

Stat 7350 - Assignment1

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1. Interesting question:

Are the top ranked source countries are the countries more threatened by the invasive species?

Paini, Sheppard, Cook and all (2016) said that “Exactly one-half (10) of the countries ranked in the top 20 source countries were also ranked in the top 20 for threatened countries.” I saw a potential positive correlation between the invasion costs(link to the literature).

In this paper, they outlined an important measure, invasion cost, to quantify the economic cost of the invasive species. Specifically, invasion costs are calculated for both threatened countries and source countries. For the threatened countries, the total invasion cost for each country, TIC_t , was calculated by summing up the cost associated with all invasive species' impact on domestic crops (see equation [5,6]). While the total invasion cost from each source country, TIC_s , was calculated by summing up the cost of source country's invasive species impacted on the crops in the threatened countries (see equation [8,9]).

Here, I am interested in the association between the invasion cost applied on threatened countries and the invasion cost that source countries can impose on other countries. In order to do so, I have followed a workflow of data cleaning, data visualization and possible interpretations of the plots as shown in the following sessions.

2. Interact with the data

2.1 Load in the data

```
# loading packages -----
suppressMessages(library("here"))
suppressMessages(library("tidyverse"))
suppressMessages(library("gridExtra"))
suppressMessages(library("sqldf"))
suppressMessages(library("Hmisc")) # for using %nin%
suppressMessages(library("skimr"))
suppressMessages(library("ggExtra")) # plot marginal histogram, density or boxplots
suppressMessages(library("scales")) # plot marginal histogram, density or boxplots
```

```
# import data -----
setwd("..")
A1_wd <- getwd()
A1_wd
```

```
## [1] "C:/Users/ZhangYang/OneDrive/Academic Life/Topics_Community_Health_Science/STAT_7350_Stat_analys
```

```
datadir <- paste(A1_wd, "data", sep = "/")
datadir
```

```
## [1] "C:/Users/ZhangYang/OneDrive/Academic Life/Topics_Community_Health_Science/STAT_7350_Stat_analys
```

```
table1 <- read_csv(paste(datadir, "table_1.csv", sep = "/")) #sorted by invasion_threat
table2 <- read_csv(paste(datadir, "table_2.csv", sep = "/")) %>% #sorted by invasion_cost
  rename(invasion_cost_threatCountry = invasion_cost)
table3 <- read_csv(paste(datadir, "table_3.csv", sep = "/")) #sorted by invasion_gdp_proportion
table4 <- read_csv(paste(datadir, "table_4.csv", sep = "/")) %>% #sorted by invasion_cost (source coun
  rename(invasion_cost_sourceCountry = invasion_cost)
invasive_species <- read_csv(paste(datadir, "table_6.csv", sep = "/")) #invasive species and impact per
africa_species <- read_csv(paste(datadir, "africa_species.csv", sep = "/"))
```

2.2 Clean up the datasets

Check if there are any duplicates in the datasets and remove all the duplicated records.

table_1:

```
# clean duplicated country in datasets -----
(table1_count <- table1 %>%
  count(country) %>%
  filter(n>1) %>% as.tibble())
```

```
## # A tibble: 0 x 2
## # ... with 2 variables: country <chr>, n <int>
```

```
# no duplicates in table1
rm(table1_count)
```

table_2:

```
(table2_count <- table2 %>%
  count(country) %>%
```

```

filter(n>1) %>% as.tibble())

## # A tibble: 1 x 2
##   country      n
##   <chr>    <int>
## 1 Guinea      2

(table2_dup <- table2[table2$country == table2_count$country,]) # or replace == by %in%

## # A tibble: 2 x 3
##   country invasion_cost_threatCountry rank
##   <chr>                <dbl> <dbl>
## 1 Guinea              977500000      60
## 2 Guinea              114300000     107

# 1 duplicated country: Guinea
(table2_nodup <- distinct(table2, country, .keep_all=T)) # keep 1 copy of Guinea

## # A tibble: 123 x 3
##   country invasion_cost_threatCountry rank
##   <chr>                <dbl> <dbl>
## 1 China              117290000000      1
## 2 USA                 70381000000      2
## 3 Brazil              33760000000      3
## 4 India               33065000000      4
## 5 Japan               23490000000      5
## 6 Korea               14349000000      6
## 7 Turkey              13267000000      7
## 8 Argentina          13204000000      8
## 9 France              12532000000      9
## 10 Mexico             11277000000     10
## # ... with 113 more rows

(table2_nodup <- table2[!table2$country == table2_count$country,]) # remove both copy of Guinea

## # A tibble: 122 x 3
##   country invasion_cost_threatCountry rank
##   <chr>                <dbl> <dbl>
## 1 China              117290000000      1
## 2 USA                 70381000000      2
## 3 Brazil              33760000000      3
## 4 India               33065000000      4
## 5 Japan               23490000000      5
## 6 Korea               14349000000      6
## 7 Turkey              13267000000      7
## 8 Argentina          13204000000      8
## 9 France              12532000000      9
## 10 Mexico             11277000000     10
## # ... with 112 more rows

rm(table2, table2_count, table2_dup)

```

table_3:

```

(table3_count <- table3 %>%
  count(country) %>%
  filter(n>1) %>% as.tibble())

```

```
## # A tibble: 1 x 2
##   country      n
##   <chr>    <int>
## 1 Guinea      2

(table3_dup <- table3[table3$country == table3_count$country,]) # or replace == by %in%

## # A tibble: 2 x 5
##   country invasion_cost  gdp_mean gdp_proportion rank
##   <chr>          <dbl>    <dbl>         <dbl> <dbl>
## 1 Guinea      978000000 3380000000      0.289      3
## 2 Guinea      114000000 513000000      0.223      4

# 1 duplicated country: Guinea
(table3_nodup <- table3[table3$country != table3_count$country,])

## # A tibble: 122 x 5
##   country      invasion_cost  gdp_mean gdp_proportion rank
##   <chr>          <dbl>    <dbl>         <dbl> <dbl>
## 1 Malawi      1071000000 3000000000      0.357      1
## 2 Burundi     398000000 1121000000      0.355      2
## 3 Mozambique  1218000000 6423000000      0.190      5
## 4 Madagascar  1074000000 5842000000      0.184      6
## 5 Cambodia    1121000000 6487000000      0.173      7
## 6 Nepal        1411000000 8411000000      0.168      8
## 7 Laos         508000000 3134000000      0.162      9
## 8 Ethiopia     2312000000 14344000000     0.161     10
## 9 Vietnam      7490000000 55702000000     0.134     11
## 10 Moldova     388000000 3130000000      0.124     12
## # ... with 112 more rows

rm(table3, table3_count, table3_dup)
```

table_4:

```
(table4_count <- table4 %>%
  count(country) %>%
  filter(n>1) %>% as.tibble())

## # A tibble: 1 x 2
##   country      n
##   <chr>    <int>
## 1 Guinea      2

(table4_dup <- table4[table4$country == table4_count$country,]) # or replace == by %in%

## # A tibble: 2 x 3
##   country invasion_cost_sourceCountry rank
##   <chr>          <dbl> <dbl>
## 1 Guinea      47400000      97
## 2 Guinea      1800000     122

# 1 duplicated country: Guinea
(table4_nodup <- table4[table4$country != table4_count$country,])

## # A tibble: 122 x 3
```

```
##      country invasion_cost_sourceCountry rank
##      <chr>                <dbl> <dbl>
## 1 China                222590000000    1
## 2 USA                   181730000000    2
## 3 Japan                 120750000000    3
## 4 Germany               85864000000    4
## 5 Italy                 44228000000    5
## 6 France                38159000000    6
## 7 Korea                 37620000000    7
## 8 India                 36913000000    8
## 9 Russian               34336000000    9
## 10 United               25670000000   10
## # ... with 112 more rows
```

```
rm(table4, table4_count, table4_dup)
```

2.3 Merge the four tables together based on the same country IDs:

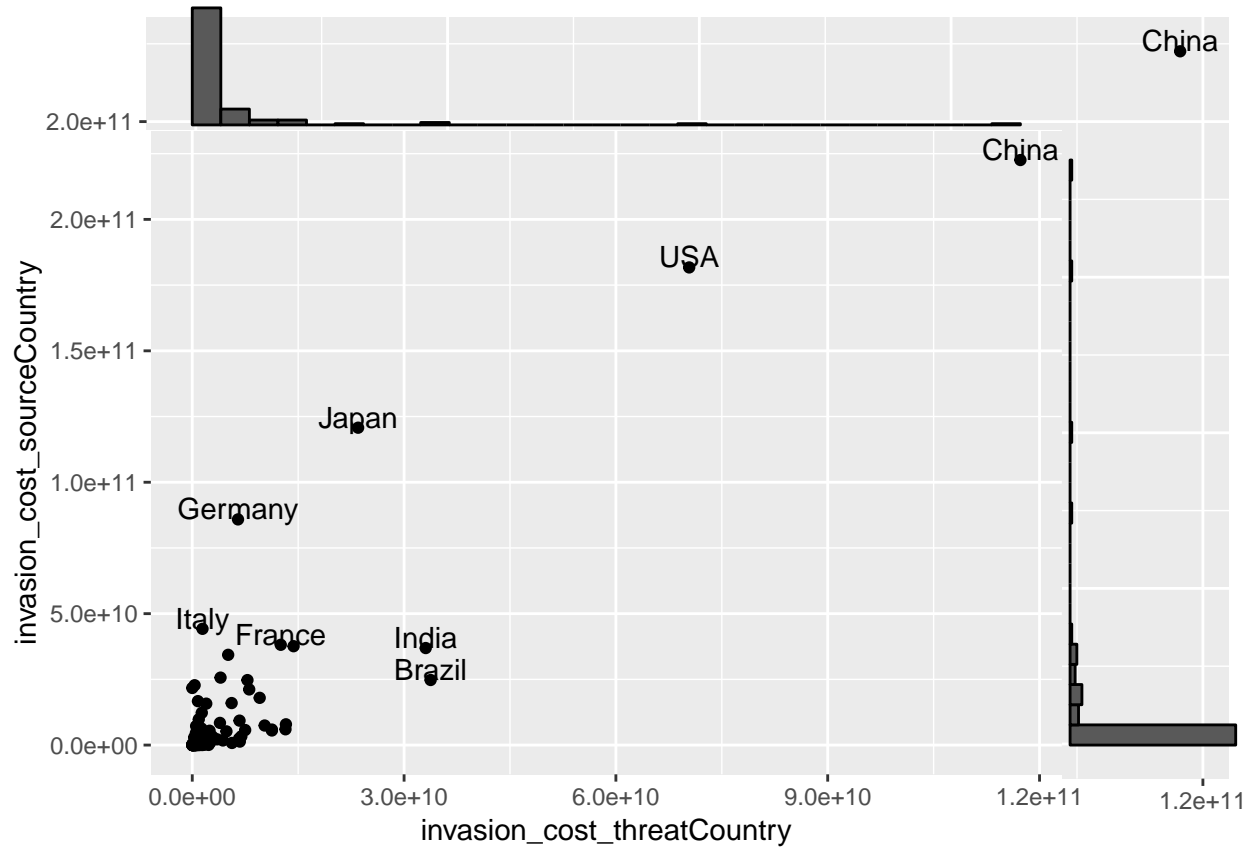
```
# join 4 tables together (full join) -----
table00 <- table1 %>%
  full_join(table2_nodup, by="country") %>%
  full_join(table3_nodup, by="country") %>%
  full_join(table4_nodup, by="country")
table00_count <- table00 %>%
  count(country) %>%
  filter(n>1)
# there is no dup country
rm(table00_count)

# clean up unwanted ranks
# and re-define the units of invasion costs (threatened and source)
table01 <- select(table00, -starts_with("rank")) %>%
  mutate(ICt_million = invasion_cost_threatCountry/(10^6),
         ICs_million = invasion_cost_sourceCountry/(10^6))
# rm(table1, table2_dup, table3_nodup, table4_nodup)
```

2.4 Preliminary plots

p1: Base plot

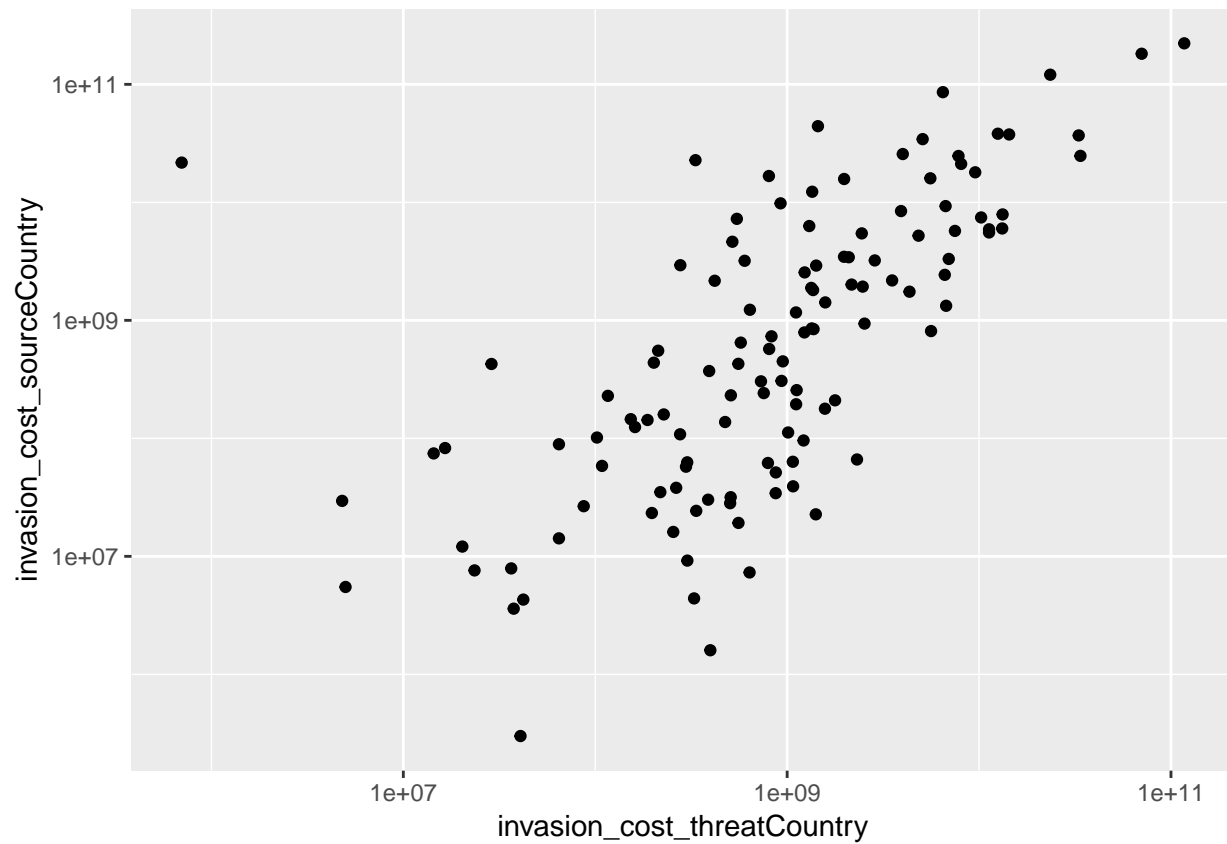
```
# base plot
(p1 <- table01
  %>% ggplot(aes(x=invasion_cost_threatCountry, y=invasion_cost_sourceCountry))
  + geom_point()
  + geom_text(data = subset(table01, ICs_million>34000 | ICt_million>14000 ), aes(label = country),
)
ggMarginal(p1, type="histogram")
```



p2: Scale x and y axes for better visualization of the data

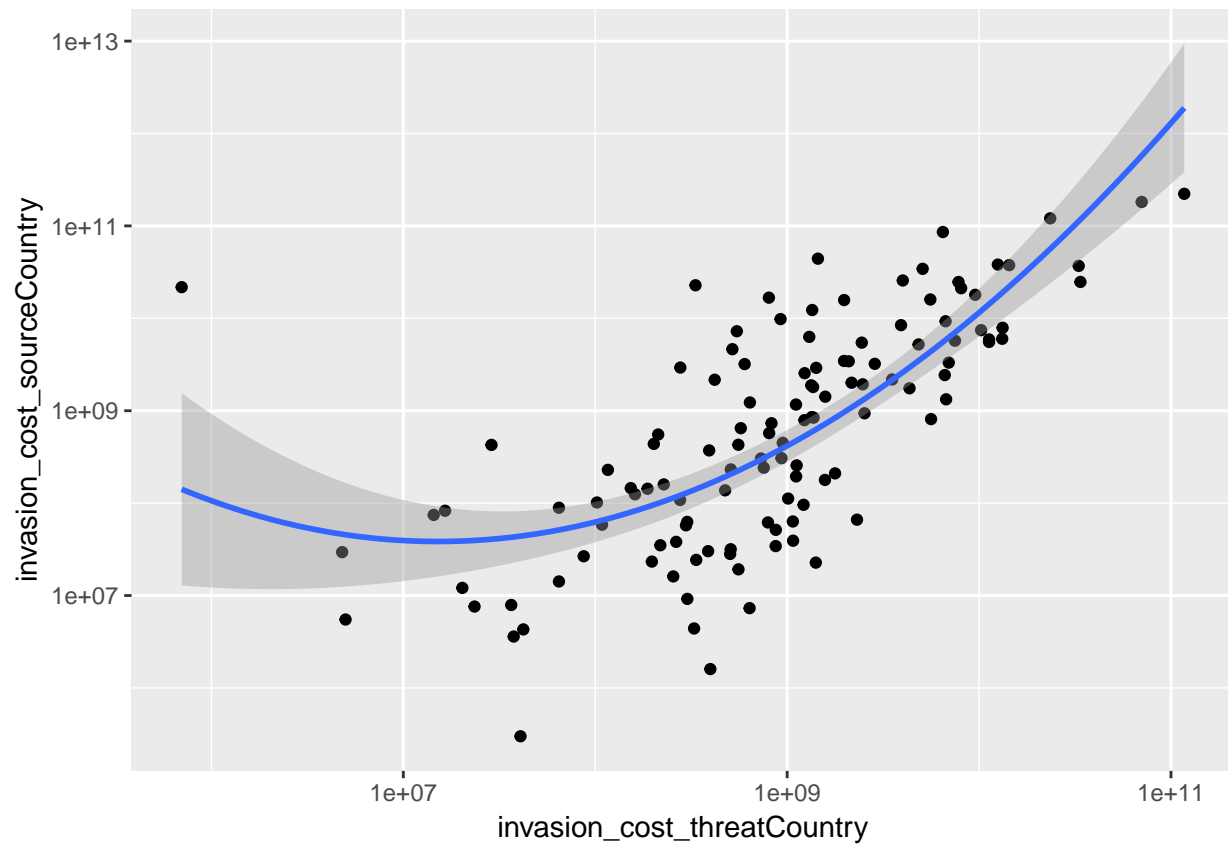
scale x and y axes and make the graph more presentable, but note that the two outliers (China, USA) i

```
(p2 <- table01
  %>% ggplot(aes(x=invasion_cost_threatCountry, y=invasion_cost_sourceCountry))
  + geom_point()
  + scale_x_log10()+scale_y_log10()
)
```



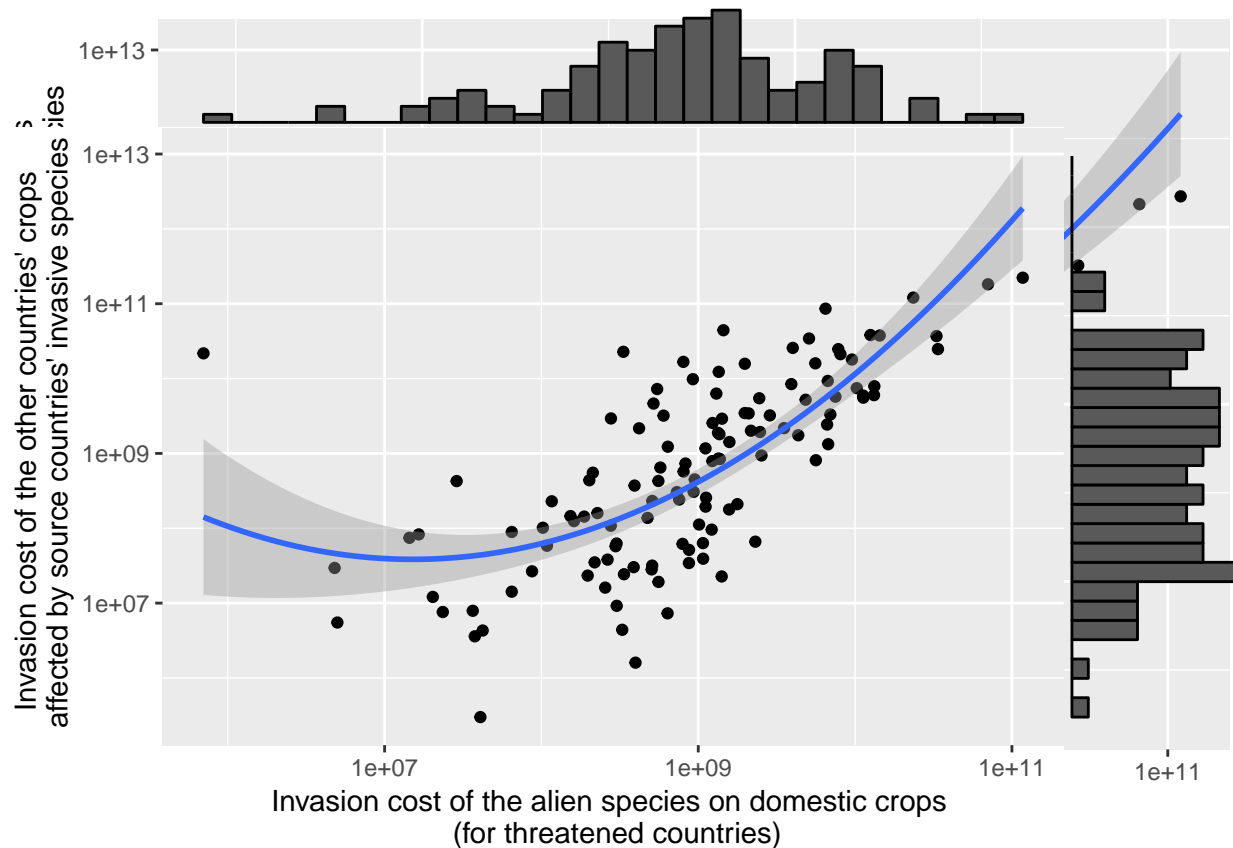
p3: Add a smooth curve to identify the association

```
# add a smooth curve to indicate the positive association
(p3 <- table01
  %>% ggplot(aes(x=invasion_cost_threatCountry, y=invasion_cost_sourceCountry))
  + geom_point()
  + scale_x_log10()+scale_y_log10()
  + geom_smooth(span=10)
  # + geom_label()
)
```



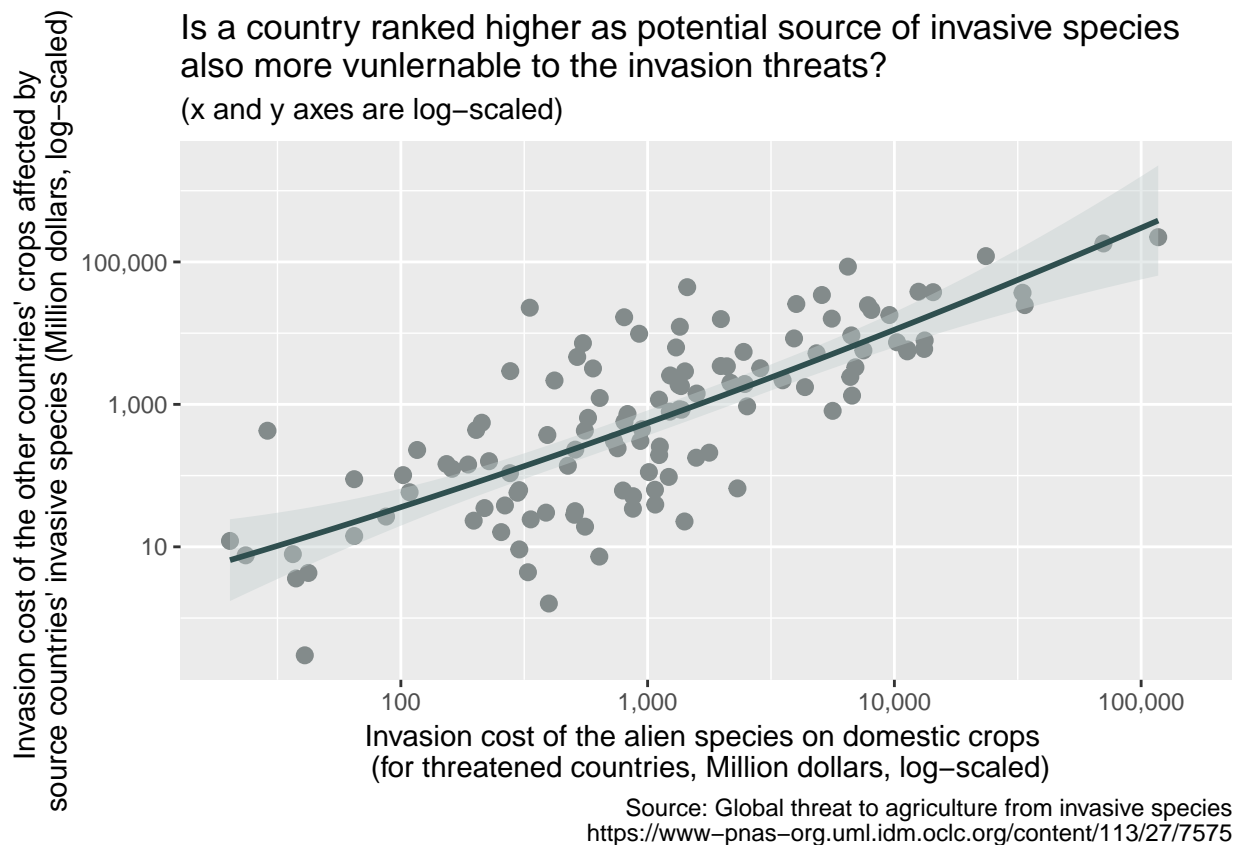
p4: Add marginal histograms

```
# modify the plot for better presentation;
# add marginal histograms (https://www.r-graph-gallery.com/277-marginal-histogram-for-ggplot2/)
(p4 <- table01
  %>% ggplot(aes(x=invasion_cost_threatCountry, y=invasion_cost_sourceCountry))
  + geom_point()
  + scale_x_log10()+scale_y_log10()
  + geom_smooth(span=10)
  + xlab("Invasion cost of the alien species on domestic crops \n (for threatened countries)")
  + ylab("Invasion cost of the other countries' crops \n affected by source countries' invasive species")
  # + geom_label()
)
(p4 <- ggMarginal(p4, type="histogram"))
```



p5: Further modification on the plot

```
# p6 - log-scaled plot (final plot)
(p5 <- table01
  # change units into million dollars:
  %>% ggplot(aes(x=ICt_million, y=ICs_million))
  + geom_point(colour="azure4", size=2.5)
  + scale_x_log10(limits=c(20, 1.5*10^5), labels=comma) + scale_y_log10(labels=comma) # labels=comma
  + xlab("Invasion cost of the alien species on domestic crops \n (for threatened countries, Million dollars, log-scaled)")
  + ylab("Invasion cost of the other countries' crops affected by \n source countries' invasive species, log-scaled")
  + labs(title="Is a country ranked higher as potential source of invasive species \n also more vulnerable to the invasion threats?",
        subtitle = "(x and y axes are log-scaled)",
        caption = "Source: Global threat to agriculture from invasive species\n https://www-pnas-org.uml.idm.oclc.org/content/113/27/7575")
  + geom_smooth(span=10, fill="azure3", colour="darkslategray")
)
```



```
# label important points:
```

```
(p5 <- p5
```

```
# + geom_text(data = subset(table01, ICt_million>70000), aes(label = country), vjust = 0, nudge_y
```

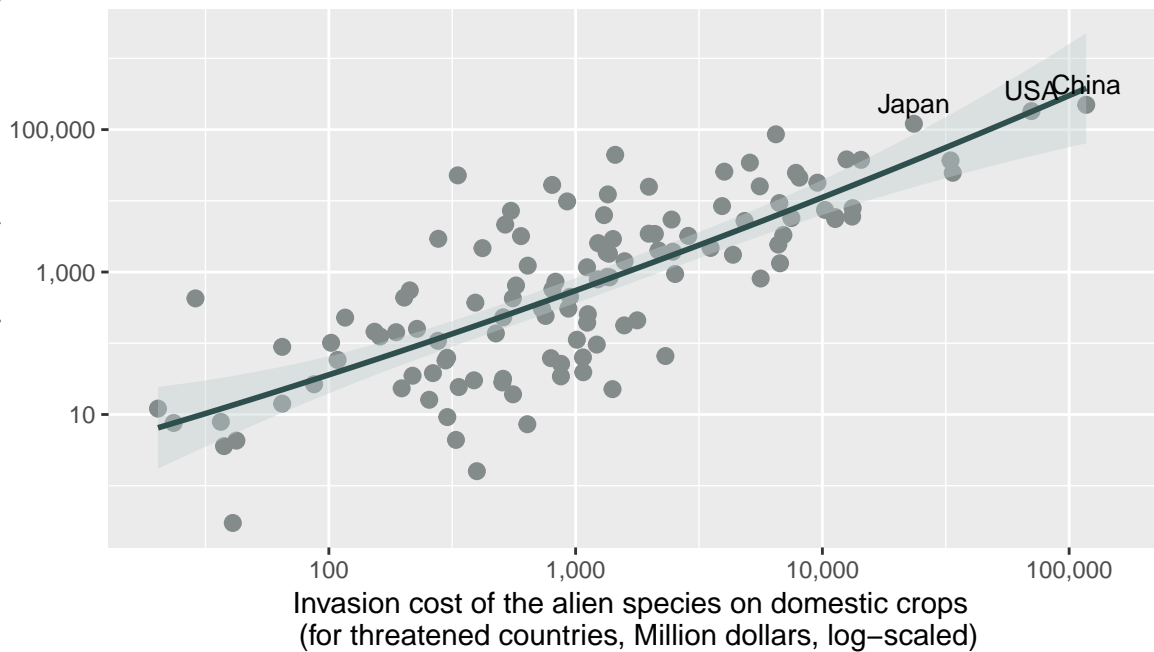
```
+ geom_text(data = subset(table01, ICs_million>100000), aes(label = country), vjust = 0, nudge_x=
```

```
)
```

Invasion cost of the other countries' crops affected by
source countries' invasive species (Million dollars, log-scaled)

Is a country ranked higher as potential source of invasive species
also more vulnerable to the invasion threats?

(x and y axes are log-scaled)

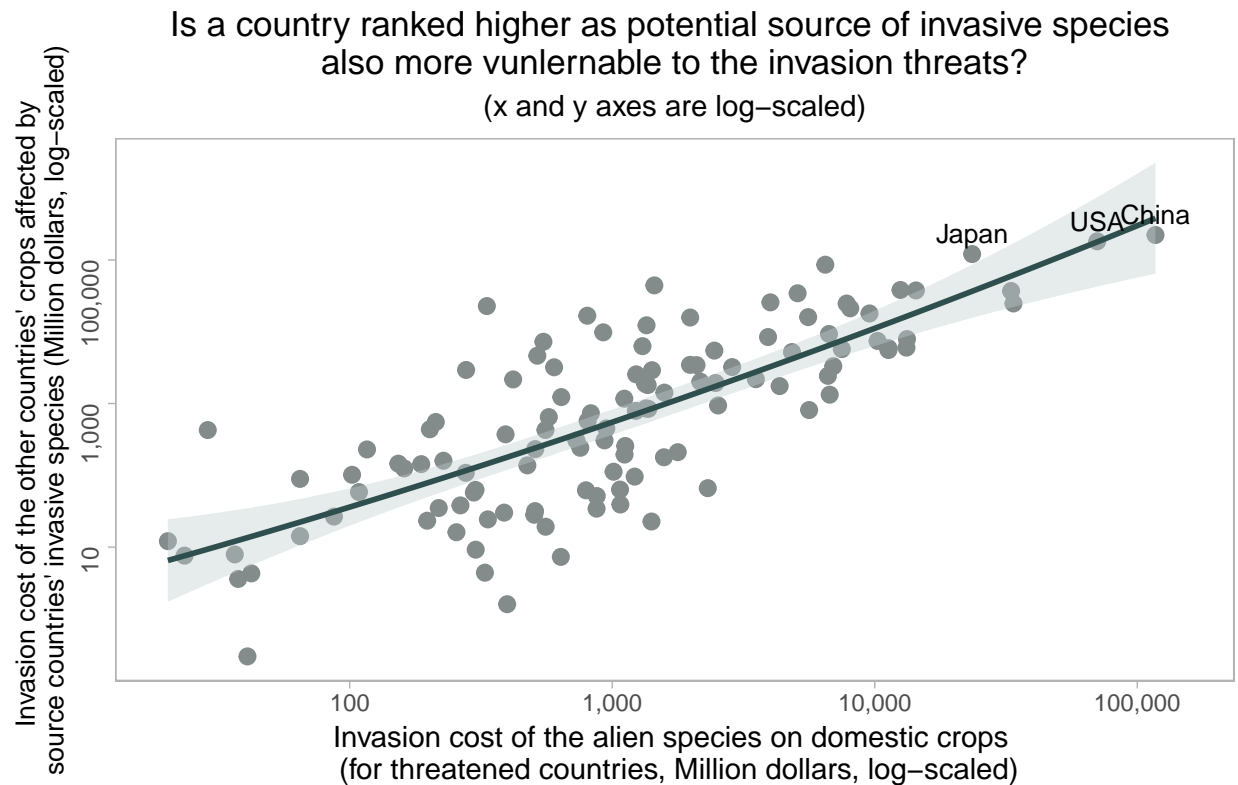


Source: Global threat to agriculture from invasive species
<https://www-pnas-org.uml.idm.oclc.org/content/113/27/7575>

```

# add theme
(p5 <- p5
  + theme_light()
  + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), #no gridline
    axis.title.y = element_text(size=10), # change the size of y axis label
    axis.text.y = element_text(angle = 90),
    plot.title = element_text(hjust =.5), # center plot title,
    plot.subtitle = element_text(hjust =.5),
    plot.caption = element_text(size=8, color = "gray8")) # change caption style
)

```



Source: Global threat to agriculture from invasive species
[https://www-pnas-org.uml.idm.oclc.org/content/113/27/7575](https://www.pnas-org.uml.idm.oclc.org/content/113/27/7575)

p6: Add the marginal histogram to finalize the plot

```
# add marginal histograms
(p6 <- ggMarginal(p5, type="histogram", fill="darkgray", colour="darkslategray", size=7))
```

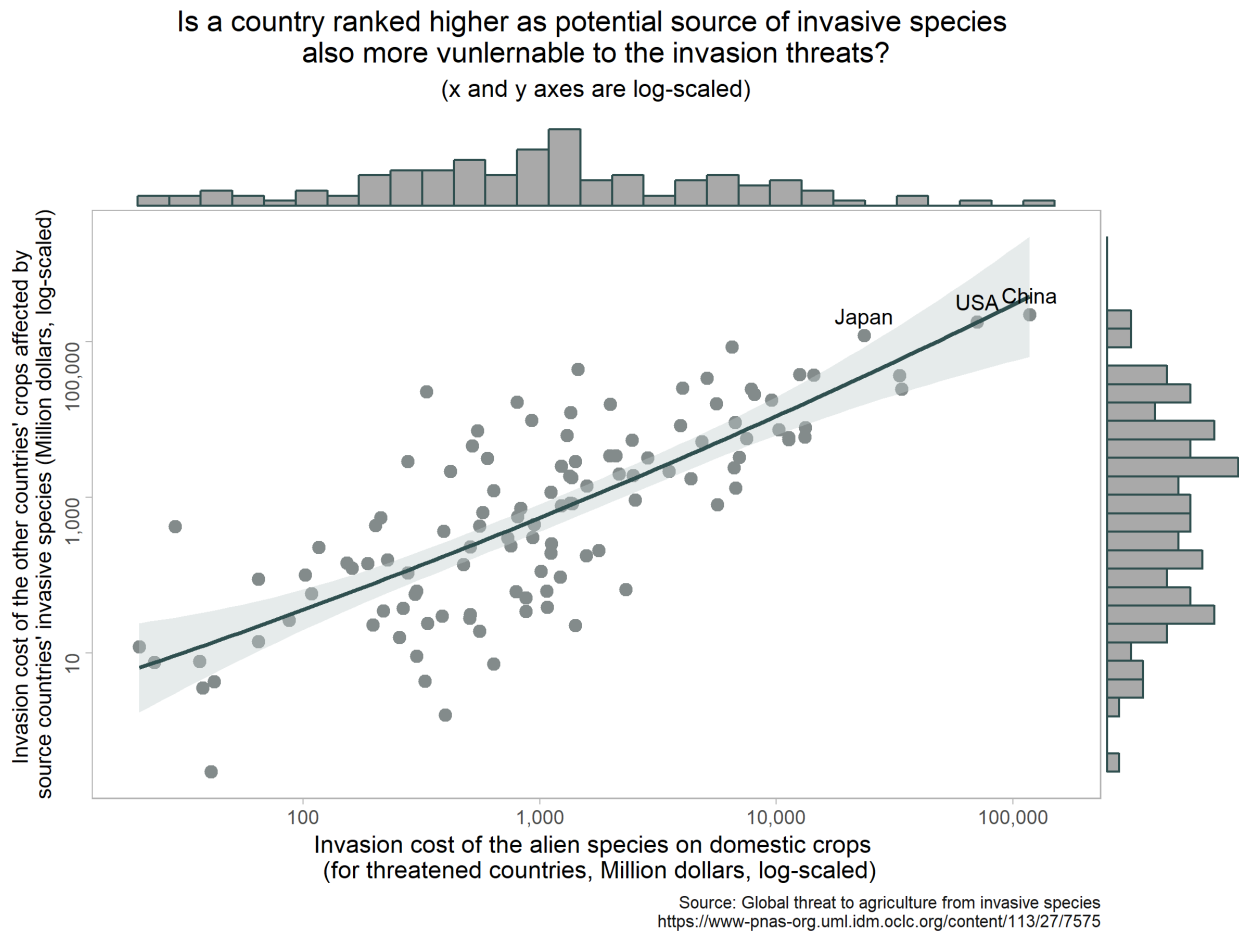


Figure 1:

Note that, this plot is saved on my computer by the ggsave function and then inserted in this document since the ggMarginal function does not plot nicely in R Markdown. As you may see, in p1 and p4, there are some points are plotted outside the axes due to the incompatibility of the ggMarginal() function.

3. Final plot

3.1 The finalized plot (p6) to address my question

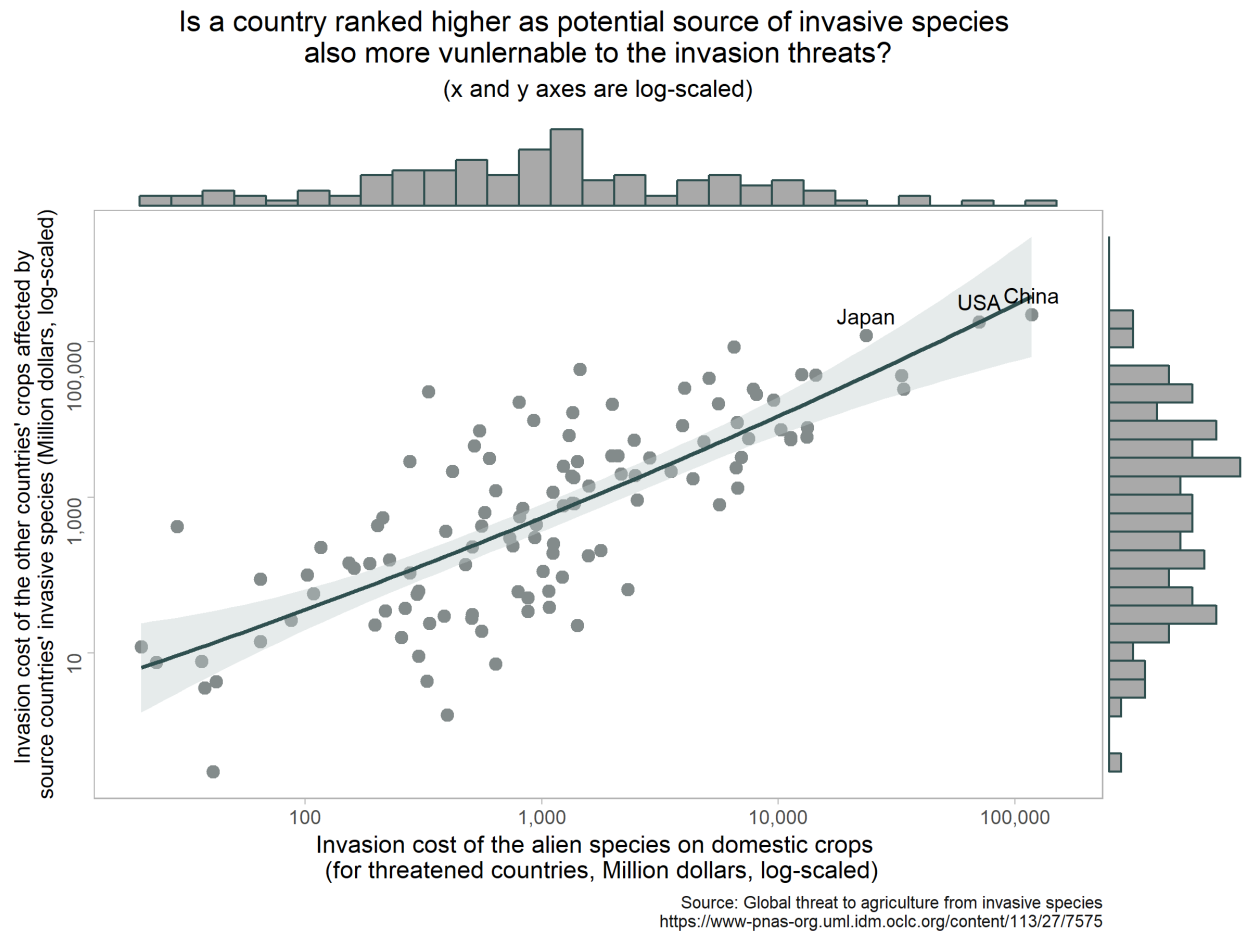


Figure 2:

3.2 The modified preliminary plot for comparison

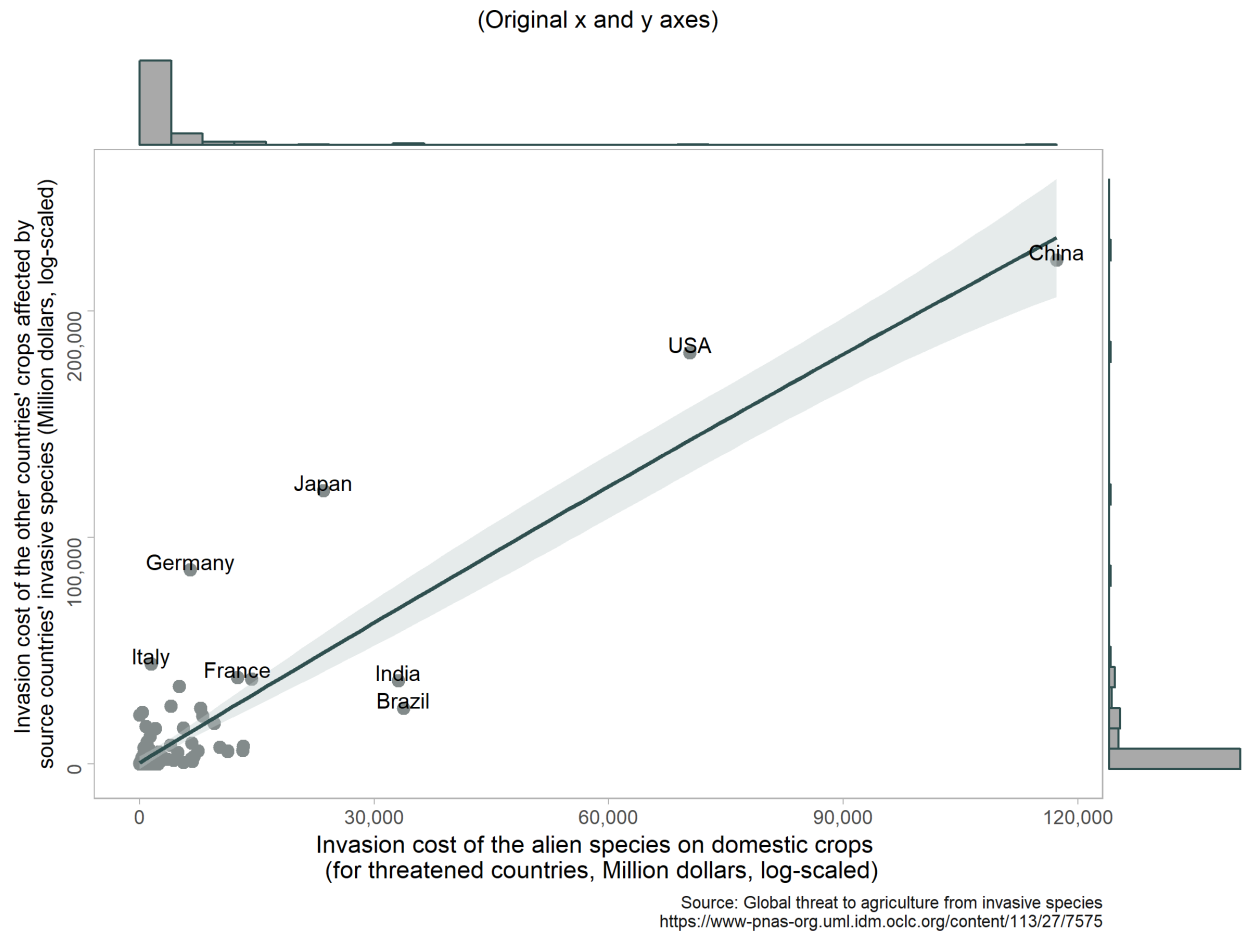


Figure 3:

3.3 Conclusion

From the finalized plot (p6), I can see that there is a relatively strong and positive association between the threat that source countries impose on the other countries and the invasion threat of this country received from foreign species invasion. Also, after scaling both axes logarithmly, the distributions of invasion cost from the source country and the invasion cost on the threatened country appear to be normal or at least somewhat symmetric. However, by no means, the positive association implies a causal relationship, as the effect are most likely to be moderated by the trading amount of a country (Paini, Sheppard, Cook and all, 2016).

Though the final plot present the clear association, the preliminary and non-log-scaled plot give us a clear look of outlining points. In the modified preliminary plot, it is shown that China and USA are the two top threatening source countries, whose invasion cost being either a threatened or source country are way higher than the rest of the countries.

Codes to generate the modified preliminary plot for comparison

```
# add the un-logged plot for comparison

# modify the units
(p1 <- table01
  # change units into million dollars:
  %>% ggplot(aes(x=ICt_million, y=ICs_million))
  + geom_point(colour="azure4", size=2.5)
  + scale_x_continuous(labels=comma)+scale_y_continuous(labels=comma) # labels=comma: no to show th
  + xlab("Invasion cost of the alien species on domestic crops \n (for threatened countries, Million
  + ylab("Invasion cost of the other countries' crops affected by \nsource countries' invasive spec
  + labs(
    # title="Is a country ranked higher as potential source of invasive species \nalso more vu
    subtitle = "(Original x and y axes)",
    caption = "Source: Global threat to agriculture from invasive species
    https://www-pnas-org.uml.idm.oclc.org/content/113/27/7575")
  + geom_smooth(span=10, fill="azure3", colour="darkslategray")
)

# label important points:
(p1 <- p1
  # + geom_text(data = subset(table01, ICt_million>70000), aes(label = country), vjust = 0, nudge_y
  + geom_text(data = subset(table01, ICs_million>34000 | ICt_million>14000 ), aes(label = country),
)

# add theme
(p1 <- p1
  + theme_light()
  + theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(), #no gridline
    axis.title.y = element_text(size=10), # change the size of y axis label
    axis.text.y = element_text(angle = 90),
    plot.title = element_text(hjust = .5), # center plot title
    plot.subtitle = element_text(hjust = .5), # center plot title
    plot.caption = element_text(size=8, color = "gray8")) # change caption style
)
```



```
# add marginal histograms  
(p1 <- ggMarginal(p1, type="histogram", fill="darkgray", colour="darkslategray", size=7))
```

4. Save the final work

```
ggsave("fig_output/A1_p6.png", p6, width = 8, height = 6)
```

To access the figure on the side, please go to the fig_output folder.

5. Potential implication

Interesting questions:

Q1. Which countries are the hosts of the most invasive species?

In order to answer to this question, extra country information of species needs to be provided in table 6.

Q2. Is the invasion threat of a country affected/driven by a country's trading amount?

To answer that, the trading amount of each country needed to be provided.

Q3. Can a country be better protected from invasion species (i.e. reduce the invasion cost) by having better agriculture inspection and imported food and animal product security check?

Extra information and measures on a country's agriculture inspection results and security level measures need to be provided for this purpose.

6. Disgarded work

Interests in finding out the spread of origin countries of the most invasive species

In table_6/invasive_species dataset, list of species and their maximum impact percentages are presented, and there are lists of countries and species in africa_species dataset. I was interested in finding out which countries are the hosts of the most invasive species (i.e. the species having the highest-ranked impact percentage). However, after joining the two tables together, little common species are present in both tables. In other words, I cannot identify which countries host the species in table 6. So, I cannot get a conclusion of which countries carries the most influentially invasive species.

```
# join species -----
species <- invasive_species[invasive_species$species %in% africa_species$species, ]
species

## # A tibble: 1 x 3
##   species      max_impact_percent rank
##   <chr>          <dbl> <dbl>
## 1 Cinara cupressi      12     17

species <- invasive_species %>%
  inner_join(africa_species, by="species")
#only 7 invasive species can be found in african speices dataset - this join is not usable
species

## # A tibble: 7 x 8
##   species max_impact_perc~ rank authority country kingdom environment_sys~
##   <chr>          <dbl> <dbl> <chr>      <chr>    <chr>    <chr>
## 1 Cinara~      12     17 (Buckton~ Libya   Animal~ host
## 2 Cinara~      12     17 (Buckton~ Morocco Animal~ host
## 3 Cinara~      12     17 (Buckton~ Rwanda  Animal~ host
## 4 Cinara~      12     17 (Buckton~ Ethiop~ Animal~ host
## 5 Cinara~      12     17 (Buckton~ Kenya Animal~ host
## 6 Cinara~      12     17 (Buckton~ Uganda  Animal~ host
## 7 Cinara~      12     17 (Buckton~ Malawi  Animal~ host
## # ... with 1 more variable: origin <chr>
```

```
summarise(species)
```

```
## # A tibble: 1 x 0
```