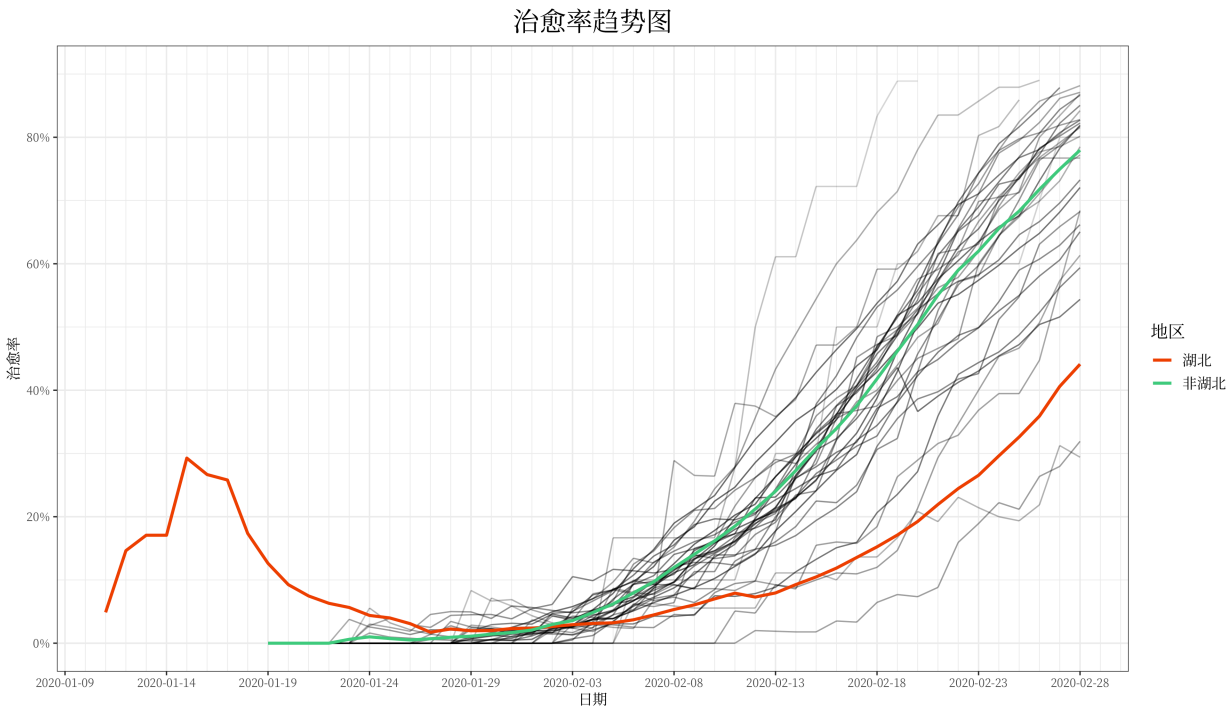




2.3 Death and Cure Rates



注：黑/灰色线为各省/市/区死亡率趋势，累计病例数表现为线条深浅。



注：黑/灰色线为各省/市/区治愈率趋势，累计病例数表现为线条深浅。