



Case Study of Autism Spectrum Disorder (ASD) with R



ABOUT 1 IN 59 CHILDREN

WERE IDENTIFIED WITH AUTISM SPECTRUM DISORDER
AMONG A 2014 SAMPLE OF 8 YEAR OLDS FROM 11 US COMMUNITIES
IN CDC'S ADDM NETWORK

[United States]

Centers for Disease Control and Prevention (CDC) - Autism Spectrum Disorder (ASD)

Autism spectrum disorder (ASD) is a developmental disability that can cause significant social, communication and behavioral challenges. CDC is committed to continuing to provide essential data on ASD, search for factors that put children at risk for ASD and possible causes, and develop resources that help identify children with ASD as early as possible.

<https://www.cdc.gov/ncbdd/autism/data/index.html>
[\(https://www.cdc.gov/ncbdd/autism/data/index.html\)](https://www.cdc.gov/ncbdd/autism/data/index.html)

[Singapore]

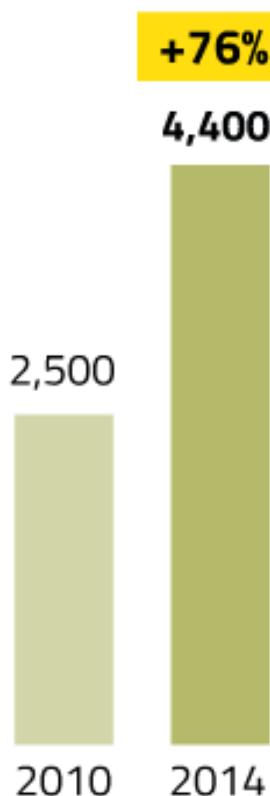
TODAY Online - More preschoolers diagnosed with developmental issues

Doctors cited better awareness among parents and preschool teachers, leading to early referrals for diagnosis.

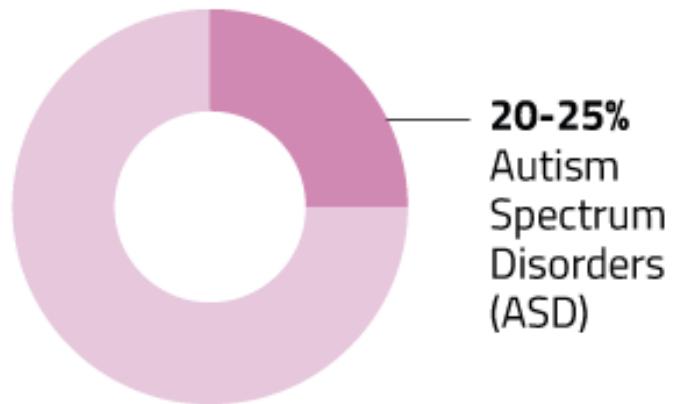
<https://www.gov.sg/news/content/today-online-more-preschoolers-diagnosed-with-developmental-issues>
<https://www.gov.sg/news/content/today-online-more-preschoolers-diagnosed-with-developmental-issues>

Jump in preschoolers diagnosed with developmental issues

● New cases



● Types of diagnosed cases



● ASD incidence

 /160
World Health Organisation

 /150
Singapore

Source: KK Women's and Children's Hospital, National University Hospital **TODAY**

<https://www.pathlight.org.sg/> (<https://www.pathlight.org.sg/>)



Highlights
Latest events and happenings at Pathlight School.



The Art Faculty
Support the products by individuals with autism.



e-Learning Portals
» Learn for Life eCampus
» MC Online
» Student Learning Space



Parents' Corner
Useful resources and information for our parents



Workshop Objective:

Use R to analyze Autism Spectrum Disorder (ASD) data from CDC USA.

<https://www.cdc.gov/ncbddd/autism/data/index.html>
[\(https://www.cdc.gov/ncbddd/autism/data/index.html\)](https://www.cdc.gov/ncbddd/autism/data/index.html)

- **R Fundamentals**
- **Data Summarization**
- **Data Visualisation (Base Graphic)**
- **Data Visualisation (Enhanced)**
- **Sampling & Normality**
- **Confidence Interval (CI)**
- **Workshop Submission**
- **Appendices**



R Fundamentals

R packaged used:

- if(!require(naniar)){install.packages("naniar")}
- if(!require(dplyr)){install.packages("dplyr")}
- if(!require(ggplot2)){install.packages("ggplot2")}
- if(!require(plotly)){install.packages("plotly")}
- if(!require(ggthemes)){install.packages("ggthemes")}
- if(!require(usmap)){install.packages("usmap")}
- if(!require(cowplot)){install.packages("cowplot")}
- if(!require(binom)){install.packages("binom")}

R Fundamentals - Get & Set working directory

Obtain current R working directory

```
In [926]: getwd()
```

```
'/Users/admin-user/Desktop/admin-desktop/vm_shared_folder/git/DDC-ASD/model_R'
```

Set new R working directory

```
In [927]: # setwd("/media/sf_vm_shared_folder/git/DDC/DDC-ASD/model_R")
# setwd('~/Desktop/admin-desktop/vm_shared_folder/git/DDC-ASD/model_R')
getwd()
```

```
'/Users/admin-user/Desktop/admin-desktop/vm_shared_folder/git/DDC-ASD/model_R'
```

Read in CSV data, storing as R dataframe

```
In [928]: # Dataset: US. National Level Children ASD Prevalence
ASD_National <- read.csv("../dataset/ADV_ASD_National.csv", stringsAsFactors = FALSE)
```

```
In [929]: # Dataset: US. State Level Children ASD Prevalence
ASD_State <- read.csv("../dataset/ADV_ASD_State.csv", stringsAsFactors = FALSE)
```

Obtain number of rows and number of columns/features/variables

```
In [930]: dim(ASD_National)
```

```
42 26
```

```
In [931]: dim(ASD_State)
```

```
1692 48
```

Obtain overview (data structure/types)

```
In [932]: str(ASD_National)
```

```
'data.frame': 42 obs. of 26 variables:  
 $ Source : chr "addm" "addm" "addm" "addm" ...  
 $ Year : int 2000 2002 2004 2006 2008 2010 201  
 2 2014 2004 2008 ...  
 $ Prevalence : num 6.7 6.6 8 9 11.3 14.7 14.8 16.8  
 9.5 16.2 ...  
 $ Upper.CI : num 7 6.8 8.4 9.3 11.7 15.1 15.2 17.3  
 12 18.1 ...  
 $ Lower.CI : num 6.3 6.3 7.6 8.6 11 14.3 14.4 16.4  
 7.4 14.5 ...  
 $ Prevalence_dup : num 6.7 6.6 8 9 11.3 14.7 14.8 16.8  
 9.5 16.2 ...  
 $ Source_Full1 : chr "Autism & Developmental Disabilities Monitoring Network" ...  
 $ Source_Full2 : chr "addm-Autism & Developmental Disabilities Monitoring Network" ...  
 - - - - -
```

```
In [933]: str(ASD_State)
```

```
'data.frame': 1692 obs. of 48 variables:  
 $ State : chr "AZ" "GA" "MD" "NJ" ...  
 $ Denominator : int 45322 43593 21532 29714 24535 2  
 3065 35472 45113 36472 11020 ...  
 $ Prevalence : num 6.5 6.5 5.5 9.9 6.3 4.5 3.3 6.2  
 6.9 5.9 ...  
 $ Lower.CI : num 5.8 5.8 4.6 8.9 5.4 3.7 2.7 5.5  
 6.1 4.6 ...  
 $ Upper.CI : num 7.3 7.3 6.6 11.1 7.4 5.5 3.9 7  
 7.8 7.5 ...  
 $ Year : int 2000 2000 2000 2000 2000 2000 2  
 002 2002 2002 2002 ...  
 $ Source : chr "addm" "addm" "addm" "addm" ...  
 $ Source_Full1 : chr "Autism & Developmental Disabilities Monitoring Network" ...  
 $ State_Full1 : chr "Arizona" "Georgia" "Maryland"  
 "New Jersey" ...  
 - - - - -
```

Look at first few rows of data

In [934]: head(ASD_National)

Source	Year	Prevalence	Upper.CI	Lower.CI	Prevalence_dup	Source_Full1	Source_Full2	Male.Prevalence
addm	2000	6.7	7.0	6.3	6.7	Autism & Developmental Disabilities Monitoring Network	addm-Autism & Developmental Disabilities Monitoring Network	No data
addm	2002	6.6	6.8	6.3	6.6	Autism & Developmental Disabilities Monitoring Network	addm-Autism & Developmental Disabilities Monitoring Network	11.5
addm	2004	8.0	8.4	7.6	8.0	Autism & Developmental Disabilities Monitoring Network	addm-Autism & Developmental Disabilities Monitoring Network	12.9

In [935]: head(ASD_State)

State	Denominator	Prevalence	Lower.CI	Upper.CI	Year	Source	Source_Full1	State_Full1	State_Full2
AZ	45322	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Arizona	AZ-Arizona
GA	43593	6.5	5.8	7.3	2000	addm	Autism & Developmental Disabilities Monitoring Network	Georgia	GA-Georgia
MD	21532	5.5	4.6	6.6	2000	addm	Autism & Developmental Disabilities Monitoring Network	Maryland	MD-Maryland
NJ	29714	9.9	8.9	11.1	2000	addm	Autism & Developmental Disabilities Monitoring Network	New Jersey	NJ-New Jersey
SC	24535	6.3	5.4	7.4	2000	addm	Autism & Developmental Disabilities Monitoring Network	South Carolina	SC-South Carolina
WV	23065	4.5	3.7	5.5	2000	addm	Autism & Developmental Disabilities Monitoring Network	West Virginia	WV-West Virginia

Obtain name of columns

```
In [936]: names(ASD_National)
```

```
'Source'  'Year'  'Prevalence'  'Upper.Cl'  'Lower.Cl'  'Prevalence_dup'  'Source_Full1'  
'Source_Full2'  'Male.Prevalence'  'Male.Lower.Cl'  'Male.Upper.Cl'  'Female.Prevalence'  
'Female.Lower.Cl'  'Female.Upper.Cl'  'Non.hispanic.white.Prevalence'  'Non.hispanic.white.Lower.Cl'  
'Non.hispanic.white.Upper.Cl'  'Non.hispanic.black.Prevalence'  'Non.hispanic.black.Lower.Cl'  
'Non.hispanic.black.Upper.Cl'  'Hispanic.Prevalence'  'Hispanic.Lower.Cl'  'Hispanic.Upper.Cl'  
'Asian.or.Pacific.Islander.Prevalence'  'Asian.or.Pacific.Islander.Lower.Cl'  
'Asian.or.Pacific.Islander.Upper.Cl'
```

```
In [937]: names(ASD_State)
```

```
'State'  'Denominator'  'Prevalence'  'Lower.Cl'  'Upper.Cl'  'Year'  'Source'  'Source_Full1'  
'State_Full1'  'State_Full2'  'Numerator_ASD'  'Numerator_NonASD'  'Proportion'  'X95_Z_CI'  
'Z_Lower.Cl'  'Z_Upper.Cl'  'Z_Lower.Cl_ABSerror'  'Z_Upper.Cl_ABSerror'  'Chi_Wilson_P'  
'X95_Chi_Wilson_CI'  'Chi_Wilson_Lower.Cl'  'Chi_Wilson_Upper.Cl'  'Chi_Wilson_Lower.Cl_ABSerror'  
'Chi_Wilson_Upper.Cl_ABSerror'  'Chi_Wilson_Corrected_w_minus.Cl'  
'Chi_Wilson_Corrected_w_plus.Cl'  'Chi_Wilson_Corrected_Lower.Cl'  'Chi_Wilson_Corrected_Upper.Cl'  
'Chi_Wilson_Corrected_Lower.Cl_ABSerror'  'Chi_Wilson_Corrected_Upper.Cl_ABSerror'  
'Male.Prevalence'  'Male.Lower.Cl'  'Male.Upper.Cl'  'Female.Prevalence'  'Female.Lower.Cl'  
'Female.Upper.Cl'  'Non.hispanic.white.Prevalence'  'Non.hispanic.white.Lower.Cl'  
'Non.hispanic.white.Upper.Cl'  'Non.hispanic.black.Prevalence'  'Non.hispanic.black.Lower.Cl'  
'Non.hispanic.black.Upper.Cl'  'Hispanic.Prevalence'  'Hispanic.Lower.Cl'  'Hispanic.Upper.Cl'  
'Asian.or.Pacific.Islander.Prevalence'  'Asian.or.Pacific.Islander.Lower.Cl'  
'Asian.or.Pacific.Islander.Upper.Cl'
```

Display column name with its index number

```
In [938]: cbind(names(ASD_National), c(1:length(names(ASD_National))))
```

Year	2
Prevalence	3
Upper.Cl	4
Lower.Cl	5
Prevalence_dup	6
Source_Full1	7
Source_Full2	8
Male.Prevalence	9
Male.Lower.Cl	10
Male.Upper.Cl	11
Female.Prevalence	12
Female.Lower.Cl	13
Female.Upper.Cl	14

Look at data structure/schema (Selected columns)

```
In [939]: str(ASD_National[, c(1:8, 24, 25, 26)])
```

```
'data.frame': 42 obs. of 11 variables:
 $ Source                  : chr  "addm" "addm" "addm" "addm" ...
 $ Year                    : int  2000 2002 2004 2006 2008 2010 201
 $ 2014 2004 2008 ...
 $ Prevalence               : num  6.7 6.6 8 9 11.3 14.7 14.8 16.8
 $ 9.5 16.2 ...
 $ Upper.CI                 : num  7 6.8 8.4 9.3 11.7 15.1 15.2 17.3
 $ 12 18.1 ...
 $ Lower.CI                 : num  6.3 6.3 7.6 8.6 11 14.3 14.4 16.4
 $ 7.4 14.5 ...
 $ Prevalence_dup           : num  6.7 6.6 8 9 11.3 14.7 14.8 16.8
 $ 9.5 16.2 ...
 $ Source_Full1              : chr  "Autism & Developmental Disabilities Monitoring Network" ...
 $ Source_Full2              : chr  "addm-Autism & Developmental Disabilities Monitoring Network" ...
 $ Asian.or.Pacific.Islander.Prevalence: chr  "No data" "No data" "No data" "No data" ...
 $ Asian.or.Pacific.Islander.Lower.CI   : chr  "No data" "No data" "No data" "No data" ...
 $ Asian.or.Pacific.Islander.Upper.CI  : chr  "No data" "No data" "No data" "No data" ...
```

Quiz:

Obtain feature/column names and column index of dataframe: ASD_State

```
In [940]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

R Fundamentals - Work with dataframe

Access column 1 as a **named list** of string/chr (dataframe alike):

```
In [941]: # use column index:  
ASD_National[1]
```

Source

addm
addm
addm
addm
addm
addm
addm
addm
nsch
nsch
nsch
nsch

```
In [942]: typeof(ASD_National[1])  
'list'
```

```
In [943]: ASD_National[1]$Source
```

'addm' 'addm' 'addm' 'addm' 'addm' 'addm' 'addm' 'addm' 'nsch' 'nsch' 'nsch'
'sped'
'sped' 'sped' 'sped' 'sped' 'sped' 'medi' 'medi' 'medi' 'medi' 'medi'
'medi' 'medi' 'medi' 'medi' 'medi' 'medi'

```
In [944]: # use column name:  
ASD_National["Source"]
```

Source

addm
addm
addm
addm
addm
addm
addm
nsch
nsch
nsch
nsch

```
In [945]: typeof(ASD_National['Source'])  
'list'
```

```
In [946]: ASD_National['Source']$Source
```

```
'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'nsch'  'nsch'  'nsch'  
'sped'  
'sped'  'sped'  'sped'  'sped'  'sped'  'medi'  'medi'  'medi'  'medi'  'medi'  
'medi'  'medi'  'medi'  'medi'  'medi'
```

Access column 1 as a set of string/chr:

```
In [947]: ASD_National[, 1]
```

```
'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'nsch'  'nsch'  'nsch'  
'sped'  
'sped'  'sped'  'sped'  'sped'  'sped'  'medi'  'medi'  'medi'  'medi'  'medi'  
'medi'  'medi'  'medi'  'medi'  'medi'
```

```
In [948]: typeof(ASD_National[, 1])
```

```
'character'
```

```
In [949]: ASD_National[, 1]
```

```
'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'nsch'  'nsch'  'nsch'  
'sped'  
'sped'  'sped'  'sped'  'sped'  'sped'  'medi'  'medi'  'medi'  'medi'  'medi'  
'medi'  'medi'  'medi'  'medi'  'medi'
```

```
In [950]: # or
```

```
ASD_National[, "Source"]
```

```
'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'nsch'  'nsch'  'nsch'  
'sped'  
'sped'  'sped'  'sped'  'sped'  'sped'  'medi'  'medi'  'medi'  'medi'  'medi'  
'medi'  'medi'  'medi'  'medi'  'medi'
```

```
In [951]: # or
```

```
ASD_National$Source
```

```
'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'addm'  'nsch'  'nsch'  'nsch'  
'sped'  
'sped'  'sped'  'sped'  'sped'  'sped'  'medi'  'medi'  'medi'  'medi'  'medi'  
'medi'  'medi'  'medi'  'medi'  'medi'
```

Count number of elements in a object:

```
In [952]: length(ASD_National) # number of features/columns
```

```
26
```

```
In [953]: length(ASD_National[1, ]) # number of features/columns
```

```
26
```

```
In [954]: length(ASD_National[, 1]) # number of elements(rows) in column 1
```

```
42
```

```
In [955]: length(ASD_National[, "Source"]) # same as above
```

```
42
```

```
In [956]: length(ASD_National$Source) # number of elements in chr list
```

```
42
```

Access elements from column 1, which is a list:

```
In [957]: # using column index  
ASD_National[1][1, ]
```

```
'addm'
```

```
In [958]: ASD_National[1][11, ]
```

```
'nsch'
```

```
In [959]: ASD_National[1][11:20, ]
```

```
'nsch'  'nsch'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'
```

```
In [960]: # using column name  
ASD_National["Source"][1, ]
```

```
'addm'
```

```
In [961]: ASD_National["Source"][11, ]
```

```
'nsch'
```

```
In [962]: ASD_National["Source"][11:20, ]
```

```
'nsch'  'nsch'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'
```

Access elements from column 1, which is a set of string/chr:

```
In [963]: # using column index  
ASD_National[, 1][1]
```

```
'addm'
```

```
In [964]: ASD_National[, 1][11]
```

```
'nsch'
```

```
In [965]: ASD_National[, 1][11:20]
```

```
'nsch'  'nsch'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'  'sped'
```

```
In [966]: # using column name  
ASD_National[, "Source"][1]  
  
'addm'
```

```
In [967]: # using column name  
ASD_National[, "Source"][11]  
  
'nsch'
```

```
In [968]: # using column name  
ASD_National[, "Source"][11:20]  
  
'nsch' 'nsch' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped'
```

```
In [969]: # using $ operator  
ASD_National$Source[1]  
  
'addm'
```

```
In [970]: ASD_National$Source[11]  
  
'nsch'
```

```
In [971]: ASD_National$Source[11:20]  
  
'nsch' 'nsch' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped' 'sped'
```

Access elements of different column:

```
In [972]: cbind(names(ASD_National), c(1:length(names(ASD_National))))
```

Source	1
Year	2
Prevalence	3
Upper.Cl	4
Lower.Cl	5
Prevalence_dup	6
Source_Full1	7
Source_Full2	8
Male.Prevalence	9
Male.Lower.Cl	10
Male.Upper.Cl	11
Female.Prevalence	12
Female.Lower.Cl	13

```
In [973]: ASD_National[1, 1] # row 1, column 1: "Source"  
  
'addm'
```

```
In [974]: ASD_National[10, 1] # row 10, column 1: "Source"
```

'nsch'

```
In [975]: ASD_National[1, 3] # row 1, column 3: "Prevalence"
```

6.7

```
In [976]: ASD_National[10, 3] # row 10, column 3: "Prevalence"
```

16.2

```
In [977]: ASD_National[1:10, 1:3] # row 1 to 10 from column 1 to 3
```

Source	Year	Prevalence
addm	2000	6.7
addm	2002	6.6
addm	2004	8.0
addm	2006	9.0
addm	2008	11.3
addm	2010	14.7
addm	2012	14.8
addm	2014	16.8
nsch	2004	9.5
nsch	2008	16.2

```
In [978]: # or using column names
```

```
ASD_National[1:10, c('Source', 'Year', 'Prevalence')]
```

Source	Year	Prevalence
addm	2000	6.7
addm	2002	6.6
addm	2004	8.0
addm	2006	9.0
addm	2008	11.3
addm	2010	14.7
addm	2012	14.8
addm	2014	16.8
nsch	2004	9.5
nsch	2008	16.2

```
In [979]: ASD_National[c(1:10, 20, 30:35), c(1:3, 9, 12)] # row 1 to 10, 20, and 20 to 25 f
```

	Source	Year	Prevalence	Male.Prevalence	Female.Prevalence
1	addm	2000	6.7	No data	No data
2	addm	2002	6.6	11.5	2.7
3	addm	2004	8.0	12.9	2.9
4	addm	2006	9.0	14.5	3.2
5	addm	2008	11.3	18.4	4
6	addm	2010	14.7	23.7	5.3
7	addm	2012	14.8	23.4	5.2
8	addm	2014	16.8	26.6	6.6
9	nsch	2004	9.5		
10	nsch	2008	16.2		
20	sped	2007	5.4		
30	medi	2000	2.3		
31	medi	2001	2.6		
32	medi	2002	2.8		
33	medi	2003	3.0		
34	medi	2004	3.5		
35	medi	2005	3.9		

[Tips] We notice missing data from above.

R Fundamentals - Process missing data

Count missing values in dataframe:

```
In [980]: sum(is.na(ASD_National)) # No missing data recognised by R (NA)
```

```
0
```

```
In [981]: sum(is.na(ASD_State)) # Some missing data recognised by R (NA)
```

```
14454
```

Empty string, "No data" arenot considered as missing value by R, thus we need to handle them manually.

```
In [982]: # Define several offending strings  
na_strings <- c("", "No data", "NA", "N A", "N / A", "N/A", "N/ A", "Not Available")
```

```
In [983]: # Load required function from packages:  
if(!require(naniar)){install.packages("naniar")}  
library(naniar)  
if(!require(dplyr)){install.packages("dplyr")}  
library(dplyr)
```

```
In [984]: # Uncomment below to show help  
# ?replace_with_na_all # Documentation
```

Replace these defined missing/offending values to R's internal NA

```
In [985]: # "~.x" is a reserved keyword of this function:  
ASD_National = replace_with_na_all(ASD_National, condition = ~.x %in% na_strings)
```

```
In [986]: # Count missing values (R's internal NA) in dataframe:  
sum(is.na(ASD_National))
```

650

R Fundamentals - Process invalid characters

Remove invalid unicode char/string: \x92

```
In [987]: ASD_National$Source_Full1[ASD_National$Source_Full1 == "National Survey of Childr  
"National Survey of Children's Health"]
```

```
In [988]: ASD_National$Source_Full2[ASD_National$Source_Full2 == "nsch-National Survey of C  
"nsch-National Survey of Children's Health"]
```

R Fundamentals - Delete/Drop dataframe variable

Delete/Drop duplicate variable: Prevalence_dup

```
In [989]: drop <- c("Prevalence_dup", "Dummy Variable Name")
```

```
In [990]: ASD_National = ASD_National[, !(names(ASD_National) %in% drop)] # Recall Datafram
```

R Fundamentals - Create/Add dataframe variable

Create one new variable: Source_UC by converting to uppercase letters

```
In [991]: ASD_National$Source_UC <- toupper(ASD_National$Source)
```

Create one new variable: Source_Full3 by combining Source and Source_Full1

```
In [992]: ASD_National$Source_Full3 <- paste(toupper(ASD_National$Source), ASD_National$Sou
```

R Fundamentals - Convert to correct data types

Review data structure and variable names:

```
In [993]: str(ASD_National)
cbind(names(ASD_National), c(1:length(names(ASD_National))))
```

Classes 'tbl_df', 'tbl' and 'data.frame': 42 obs. of 27 variables:
 \$ Source : chr "addm" "addm" "addm" "addm" ...
 \$ Year : int 2000 2002 2004 2006 2008 2010 201
 2 2014 2004 2008 ...
 \$ Prevalence : num 6.7 6.6 8 9 11.3 14.7 14.8 16.8
 9.5 16.2 ...
 \$ Upper.CI : num 7 6.8 8.4 9.3 11.7 15.1 15.2 17.3
 12 18.1 ...
 \$ Lower.CI : num 6.3 6.3 7.6 8.6 11 14.3 14.4 16.4
 7.4 14.5 ...
 \$ Source_Full1 : chr "Autism & Developmental Disabilities Monitoring Network" ...
 \$ Source_Full2 : chr "addm-Autism & Developmental Disabilities Monitoring Network" ...
 \$ Male.Prevalence : chr NA "11.5" "12.9" "14.5" ...
 ^ ^

Convert Prevalence and CIs from categorical/chr to numeric, column 8 to 25

```
In [994]: ix <- 8:25 # define an index
# apply()
ASD_National[ix] <- apply(ASD_National[ix], 2, as.numeric) # "2" means column-wise
```

```
In [995]: # Uncomment below to show help
# ?apply # Documentation
```

```
In [996]: # or lapply()
ASD_National[ix] <- lapply(ASD_National[ix], as.numeric) # column-wise
```

```
In [997]: # Uncomment below to show help
# ?lapply # Documentation
```

Convert Source from categorical/chr to categorical/factor

```
In [998]: ix <- c(1, 6, 7, 26, 27) # define an index  
ASD_National[ix] <- lapply(ASD_National[ix], as.factor)
```

Create new ordered factor Year_Factor from Year

```
In [999]: ASD_National$Year_Factor <- factor(ASD_National$Year, ordered = TRUE)
```

```
In [1000]: # Observe the difference of 'Levels' in below two factors  
ASD_National$Year_Factor # Ordinal categorical variable  
str(ASD_National$Year_Factor)
```

```
ASD_National$Source # Nominal categorical variable  
str(ASD_National$Source)
```

2000	2002	2004	2006	2008	2010	2012	2014	2004	2008	2012	2016	2000	2001	2002
2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2000
2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012			

► Levels:

```
Ord.factor w/ 17 levels "2000"<"2001"<...: 1 3 5 7 9 11 13 15 5 9 ...
```

```
addm addm addm addm addm addm nsch nsch nsch sped sped  
sped sped sped sped sped sped sped sped sped sped sped sped  
medi medi
```

► Levels:

```
Factor w/ 4 levels "addm","medi",...: 1 1 1 1 1 1 1 3 3 ...
```

```
In [1001]: # Optionally, below is manual conversion examples:  
# ASD_National$Male.Prevalence = as.numeric(ASD_National$Male.Prevalence)  
# ASD_National$Source = as.factor(ASD_National$Source)
```

Optionally, export the processed dataframe data to CSV file.

```
In [1002]: write.csv(ASD_National, file = ".../dataset/ADV_ASD_National_R.csv", row.names = F
```

```
In [1003]: # Read back in above saved file:  
# ASD_National <- read.csv("../dataset/ADV_ASD_National_R.csv")  
# ASD_National$Year_Factor <- factor(ASD_National$Year_Factor, ordered = TRUE) #
```

Data Summarization

Data Summarization - High Level Data Summary

```
In [1004]: summary(ASD_National)
```

Source	Year	Prevalence	Upper.CI	Lower.CI
addm: 8	Min. :2000	Min. : 1.800	Min. : 1.800	Min. : 1.700
medi:13	1st Qu.:2004	1st Qu.: 3.950	1st Qu.: 3.950	1st Qu.: 3.875
nsch: 4	Median :2008	Median : 6.650	Median : 6.900	Median : 6.350
sped:17	Mean :2007	Mean : 7.952	Mean : 8.207	Mean : 7.712
	3rd Qu.:2011	3rd Qu.: 9.725	3rd Qu.:10.350	3rd Qu.: 9.625
	Max. :2016	Max. :29.200	Max. :30.700	Max. :27.700

Source_Full1

Autism & Developmental Disabilities Monitoring Network: 8
Medicaid :13
National Survey of Children's Health : 4
Special Education Child Count :17

Source_Full2

addm-Autism & Developmental Disabilities Monitoring Network: 8
medi-Medicaid :13

Data Summarization - Summary of numeric variables

```
In [1005]: # Filter only numeric variables/columns
select_if(ASD_National, is.numeric) # library(dplyr)
```

Year	Prevalence	Upper.CI	Lower.CI	Male.Prevalence	Male.Lower.CI	Male.Upper.CI	Female.Prevalence	Female.Upper.CI	Female.Lower.CI
2000	6.7	7.0	6.3	NA	NA	NA	NA	NA	NA
2002	6.6	6.8	6.3	11.5	NA	NA	NA	2.7	NA
2004	8.0	8.4	7.6	12.9	12.2	13.7	NA	2.9	NA
2006	9.0	9.3	8.6	14.5	13.9	15.1	NA	3.2	NA
2008	11.3	11.7	11.0	18.4	17.7	19.0	NA	4.0	NA
2010	14.7	15.1	14.3	23.7	23.0	24.4	NA	5.3	NA
2012	14.8	15.2	14.4	23.4	22.7	24.1	NA	5.2	NA
2014	16.8	17.3	16.4	26.6	25.8	27.4	NA	6.6	NA
2004	9.5	12.0	7.4	NA	NA	NA	NA	NA	NA
2008	16.2	18.1	14.5	NA	NA	NA	NA	NA	NA
2012	21.2	22.3	20.1	NA	NA	NA	NA	NA	NA
2016	29.2	30.7	27.7	NA	NA	NA	NA	NA	NA

```
In [1006]: # Data summarization  
summary(select_if(ASD_National, is.numeric))
```

Year	Prevalence	Upper.CI	Lower.CI
Min. :2000	Min. : 1.800	Min. : 1.800	Min. : 1.700
1st Qu.:2004	1st Qu.: 3.950	1st Qu.: 3.950	1st Qu.: 3.875
Median :2008	Median : 6.650	Median : 6.900	Median : 6.350
Mean :2007	Mean : 7.952	Mean : 8.207	Mean : 7.712
3rd Qu.:2011	3rd Qu.: 9.725	3rd Qu.:10.350	3rd Qu.: 9.625
Max. :2016	Max. :29.200	Max. :30.700	Max. :27.700
Male.Prevalence	Male.Lower.CI	Male.Upper.CI	Female.Prevalence
Min. :11.50	Min. :12.20	Min. :13.70	Min. :2.700
1st Qu.:13.70	1st Qu.:14.85	1st Qu.:16.07	1st Qu.:3.050
Median :18.40	Median :20.20	Median :21.55	Median :4.000
Mean :18.71	Mean :19.22	Mean :20.62	Mean :4.271
3rd Qu.:23.55	3rd Qu.:22.93	3rd Qu.:24.32	3rd Qu.:5.250
Max. :26.60	Max. :25.80	Max. :27.40	Max. :6.600
NA's :35	NA's :36	NA's :36	NA's :35
Female.Lower.CI	Female.Upper.CI	Non.hispanic.white.Prevalence	
Min. :2.600	Min. :3.300	Min. : 7.70	
1st Qu.:3.100	1st Qu.:3.700	1st Qu.: 9.80	
..

[Tips] We notice missing data in a few Prevalence variables.

```
In [1007]: # Calculate average Prevalence, no error  
mean(ASD_National$Prevalence)  
mean(ASD_National$Prevalence[ASD_National$Source == 'addm'])  
mean(ASD_National$Prevalence[ASD_National$Source == 'medi'])  
mean(ASD_National$Prevalence[ASD_National$Source == 'nsch'])  
mean(ASD_National$Prevalence[ASD_National$Source == 'sped'])
```

7.95238095238095

10.9875

4.67692307692308

19.025

6.42352941176471

```
In [1008]: # Calculate average Male.Prevalence, there is error!  
mean(ASD_National$Male.Prevalence)
```

<NA>

```
In [1009]: # Because of NA, mean() cannot process, thus we use na.rm to ignore NAs  
mean(ASD_National$Male.Prevalence, na.rm = TRUE)
```

18.7142857142857

```
In [1010]: mean(ASD_National$Female.Prevalence, na.rm = TRUE)
```

4.27142857142857

```
In [1011]: # Count occurrences of uniques values in a variable/column: number of rows (of data
table(ASD_National$Year) # ?table
```

2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
3	2	3	2	4	2	3	2	4	2	3	2	4	1	2	1
2016															
	2														

Data Summarization - Summary of categorical variables

```
In [1012]: # List of categorical variables
names(select_if(ASD_National, is.factor)) # All categorical variables are factor
names(select_if(ASD_National, is.character)) # No categorical variable is character

'Source' 'Source_Full1' 'Source_Full2' 'Source_UC' 'Source_Full3' 'Year_Factor'
```

```
In [1013]: # Look at summary
summary(select_if(ASD_National, is.factor))
```

Source	Source_Full1
addm: 8	Autism & Developmental Disabilities Monitoring Network: 8
medi:13	Medicaid :13
nsch: 4	National Survey of Children's Health : 4
sped:17	Special Education Child Count :17

Source_Full2	Source_UC
addm-Autism & Developmental Disabilities Monitoring Network: 8	ADDM: 8
medi-Medicaid :13	MEDI:13
nsch-National Survey of Children's Health : 4	NSCH: 4
sped-Special Education Child Count :17	SPED:17

Source_Full3	Year_Factor
ADDM Autism & Developmental Disabilities Monitoring Network: 8	2004 : 4
MEDI Medicaid :13	2008 : 4
NSCH National Survey of Children's Health : 4	2012 : 4
SPED Special Education Child Count :17	2000 : 3
	2002 : 3
	2006 : 3
(Other):21	

```
In [1014]: summary(select_if(ASD_National, is.character))

< table of extent 0 x 0 >
```

```
In [1015]: # Count occurrences of uniques values in a variable/column
table(ASD_National$Source)
```

addm	medi	nsch	sped
8	13	4	17

```
In [1016]: table(ASD_National$Source_Full3)
```

ADDM Autism & Developmental Disabilities Monitoring Network	
	8
MEDI Medicaid	
	13
NSCH National Survey of Children's Health	
	4
SPED Special Education Child Count	
	17

```
In [1017]: table(ASD_National$Year_Factor)
```

2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
3	2	3	2	4	2	3	2	4	2	3	2	4	1	2	1
2016															
	2														

```
In [1018]: table(ASD_National$Prevalence) # numeric is also possible
```

1.8	2.1	2.3	2.6	2.8	3	3.5	3.6	3.9	4.1	4.4	4.8	5.1	5.4	5.6	5.9
1	1	1	2	1	2	1	1	1	1	1	1	1	1	1	1
6.2	6.4	6.6	6.7	7	7.1	7.7	8	8.2	8.4	9	9.1	9.5	9.8	10.5	11.2
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
11.3	11.9	14.7	14.8	16.2	16.8	21.2	29.2								
1	1	1	1	1	1	1	1								

```
In [1019]: # Display unique values (levels) of a factor categorical
lapply(select_if(ASD_National, is.factor), levels)
```

\$Source

'addm' 'medi' 'nsch' 'sped'

\$Source_Full1

'Autism & Developmental Disabilities Monitoring Network' 'Medicaid'

'National Survey of Children's Health' 'Special Education Child Count'

\$Source_Full2

'addm-Autism & Developmental Disabilities Monitoring Network' 'medi-Medicaid'

'nsch-National Survey of Children's Health' 'sped-Special Education Child Count'

\$Source_UC

'ADDM' 'MEDI' 'NSCH' 'SPED'

\$Source_Full3

'ADDM Autism & Developmental Disabilities Monitoring Network' 'MEDI Medicaid'

'NSCH National Survey of Children's Health' 'SPED Special Education Child Count'

\$Year_Factor

'2000' '2001' '2002' '2003' '2004' '2005' '2006' '2007' '2008' '2009' '2010' '2011'

'2012' '2013' '2014' '2015' '2016'

```
In [1020]: # or using variable names
lapply(ASD_National[c('Source_UC', 'Year_Factor')], levels)

$Source_UC
'ADDM' 'MEDI' 'NSCH' 'SPED'

$Year_Factor
'2000' '2001' '2002' '2003' '2004' '2005' '2006' '2007' '2008' '2009' '2010' '2011'
'2012' '2013' '2014' '2015' '2016'
```

```
In [1021]: # Pivot of counting occurrences
table(ASD_National$Source_Full3, ASD_National$Year) # table(ASD_National$Year, AS
```

	2000	2001	2002
ADDM Autism & Developmental Disabilities Monitoring Network	1	0	1
MEDI Medicaid	1	1	1
NSCH National Survey of Children's Health	0	0	0
SPED Special Education Child Count	1	1	1
	2003	2004	2005
ADDM Autism & Developmental Disabilities Monitoring Network	0	1	0
MEDI Medicaid	1	1	1
NSCH National Survey of Children's Health	0	1	0
SPED Special Education Child Count	1	1	1
	2006	2007	2008
ADDM Autism & Developmental Disabilities Monitoring Network	1	0	1
MEDI Medicaid	1	1	1
NSCH National Survey of Children's Health	0	0	1
SPED Special Education Child Count	1	1	1

~~~~~ ~~~~ ~~~~

## Data Visualisation (Base Graphic)

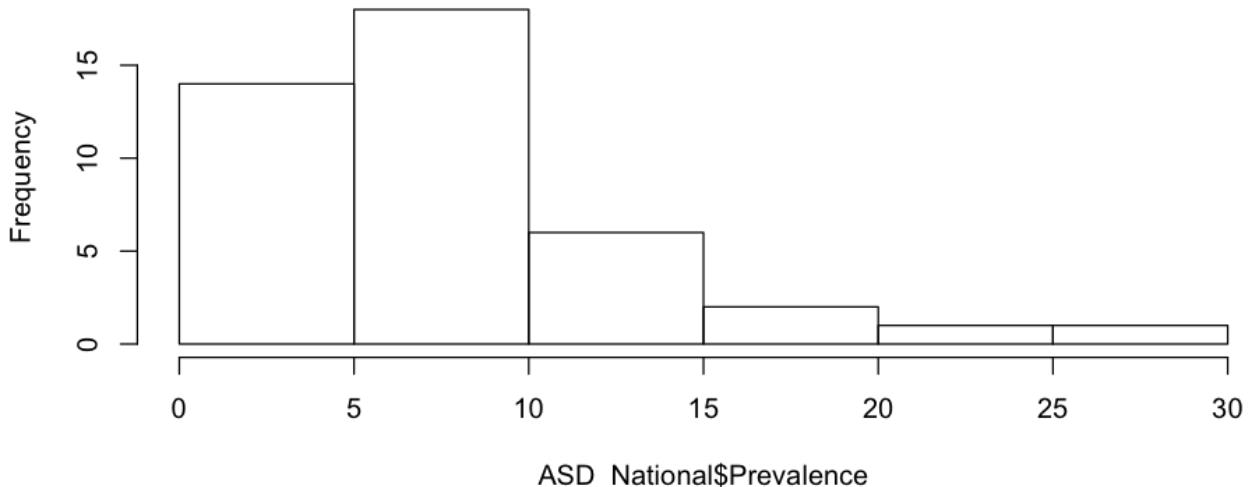
```
In [1022]: # library(repr)
# Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

**Data Visualisation (Base Graphic) - Histogram (distribution of binned continuous variable)**

<https://www.statmethods.net/graphs/density.html> (<https://www.statmethods.net/graphs/density.html>)

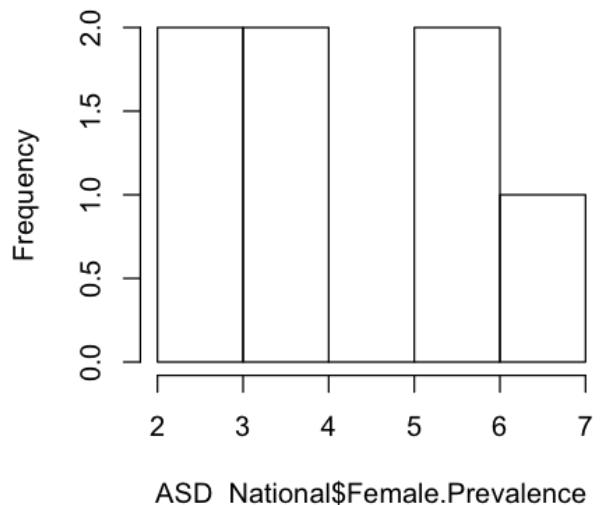
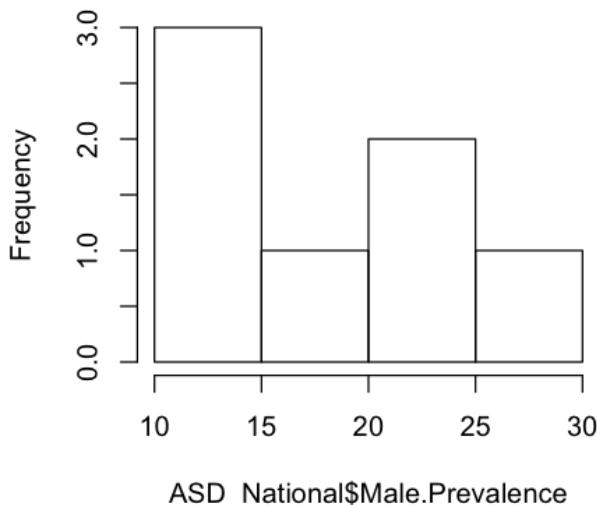
```
In [1023]: hist(ASD_National$Prevalence)
```

Histogram of ASD\_National\$Prevalence

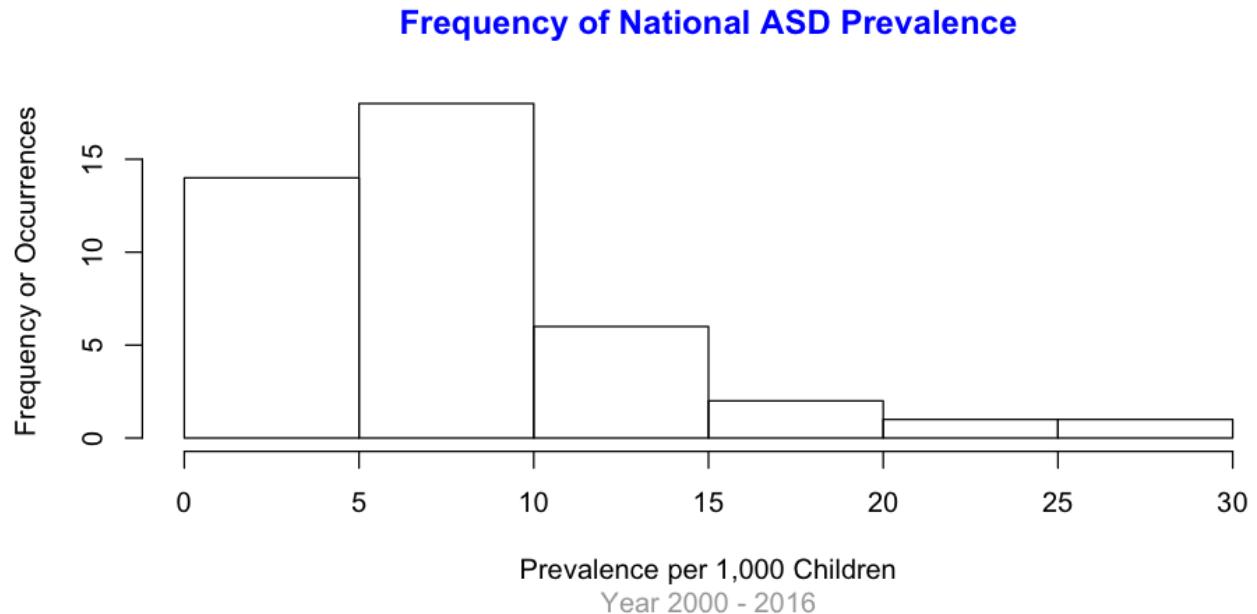


```
In [1024]: par(mfrow=c(1, 2)) # multiple plots on one page: row split to: 1, column split to: 2  
hist(ASD_National$Male.Prevalence)  
hist(ASD_National$Female.Prevalence)  
par(mfrow=c(1, 1)) # Reset to one plot on one page
```

Histogram of ASD\_National\$Male.Prevalence | Histogram of ASD\_National\$Female.Prevalence



```
In [1025]: # Histogram with annotations
hist(ASD_National$Prevalence,
      main = "Frequency of National ASD Prevalence", # Chart title
      xlab = "Prevalence per 1,000 Children", # x axis label
      ylab = "Frequency or Occurrences",# y axis label
      sub = "Year 2000 - 2016", # Chart subtitle at bottom
      col.main="blue", col.lab="black", col.sub="darkgrey") # Colours
```



**Density plot (distribution for continuous variable normalized to 100% area under curve)**

<https://www.statmethods.net/graphs/density.html> (<https://www.statmethods.net/graphs/density.html>)

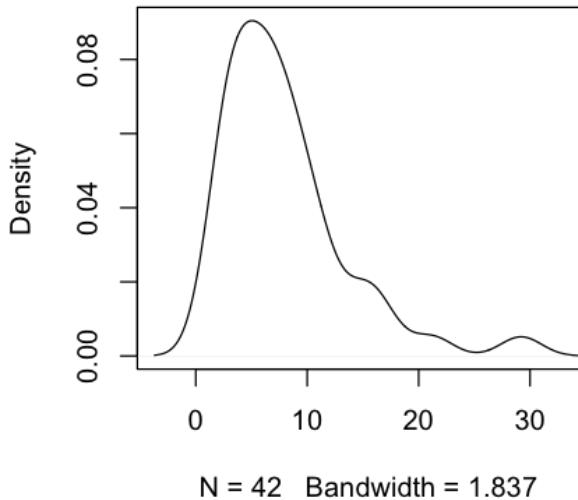
```
In [1026]: par(mfrow=c(1, 2)) # multiple plots on one page: row split to: 1, column split to: 2

plot(density(ASD_National$Prevalence))

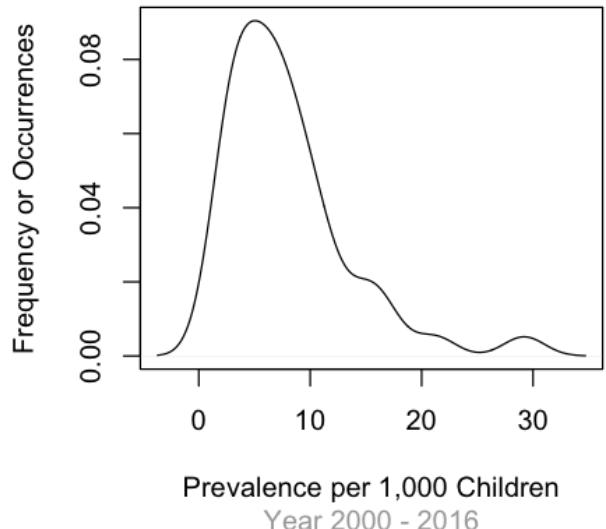
# Density plot with annotations
plot(density(ASD_National$Prevalence),
     main = "Density of National ASD Prevalence",
     xlab = "Prevalence per 1,000 Children",
     ylab = "Frequency or Occurrences",
     sub = "Year 2000 - 2016",
     col.main="blue", col.lab="black", col.sub="darkgrey")

par(mfrow=c(1, 1))
```

**density.default(x = ASD\_National\$Prevalence)**



**Density of National ASD Prevalence**



### Boxplot plot (median, 25% quantile, 75% quantile)

<https://www.statmethods.net/graphs/boxplot.html> (<https://www.statmethods.net/graphs/boxplot.html>)

<https://stats.stackexchange.com/questions/156778/percentile-vs-quantile-vs-quartile>  
(<https://stats.stackexchange.com/questions/156778/percentile-vs-quantile-vs-quartile>)

0 quartile = 0 quantile = 0 percentile

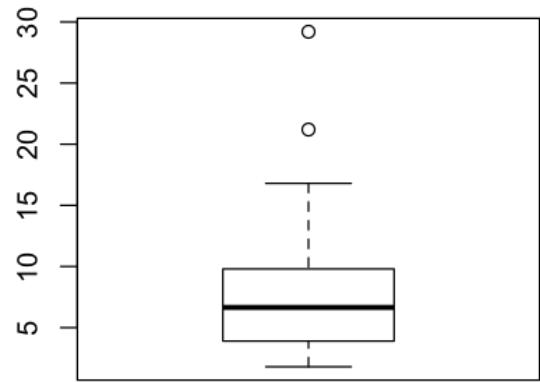
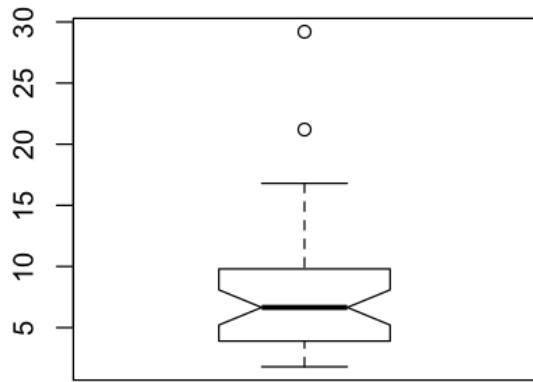
1 quartile = 0.25 quantile = 25 percentile

2 quartile = .5 quantile = 50 percentile (median)

3 quartile = .75 quantile = 75 percentile

4 quartile = 1 quantile = 100 percentile

```
In [1027]: par(mfrow=c(1, 2)) # multiple plots on one page: row split to: 1, column split to:  
  
# All children prevalence with and without 95% confidence side by side:  
boxplot(ASD_National$Prevalence, notch = TRUE) # 95% confidence interval - a notch  
boxplot(ASD_National$Prevalence) # All children  
  
par(mfrow=c(1, 1))
```

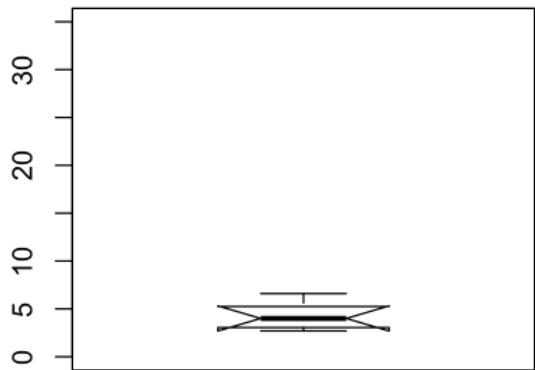
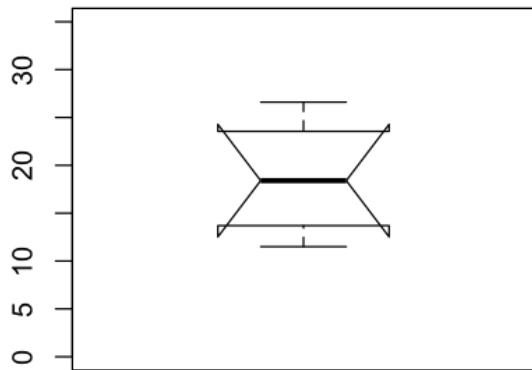


```
In [1028]: par(mfrow=c(1, 2)) # multiple plots on one page: row split to: 1, column split to: 2

# Male prevalence and Female prevalence side by side:
boxplot(ASD_National$Male.Prevalence, ylim = c(0, 35), notch = TRUE) # Male child
boxplot(ASD_National$Female.Prevalence, ylim = c(0, 35), notch = TRUE) # Female child

par(mfrow=c(1, 1))

Warning message in bxp(list(stats = structure(c(11.5, 13.7, 18.4, 23.55, 26.6),
.Dim = c(5L, :
"some notches went outside hinges ('box'): maybe set notch=FALSE"
Warning message in bxp(list(stats = structure(c(2.7, 3.05, 4, 5.25, 6.6), .Dim = c(5L, :
"some notches went outside hinges ('box'): maybe set notch=FALSE"
```



```
In [1029]: # Display value ranges
# numeric:
range(ASD_National$Prevalence)
```

1.8 29.2

```
In [1030]: range(ASD_National$Year)
```

2000 2016

```
In [1031]: # categorical:
min(ASD_National$Year_Factor)
```

2000

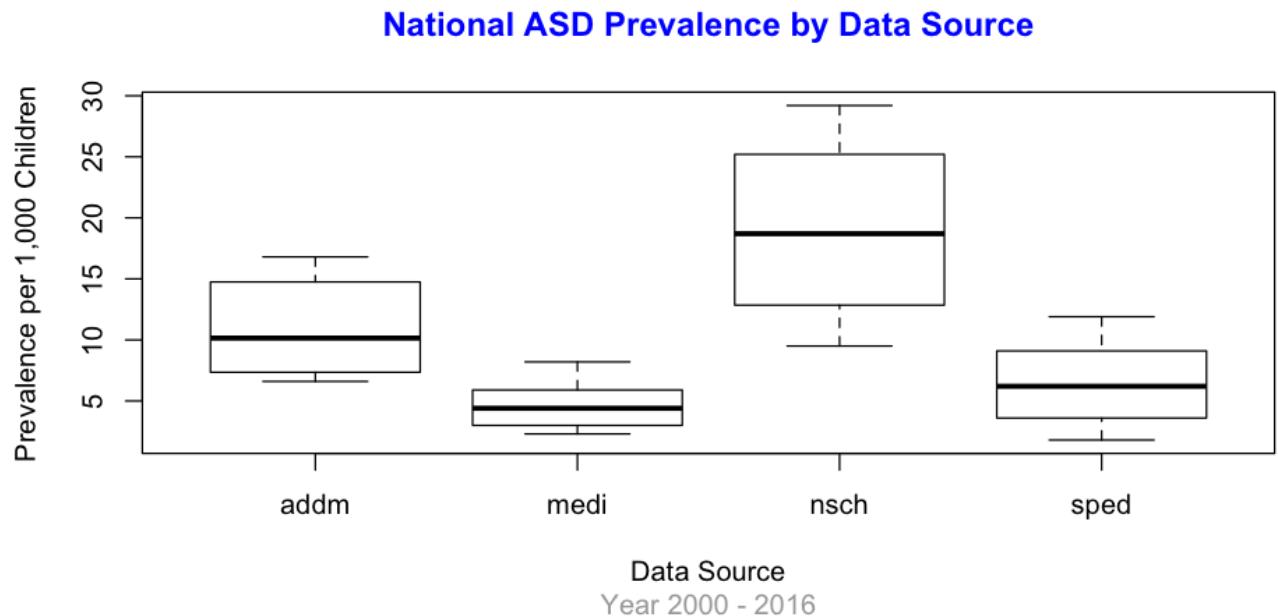
► Levels:

```
In [1032]: max(ASD_National$Year_Factor)
```

2016

► Levels:

```
In [1033]: # Create 'Prevalence' box plots break by 'Source'  
boxplot(ASD_National$Prevalence ~ ASD_National$Source,  
        main = "National ASD Prevalence by Data Source",  
        xlab = "Data Source",  
        ylab = "Prevalence per 1,000 Children",  
        sub = "Year 2000 - 2016",  
        col.main="blue", col.lab="black", col.sub="darkgrey")
```



### Quiz:

Set `notch=TRUE` to above boxplot. Are there overlapping among four data sources?

```
In [1034]: # Write your code below and press Shift+Enter to execute
```

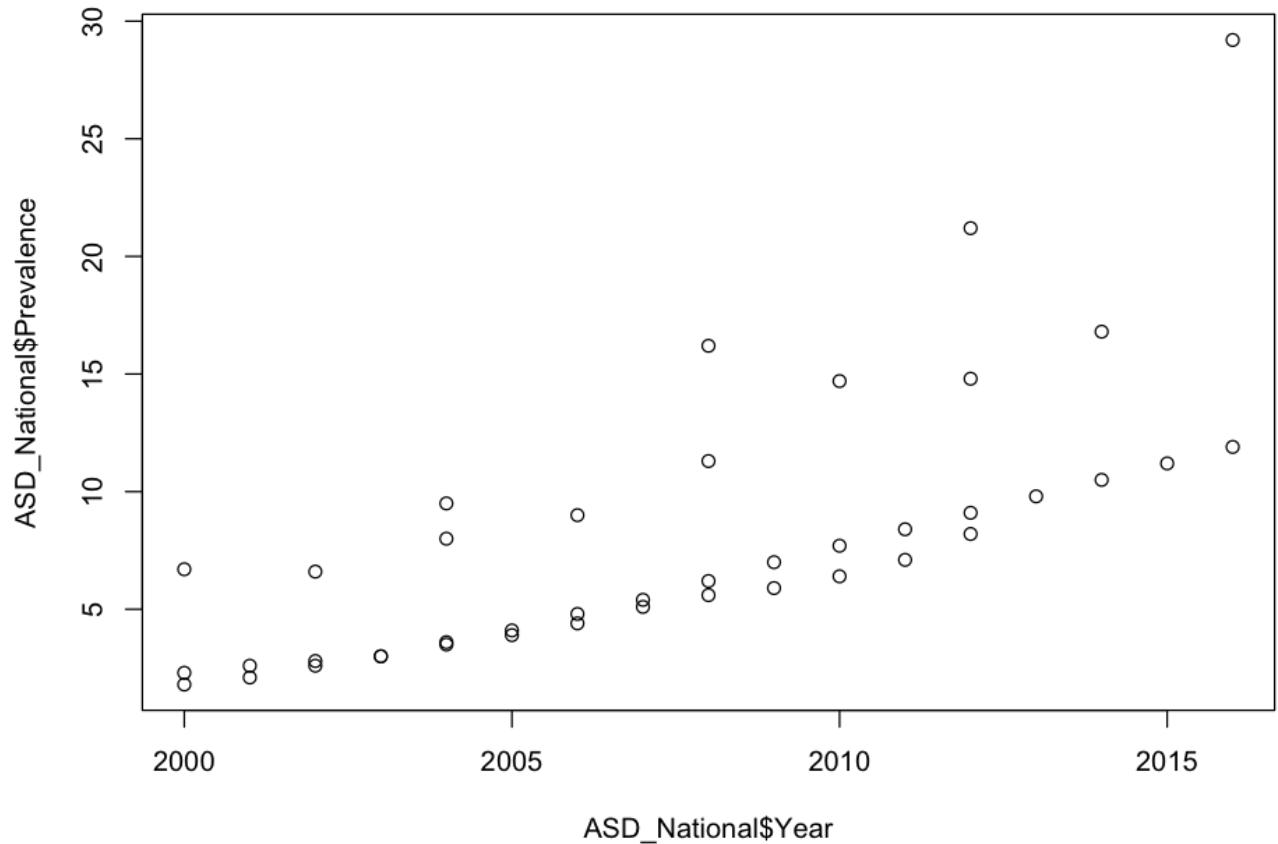
Double-click **here** for the solution.

### Data Visualisation (Base Graphic) - Line chart

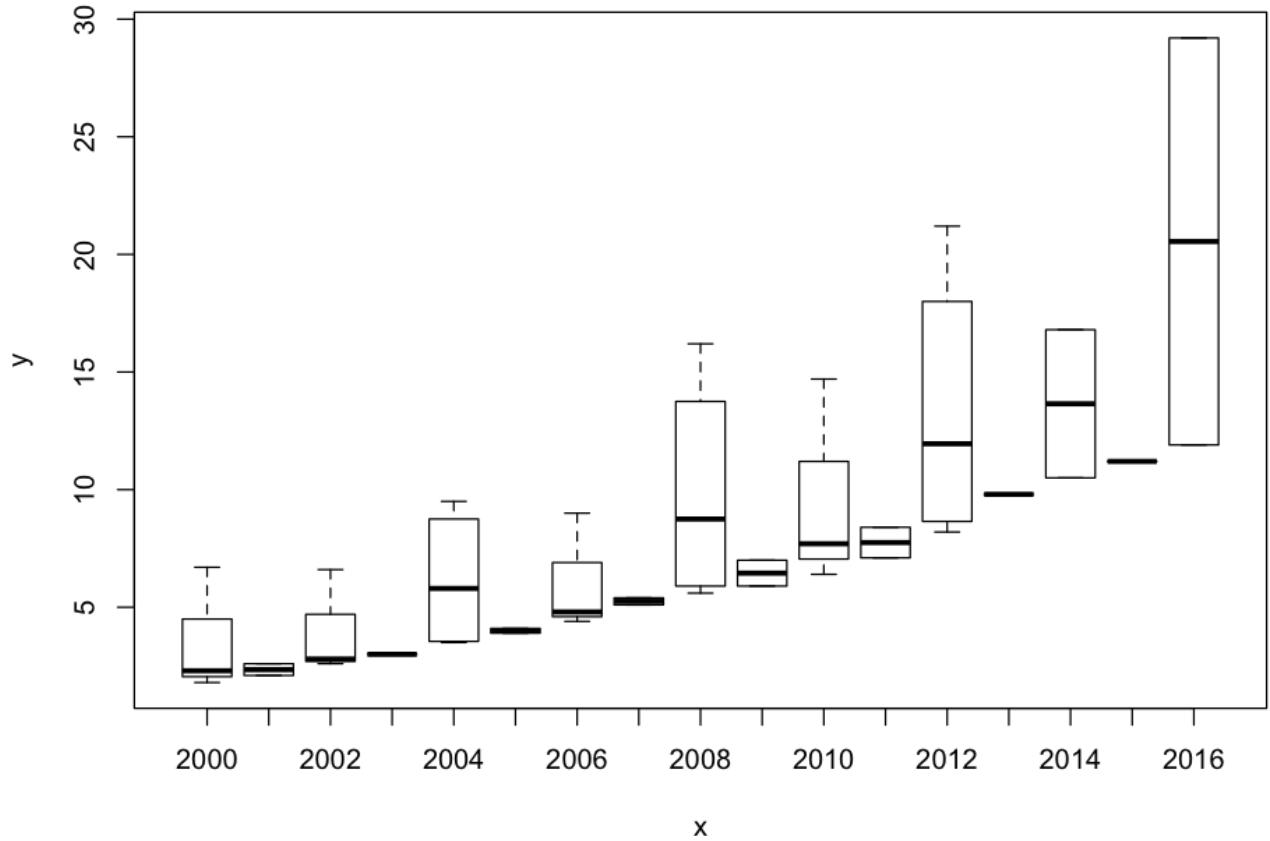
```
In [1035]: # Adjust in-line plot size to M x N  
options(repr.plot.width=8, repr.plot.height=6)
```

In [1036]:

```
# -----  
# [National] < Prevalence has changed over Time >  
# -----  
# Prevalence over Year  
# Use Year      as x-axis: y value Prevalence is NOT aggregated for different d  
plot(ASD_National$Year, ASD_National$Prevalence)
```



```
In [1037]: # Use Year_factor as x-axis: y value Prevalence is aggregated for different d  
plot(ASD_National$Year_Factor, ASD_National$Prevalence)
```



```
In [1038]: # table(ASD_National$Source_Full13)
```

```
In [1039]: par(mfrow=c(2, 2))

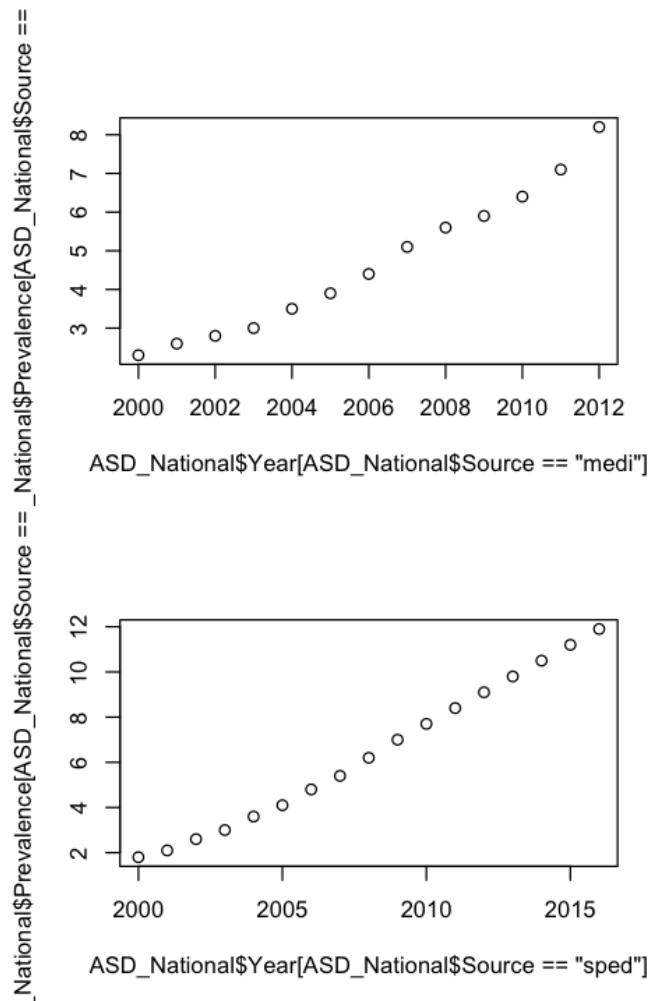
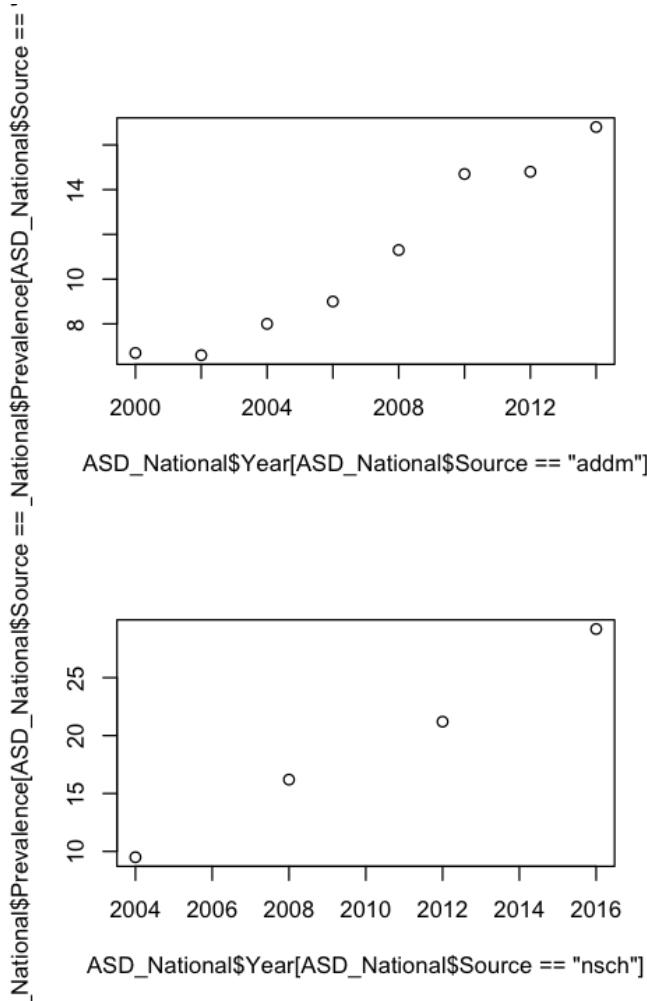
# Prevalence over Year, from data source:
# addm-Autism & Developmental Disabilities Monitoring Network
plot(ASD_National$Year[ASD_National$Source == 'addm'],
     ASD_National$Prevalence[ASD_National$Source == 'addm'])

# Prevalence over Year, from data source:
# medi-Medicaid
plot(ASD_National$Year[ASD_National$Source == 'medi'],
     ASD_National$Prevalence[ASD_National$Source == 'medi'])

# Prevalence over Year, from data source:
# nsch-National Survey of Children Health
plot(ASD_National$Year[ASD_National$Source == 'nsch'],
     ASD_National$Prevalence[ASD_National$Source == 'nsch'])

# Prevalence over Year, from data source:
# sped-Special Education Child Count
plot(ASD_National$Year[ASD_National$Source == 'sped'],
     ASD_National$Prevalence[ASD_National$Source == 'sped'])

par(mfrow=c(1, 1)) # Reset to one plot on one page
```



\_National\$Prevalence[ASD\_National\$Source == "nsch"]

\_National\$Prevalence[ASD\_National\$Source == "sped"]

In [1040]:

```
# -----
# Add more annotations to above plots
# -----
# Color list
# addm : darkblue
# medi : orange
# nsch : darkred
# sped : skyblue

par(mfrow=c(2, 2))

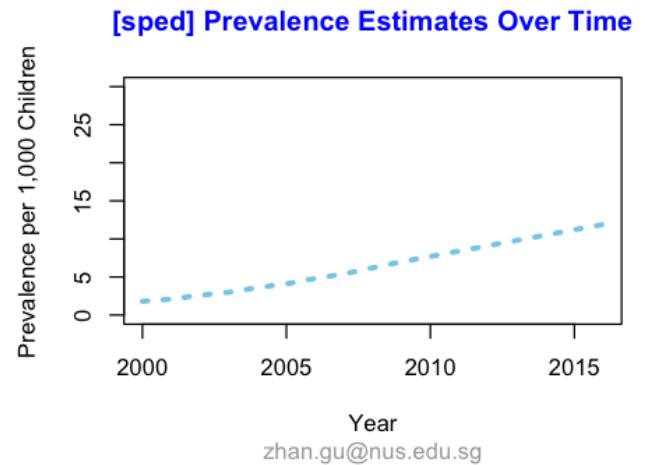
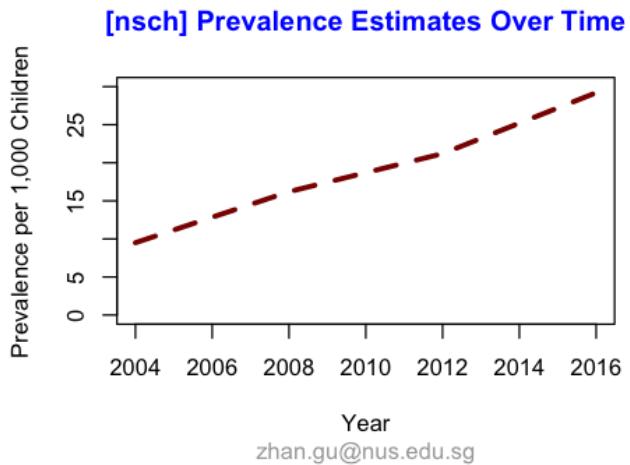
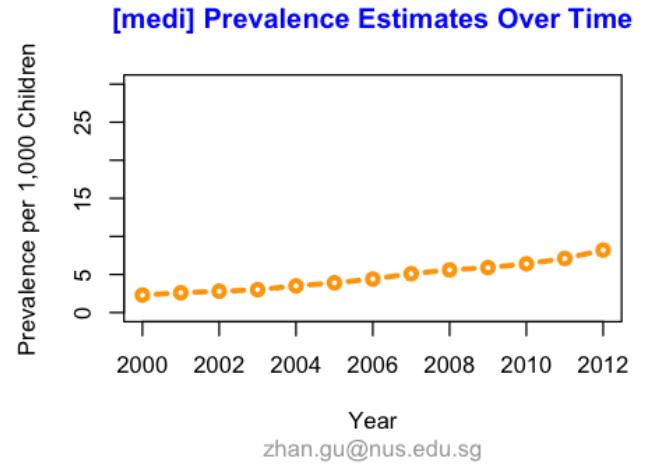
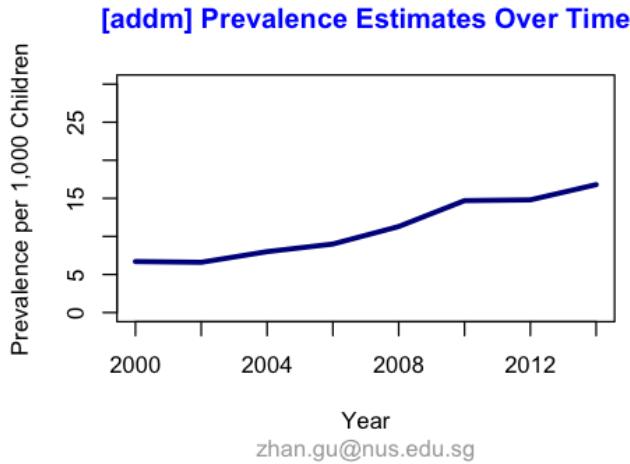
# Prevalence over Year, from data source:
# addm-Autism & Developmental Disabilities Monitoring Network
plot(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Prevalence[ASD_National$Source == 'addm'],
      type="l", # dot/point type
      lty=1, # line type
      lwd=3, # line width
      col="darkblue", # line color
      xlab="Year",
      ylab="Prevalence per 1,000 Children",
      ylim = c(0, 30), # Set value range of y axis
      main="[addm] Prevalence Estimates Over Time",
      sub = "zhan.gu@nus.edu.sg",
      col.main="blue", col.lab="black", col.sub="darkgrey")

# Prevalence over Year, from data source:
# medi-Medicaid
plot(ASD_National$Year[ASD_National$Source == 'medi'],
      ASD_National$Prevalence[ASD_National$Source == 'medi'],
      type="b", lty=1, lwd=3, col="orange",
      xlab="Year",
      ylab="Prevalence per 1,000 Children",
      ylim = c(0, 30), # Set value range of y axis
      main="[medi] Prevalence Estimates Over Time",
      sub = "zhan.gu@nus.edu.sg",
      col.main="blue", col.lab="black", col.sub="darkgrey")

# Prevalence over Year, from data source:
# nsch-National Survey of Children Health
plot(ASD_National$Year[ASD_National$Source == 'nsch'],
      ASD_National$Prevalence[ASD_National$Source == 'nsch'],
      type="l", lty=2, lwd=3, col="darkred",
      xlab="Year",
      ylab="Prevalence per 1,000 Children",
      ylim = c(0, 30), # Set value range of y axis
      main="[nsch] Prevalence Estimates Over Time",
      sub = "zhan.gu@nus.edu.sg",
      col.main="blue", col.lab="black", col.sub="darkgrey")

# Prevalence over Year, from data source:
# sped-Special Education Child Count
plot(ASD_National$Year[ASD_National$Source == 'sped'],
      ASD_National$Prevalence[ASD_National$Source == 'sped'],
      type="l", lty=3, lwd=3, col="skyblue",
      xlab="Year",
      ylab="Prevalence per 1,000 Children",
      ylim = c(0, 30), # Set value range of y axis
      main="[sped] Prevalence Estimates Over Time",
      sub = "zhan.gu@nus.edu.sg",
      col.main="blue", col.lab="black", col.sub="darkgrey")
```

```
par(mfrow=c(1, 1)) # Reset to one plot on one page
```



Data Visualisation (Base Graphic) - [ R ] REPORTED PREVALENCE HAS CHANGED OVER TIME by [ Data Source ]

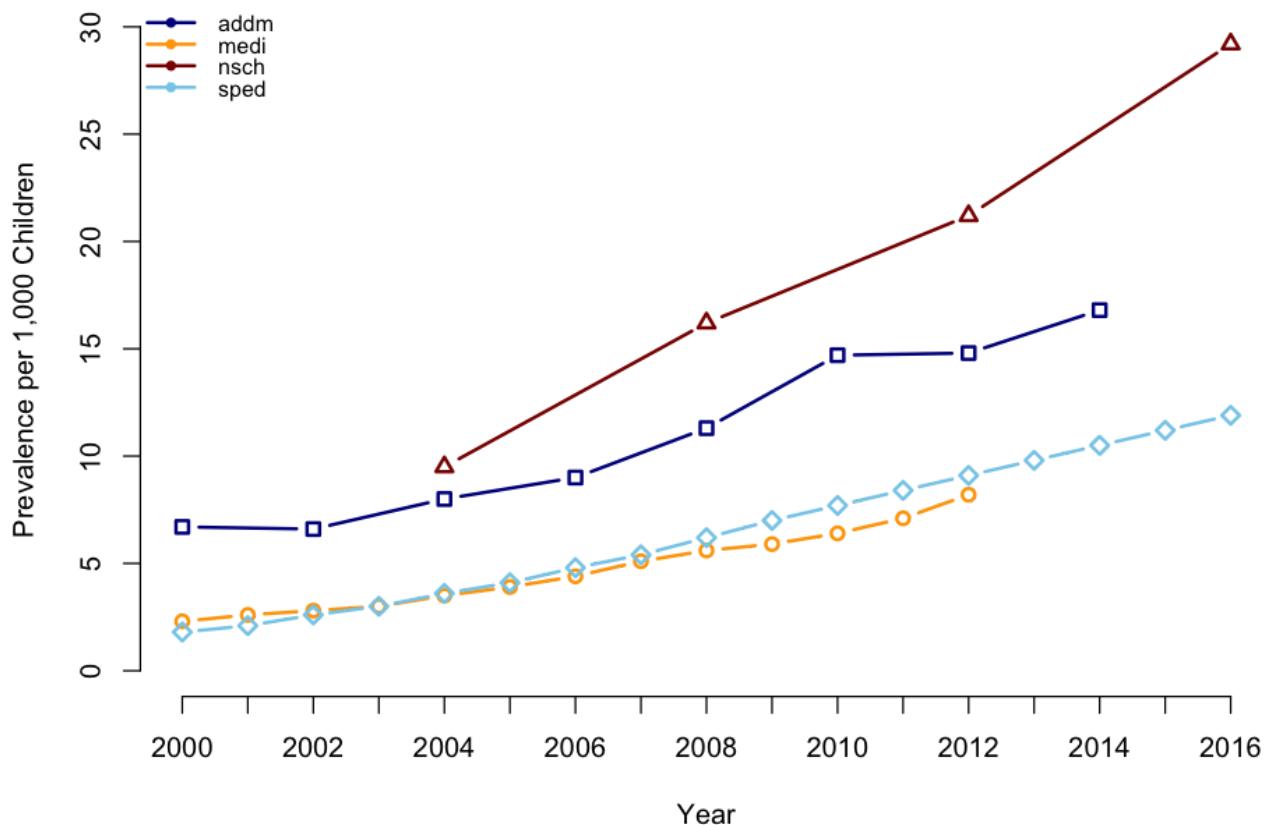
Create multiple lines within a single chart

In [1041]:

```
# -----
# [National] < Prevalence Varies over Time/Year by Data Source >
# -----
# Create a first line
plot(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Prevalence[ASD_National$Source == 'addm'],
      col = "darkblue", lty = 1, lwd = 2,
      type = "b", # use dot/point
      pch = 0, # dot/point type: http://www.endmemo.com/program/R/pchsymbols.php
      xlab="Year",
      xlim=c(2000, 2016), # Set x axis value range
      ylab="Prevalence per 1,000 Children",
      ylim=c(0, 30), # Set y axis value range
      main="Prevalence Estimates Over Time by Data Source",
      col.main="black", col.lab="black", col.sub="grey",
      frame = FALSE, # Remove frame
      axes=FALSE # Remove x and y axis
)
axis(1, at=seq(2000, 2016, 1)) # Customize x axis
axis(2, at=seq(0, 30, 5)) # Customize y axis

# Add another line
lines(ASD_National$Year[ASD_National$Source == 'medi'],
      ASD_National$Prevalence[ASD_National$Source == 'medi'],
      pch = 1, col = "orange", type = "b", lty = 1, lwd = 2
)
# Add another line
lines(ASD_National$Year[ASD_National$Source == 'nsch'],
      ASD_National$Prevalence[ASD_National$Source == 'nsch'],
      pch = 2, col = "darkred", type = "b", lty = 1, lwd = 2
)
# Add another line
lines(ASD_National$Year[ASD_National$Source == 'sped'],
      ASD_National$Prevalence[ASD_National$Source == 'sped'],
      pch = 5, col = "skyblue", type = "b", lty = 1, lwd = 2
)
# Add a legend to the plot
legend("topleft", legend=levels(ASD_National$Source),
       col=c("darkblue", "orange", "darkred", "skyblue"),
       pch = 20, # dot in a line
       lty = 1, # line type
       lwd = 2, # line width
       cex=0.8, # size of text
       bty = 'n' # Without frame
)
```

## Prevalence Estimates Over Time by Data Source



R pch: dot/point type: <http://www.endmemo.com/program/R/pchsymbols.php>  
[\(http://www.endmemo.com/program/R/pchsymbols.php\)](http://www.endmemo.com/program/R/pchsymbols.php).

R plot colour list: <https://www.r-graph-gallery.com/42-colors-names.html> (<https://www.r-graph-gallery.com/42-colors-names.html>)

**Data Visualisation (Base Graphic) - [ R ] REPORTED PREVALENCE VARIES BY SEX [ Source: ADDM ] over [ Year ]**

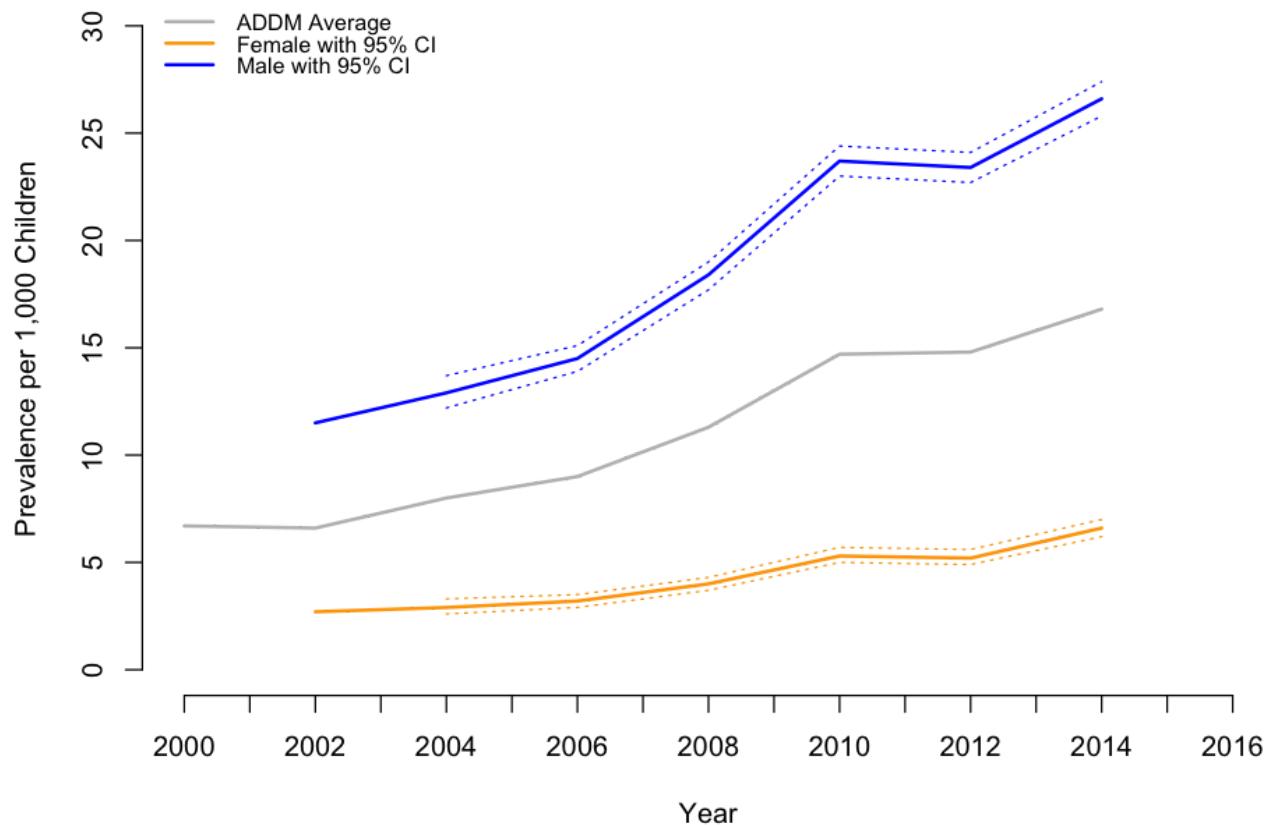
In [1042]:

```
# -----
# [addm] < Prevalence Varies by Sex >
# -----
# Create a first line
plot(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Prevalence[ASD_National$Source == 'addm'],
      col = "grey", lty = 1, lwd = 2,
      type = "l", # use dot/point
      pch = 0, # dot/point type: http://www.endmemo.com/program/R/pchsymbols.php
      xlab="Year",
      xlim=c(2000, 2016), # Set x axis value range
      ylab="Prevalence per 1,000 Children",
      ylim=c(0, 30), # Set y axis value range
      main="Prevalence Estimates by Sex [ADDM]",
      col.main="black", col.lab="black", col.sub="grey",
      frame = FALSE, # Remove frame
      axes=FALSE # Remove x and y axis
)
axis(1, at=seq(2000, 2016, 1)) # Customize x axis
axis(2, at=seq(0, 30, 5)) # Customize y axis

# Add Female prevalence
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Female.Prevalence[ASD_National$Source == 'addm'],
      pch = 1, col = "orange", type = "l", lty = 1, lwd = 2)
# Add Female prevalence lower CI
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Female.Lower.CI[ASD_National$Source == 'addm'],
      pch = 1, col = "orange", type = "l", lty = 3, lwd = 1)
# Add Female prevalence upper CI
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Female.Upper.CI[ASD_National$Source == 'addm'],
      pch = 1, col = "orange", type = "l", lty = 3, lwd = 1)

# Add Male prevalence
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Male.Prevalence[ASD_National$Source == 'addm'],
      pch = 1, col = "blue", type = "l", lty = 1, lwd = 2)
# Add Male prevalence lower CI
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Male.Lower.CI[ASD_National$Source == 'addm'],
      pch = 1, col = "blue", type = "l", lty = 3, lwd = 1)
# Add Male prevalence upper CI
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Male.Upper.CI[ASD_National$Source == 'addm'],
      pch = 1, col = "blue", type = "l", lty = 3, lwd = 1)
# Add a legend to the plot
legend("topleft", legend=c('ADDM Average', 'Female with 95% CI', 'Male with 95% CI'),
       col=c("grey", "orange", "blue"),
       # pch = 20, # dot in a line
       lty = 1, # line type
       lwd = 2, # line width
       cex=0.8, # size of text
       bty = 'n' # Without frame
)
```

## Prevalence Estimates by Sex [ADDM]



Data Visualisation (Base Graphic) - [ R ] REPORTED PREVALENCE VARIES BY RACE AND ETHNICITY [ Source: ADDM ]

In [1043]:

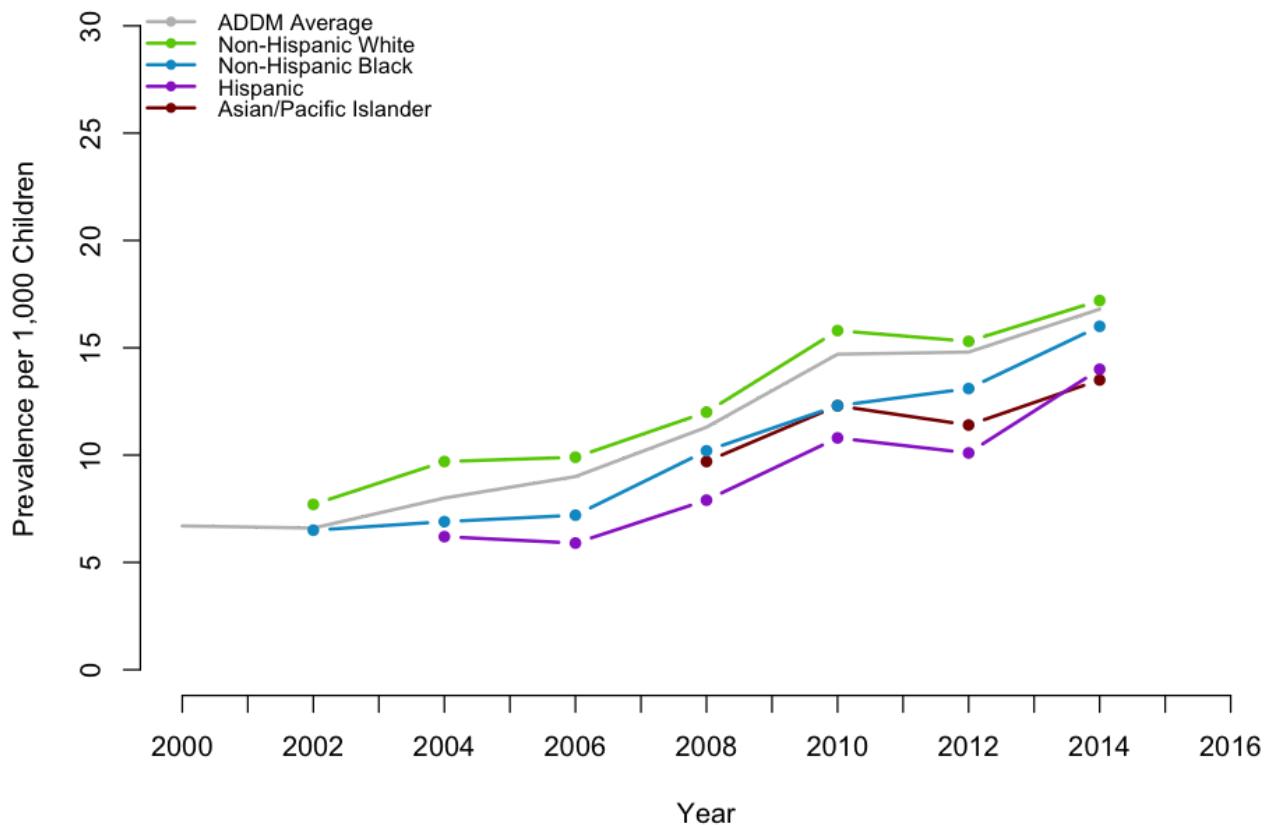
```
# -----
# [addm] < Prevalence Varies by Race and Ethnicity >
# -----
# Create a first line
plot(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Prevalence[ASD_National$Source == 'addm'],
      col = "grey", lty = 1, lwd = 2,
      type = "l", # use dot/point
      pch = 0, # dot/point type: http://www.endmemo.com/program/R/pchsymbols.php
      xlab="Year",
      xlim=c(2000, 2016), # Set x axis value range
      ylab="Prevalence per 1,000 Children",
      ylim=c(0, 30), # Set y axis value range
      main="Prevalence Estimates by Race/Ethnicity [ADDM]",
      col.main="black", col.lab="black", col.sub="grey",
      frame = FALSE, # Remove frame
      axes=FALSE # Remove x and y axis
)
axis(1, at=seq(2000, 2016, 1)) # Customize x axis
axis(2, at=seq(0, 30, 5)) # Customize y axis

# R plot colour list: https://www.r-graph-gallery.com/42-colors-names.html

# Add Asian.or.Pacific.Islander.Prevalence
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Asian.or.Pacific.Islander.Prevalence[ASD_National$Source == 'a',
      pch = 20, col = "darkred", type = "b", lty = 1, lwd = 2)
# Add Hispanic.Prevalence
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Hispanic.Prevalence[ASD_National$Source == 'addm'],
      pch = 20, col = "darkorchid3", type = "b", lty = 1, lwd = 2)
# Add Non.hispanic.black.Prevalence
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Non.hispanic.black.Prevalence[ASD_National$Source == 'addm'],
      pch = 20, col = "deepskyblue3", type = "b", lty = 1, lwd = 2)
# Add Non.hispanic.white.Prevalence
lines(ASD_National$Year[ASD_National$Source == 'addm'],
      ASD_National$Non.hispanic.white.Prevalence[ASD_National$Source == 'addm'],
      pch = 20, col = "chartreuse3", type = "b", lty = 1, lwd = 2)

# Add a legend to the plot
legend("topleft", legend=c('ADDM Average',
                           'Non-Hispanic White',
                           'Non-Hispanic Black',
                           'Hispanic',
                           'Asian/Pacific Islander'),
       col=c("grey", "chartreuse3", "deepskyblue3", "darkorchid3", "darkred"),
       pch = 20, # dot in a line
       lty = 1, # line type
       lwd = 2, # line width
       cex=0.8, # size of text
       bty = 'n' # Without frame
)
```

## Prevalence Estimates by Race/Ethnicity [ADDM]



```
In [1044]: # Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

### Quiz:

Add 95% Confidence Interval to above plot

```
In [1045]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

### Quiz:

Use `table()` to count No. prevalence records for each Data Source. Then use `barplot()` to visualize.

In [1046]: *# Write your code below and press Shift+Enter to execute*

Double-click **here** for the solution.

In [ ]:

### Quiz:

Which Data Sources are available in which years?

In [1047]: *# Write your code below and press Shift+Enter to execute*

Double-click **here** for the solution.

### Quiz:

Which Data Source has breakdown Prevalence data by sex/gender?

In [1048]: *# Write your code below and press Shift+Enter to execute*

Double-click **here** for the solution.

### Quiz:

Which Data Source has breakdown Prevalence data by race and ethnicity?

In [1049]: *# Write your code below and press Shift+Enter to execute*

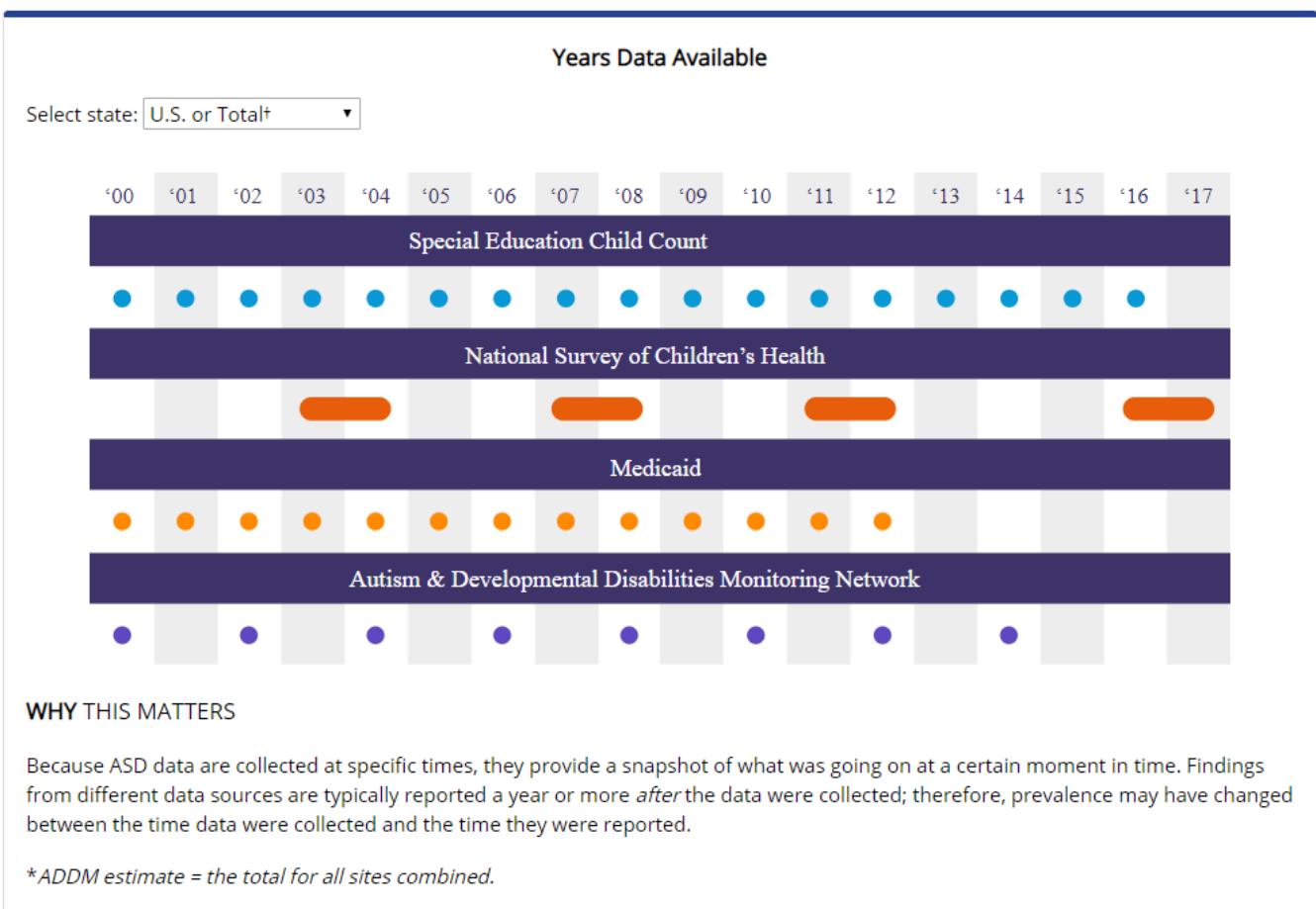
Double-click **here** for the solution.

## Data Visualisation (Enhanced)

```
In [1050]: if(!require(ggplot2)){install.packages("ggplot2")}  
library(ggplot2)
```

```
In [1051]: # Adjust in-line plot size to M x N  
options(repr.plot.width=8, repr.plot.height=4)
```

## Data Visualisation (Enhanced) - [ CDC ] Explore the Data

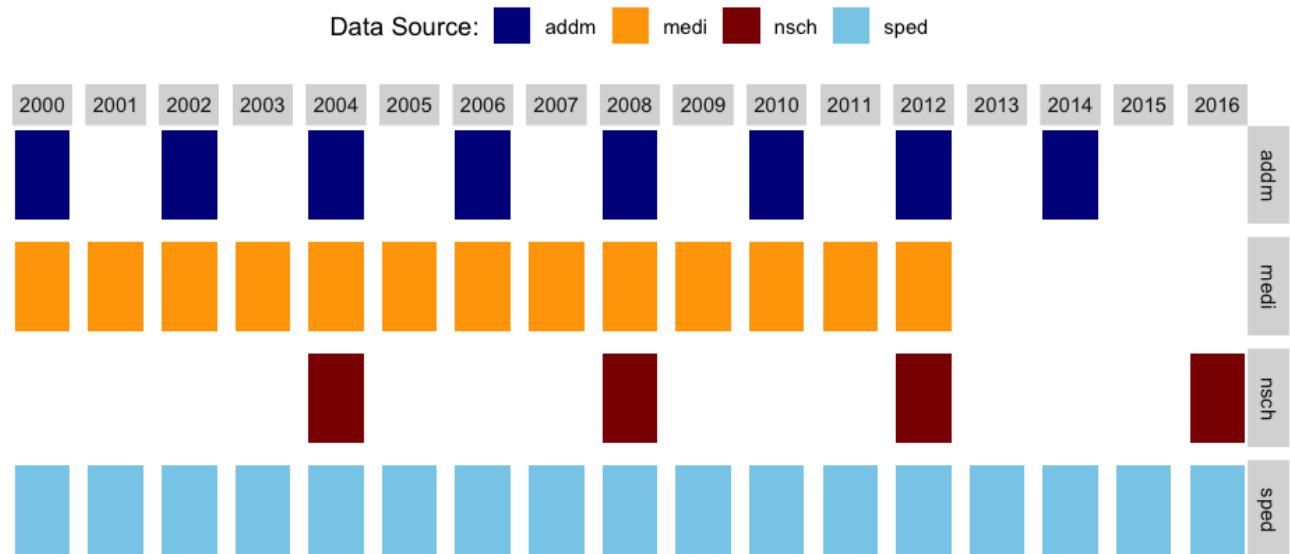


## Data Visualisation (Enhanced) - [ R ] Explore the Data

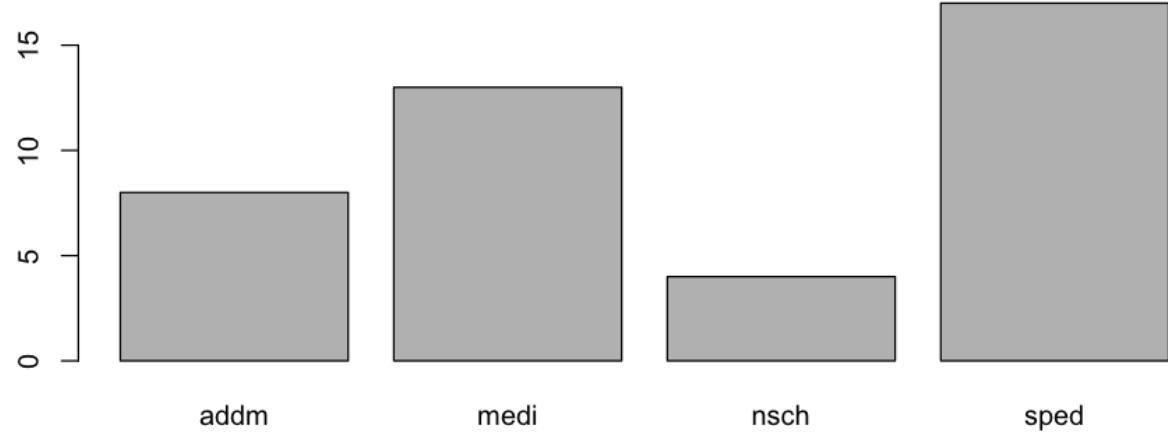
In [1052]:

```
# -----  
# [National] < Years Data Available >  
# -----  
p = ggplot(ASD_National, aes(x = 1, fill = Source)) +  
  geom_bar() + theme(axis.text.x=element_blank(), # Hide axis  
                      axis.ticks.x=element_blank(), # Hide axis  
                      axis.text.y=element_blank(), # Hide axis  
                      axis.ticks.y=element_blank(), # Hide axis  
                      panel.background = element_blank(), # Remove panel background  
                      legend.position="top"  
) +  
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",  
                                              "medi" = "orange",  
                                              "nsch" = "darkred",  
                                              "sped" = "skyblue")) +  
  labs(x="", y="", title="Years Data Available") + # layers of graphics  
  facet_grid(facets = Source~Year)  
# Show plot  
p
```

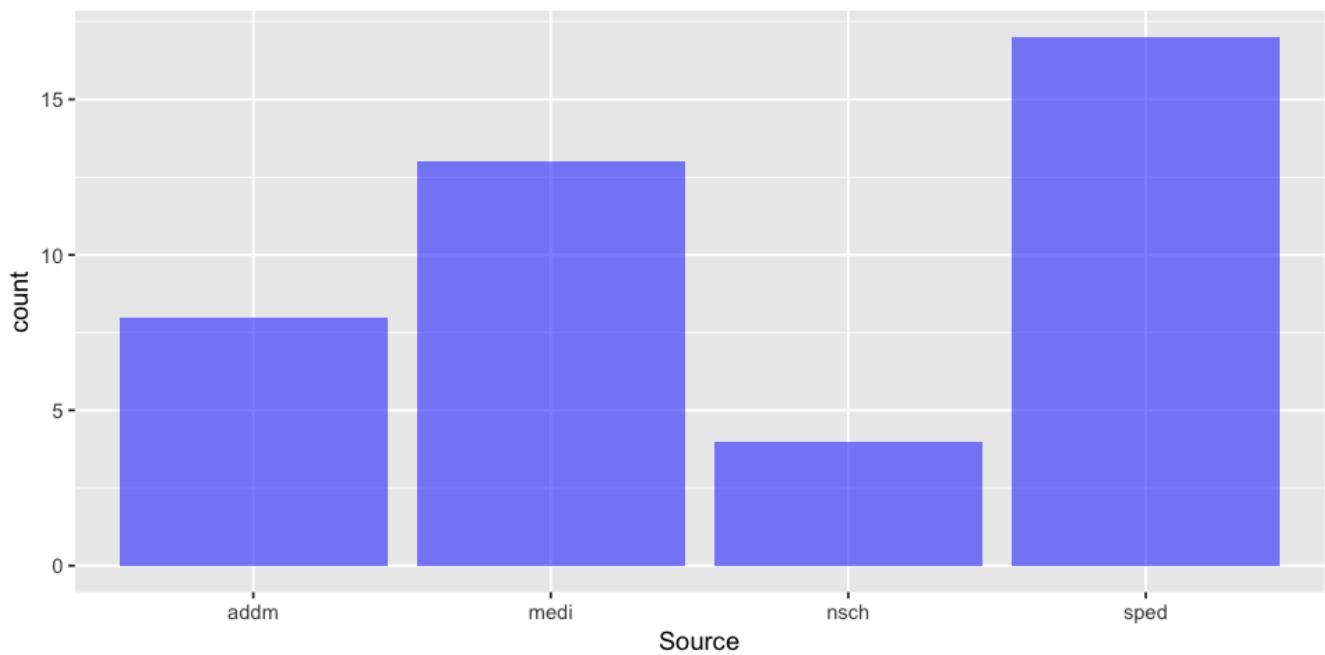
Years Data Available



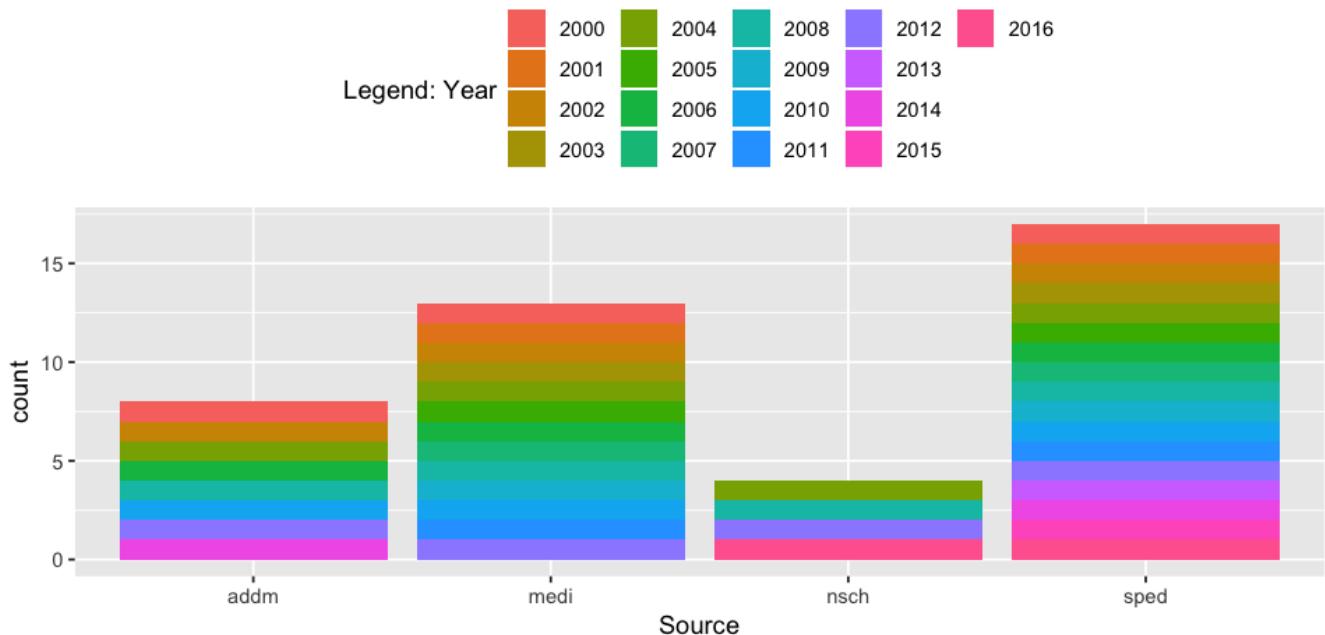
```
In [1053]: # Create bar chart using R graphics  
barplot(table(ASD_National$Source))
```



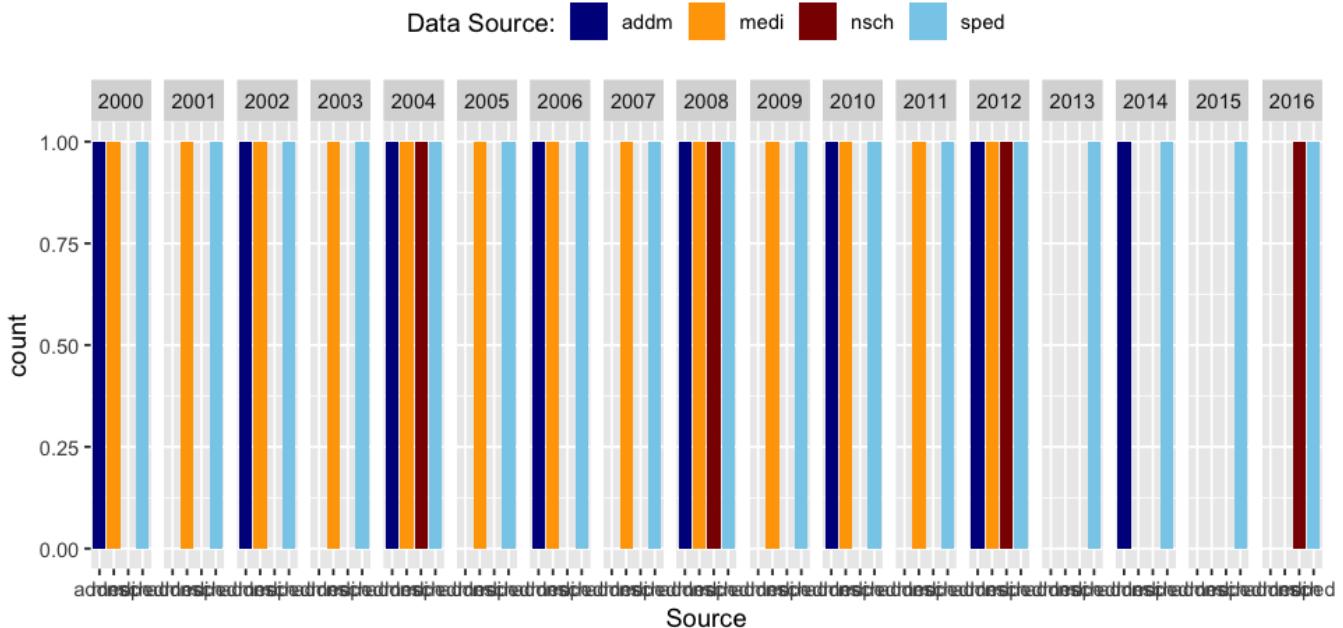
```
In [1054]: # Create bar chart using ggplot2  
ggplot(ASD_National, aes(x = Source)) + geom_bar(fill = "blue", alpha=0.5)
```



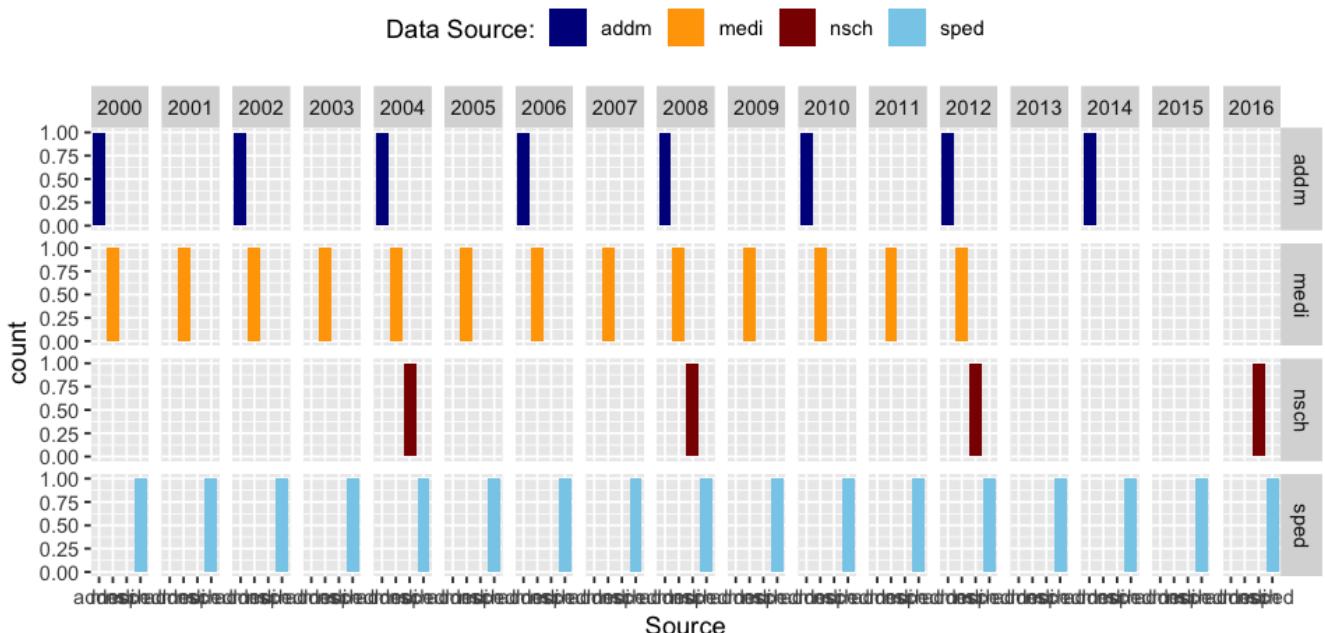
```
In [1055]: # Use color to differentiate sub-group data (Year)
ggplot(ASD_National, aes(x = Source, fill = factor(Year))) + geom_bar() +
    theme(legend.position="top") + labs(fill = "Legend: Year")
```



```
In [1056]: # Split chart to multiple columns by using: facets = . ~ Year
ggplot(ASD_National, aes(x = Source, fill = Source)) + geom_bar() +
  theme(legend.position="top") +
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue")) +
  facet_grid(facets = . ~ Year)
```

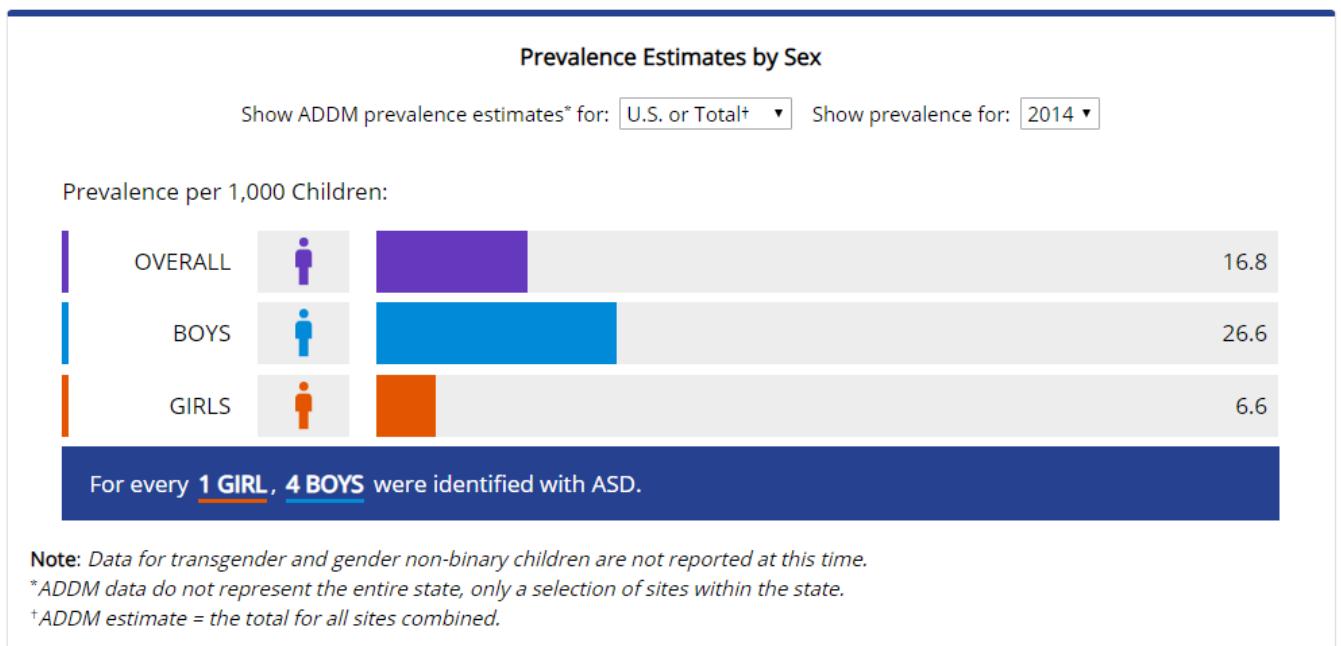


```
In [1057]: # Split chart to multiple rows and columns by using: facets = Source ~ Year
ggplot(ASD_National, aes(x = Source, fill = Source)) + geom_bar() +
  theme(legend.position="top") +
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue")) +
  facet_grid(facets = Source~Year)
```



## Barplot / Column plot

## Data Visualisation (Enhanced) - [ CDC ] REPORTED PREVALENCE VARIES BY SEX



## Data Visualisation (Enhanced) - [ R ] REPORTED PREVALENCE VARIES BY SEX [ Source: ADDM ] [ Year: 2014 ]

In [1058]: # Filter only data of ADDM

```
ASD_National_ADDM <- subset(ASD_National, Source == 'addm')
#
ASD_National_ADDM
```

| Source | Year | Prevalence | Upper.CI | Lower.CI | Source_Full1                                           | Source_Full2                                                | Male.Prevalence | Male.Lower.Cl |
|--------|------|------------|----------|----------|--------------------------------------------------------|-------------------------------------------------------------|-----------------|---------------|
| addm   | 2000 | 6.7        | 7.0      | 6.3      | Autism & Developmental Disabilities Monitoring Network | addm-Autism & Developmental Disabilities Monitoring Network | NA              | NA            |
| addm   | 2002 | 6.6        | 6.8      | 6.3      | Autism & Developmental Disabilities Monitoring Network | addm-Autism & Developmental Disabilities Monitoring Network | 11.5            | NA            |
| addm   | 2004 | 8.0        | 8.4      | 7.6      | Autism & Developmental Disabilities Monitoring Network | addm-Autism & Developmental Disabilities Monitoring Network | 12.9            | 12.2          |

```
In [1059]: # Construct a new re-shaped dataframe of [ Source: ADDM ] [Year: 2014]
#
Process_Source = 'addm'
Process_Year = 2014
```

```
In [1060]: # Create the vectors:
Sex.Group = c('Overall',
             'Boys',
             'Girls')
Sex.Group

Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year],
              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],
              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year])
Prevalence

# Combine all the vectors into a data frame:
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)

# Add new columns:
ASD_National_ADDM_Rshaped$Source = Process_Source
ASD_National_ADDM_Rshaped$Year = Process_Year
#
ASD_National_ADDM_Rshaped
```

'Overall' 'Boys' 'Girls'

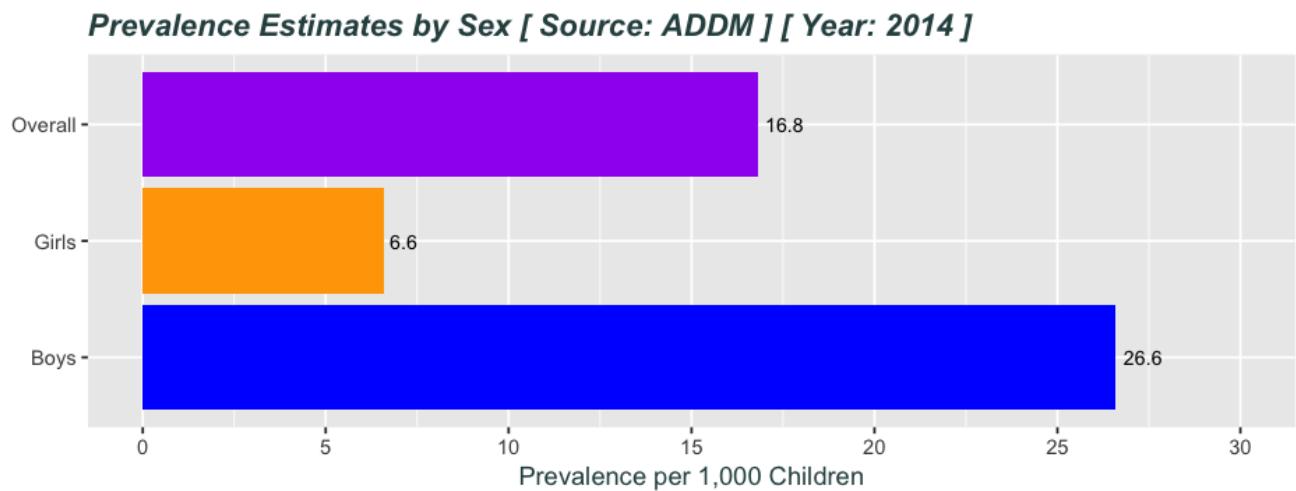
16.8 26.6 6.6

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 16.8       | addm   | 2014 |
| Boys      | 26.6       | addm   | 2014 |
| Girls     | 6.6        | addm   | 2014 |

### Visualise: Prevalence Estimates by Sex [ Source: ADDM ] [ Year: 2014 ]

```
In [1061]: # Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=3)
```

```
In [1062]: ggplot(ASD_National_ADDM_Reshaped, aes(Sex.Group, Prevalence)) +
  geom_col(aes(fill = Sex.Group, colours = )) + # Use column chart
  geom_text(aes(label = Prevalence), vjust = +0.5, hjust = -0.2, size = 3) +
  scale_y_continuous(name = "Prevalence per 1,000 Children",
                      breaks = seq(0, 30, 5),
                      limits=c(0, 30)) +
  scale_x_discrete(name = "") +
  scale_fill_manual("Sex Group:", values = c("Overall" = "purple",
                                             "Boys" = "blue",
                                             "Girls" = "orange")) +
  ggtitle("Prevalence Estimates by Sex [ Source: ADDM ] [ Year: 2014 ]") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey"),
        legend.position = 'none') +
  coord_flip() # Rotate chart
# facet_grid(facets = Year ~ .)
```



## Data Visualisation (Enhanced) - [ R ] REPORTED PREVALENCE VARIES BY SEX [ Source: ADDM ] [ Year: ALL ]

```
In [1063]: # Create a new datafarme to hold re-shaped data for all years.
ASD_National_ADDM_Reshaped_All = ASD_National_ADDM_Reshaped
```

```
In [1064]: Process_Source = 'addm'
unique(ASD_National_ADDM$Year[!is.na(ASD_National_ADDM$Male.Prevalance)])
```

Warning message:  
"Unknown or uninitialized column: 'Male.Prevalance'."

```
In [1065]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2012
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year,  
                                              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              #Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source
```

```
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped_All, ASD_National_ADDM_Rshaped)
```

```
#ASD_National_ADDM_Rshaped_All
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 14.8       | addm   | 2012 |
| Boys      | 23.4       | addm   | 2012 |
| Girls     | 5.2        | addm   | 2012 |

```
In [1066]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2010
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year,  
                                              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              #Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source  
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped, ASD_National_ADDM_Rshaped)
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 14.7       | addm   | 2010 |
| Boys      | 23.7       | addm   | 2010 |
| Girls     | 5.3        | addm   | 2010 |

```
In [1067]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2008
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year,  
                                              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              #Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source  
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped, ASD_National_ADDM_Rshaped)
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 11.3       | addm   | 2008 |
| Boys      | 18.4       | addm   | 2008 |
| Girls     | 4.0        | addm   | 2008 |

```
In [1068]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2006
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year,  
                                              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              #Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source  
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped, ASD_National_ADDM_Rshaped)
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 9.0        | addm   | 2006 |
| Boys      | 14.5       | addm   | 2006 |
| Girls     | 3.2        | addm   | 2006 |

```
In [1069]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2004
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year,  
                                              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              #Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source
```

```
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped_All, ASD_National_ADDM_Rshaped)
```

```
#ASD_National_ADDM_Rshaped_All
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 8.0        | addm   | 2004 |
| Boys      | 12.9       | addm   | 2004 |
| Girls     | 2.9        | addm   | 2004 |

```
In [1070]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2002
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year == 2002],  
             ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year == 2002],  
             ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year == 2002])
```

```
#Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source
```

```
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped, ASD_National_ADDM_Rshaped)
```

```
#ASD_National_ADDM_Rshaped_All
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 6.6        | addm   | 2002 |
| Boys      | 11.5       | addm   | 2002 |
| Girls     | 2.7        | addm   | 2002 |

```
In [1071]: # 2000 2002 2004 2006 2008 2010 2012 2014
```

```
Process_Year = 2000
```

```
# Create the vectors:
```

```
Sex.Group = c('Overall',  
            'Boys',  
            'Girls')
```

```
#Sex.Group
```

```
Prevalence = c(ASD_National_ADDM$Prevalence[ASD_National_ADDM$Year == Process_Year,  
                                              ASD_National_ADDM$Male.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              ASD_National_ADDM$Female.Prevalence[ASD_National_ADDM$Year == Process_Year],  
                                              #Prevalence
```

```
# Combine all the vectors into a data frame:
```

```
ASD_National_ADDM_Rshaped = data.frame(Sex.Group, Prevalence, stringsAsFactors=TRUE)
```

```
# Add new columns:
```

```
ASD_National_ADDM_Rshaped$Source = Process_Source  
ASD_National_ADDM_Rshaped$Year = Process_Year
```

```
#
```

```
ASD_National_ADDM_Rshaped
```

```
# Append rows to existing dataframe
```

```
ASD_National_ADDM_Rshaped_All = rbind(ASD_National_ADDM_Rshaped, ASD_National_ADDM_Rshaped)
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 6.7        | addm   | 2000 |
| Boys      | NA         | addm   | 2000 |
| Girls     | NA         | addm   | 2000 |

```
In [1072]: ASD_National_ADDM_Reshaped_All
```

| Sex.Group | Prevalence | Source | Year |
|-----------|------------|--------|------|
| Overall   | 16.8       | addm   | 2014 |
| Boys      | 26.6       | addm   | 2014 |
| Girls     | 6.6        | addm   | 2014 |
| Overall   | 14.8       | addm   | 2012 |
| Boys      | 23.4       | addm   | 2012 |
| Girls     | 5.2        | addm   | 2012 |
| Overall   | 14.7       | addm   | 2010 |
| Boys      | 23.7       | addm   | 2010 |
| Girls     | 5.3        | addm   | 2010 |
| Overall   | 11.3       | addm   | 2008 |
| Boys      | 18.4       | addm   | 2008 |
| Girls     | 4.0        | addm   | 2008 |
| Overall   | 9.0        | addm   | 2006 |
| Boys      | 14.5       | addm   | 2006 |
| Girls     | 3.2        | addm   | 2006 |
| Overall   | 8.0        | addm   | 2004 |
| Boys      | 12.9       | addm   | 2004 |
| Girls     | 2.9        | addm   | 2004 |
| Overall   | 6.6        | addm   | 2002 |
| Boys      | 11.5       | addm   | 2002 |
| Girls     | 2.7        | addm   | 2002 |
| Overall   | 6.7        | addm   | 2000 |
| Boys      | NA         | addm   | 2000 |
| Girls     | NA         | addm   | 2000 |

Visualise: Prevalence Estimates by Sex [ Source: ADDM ] [ Year: ALL ]

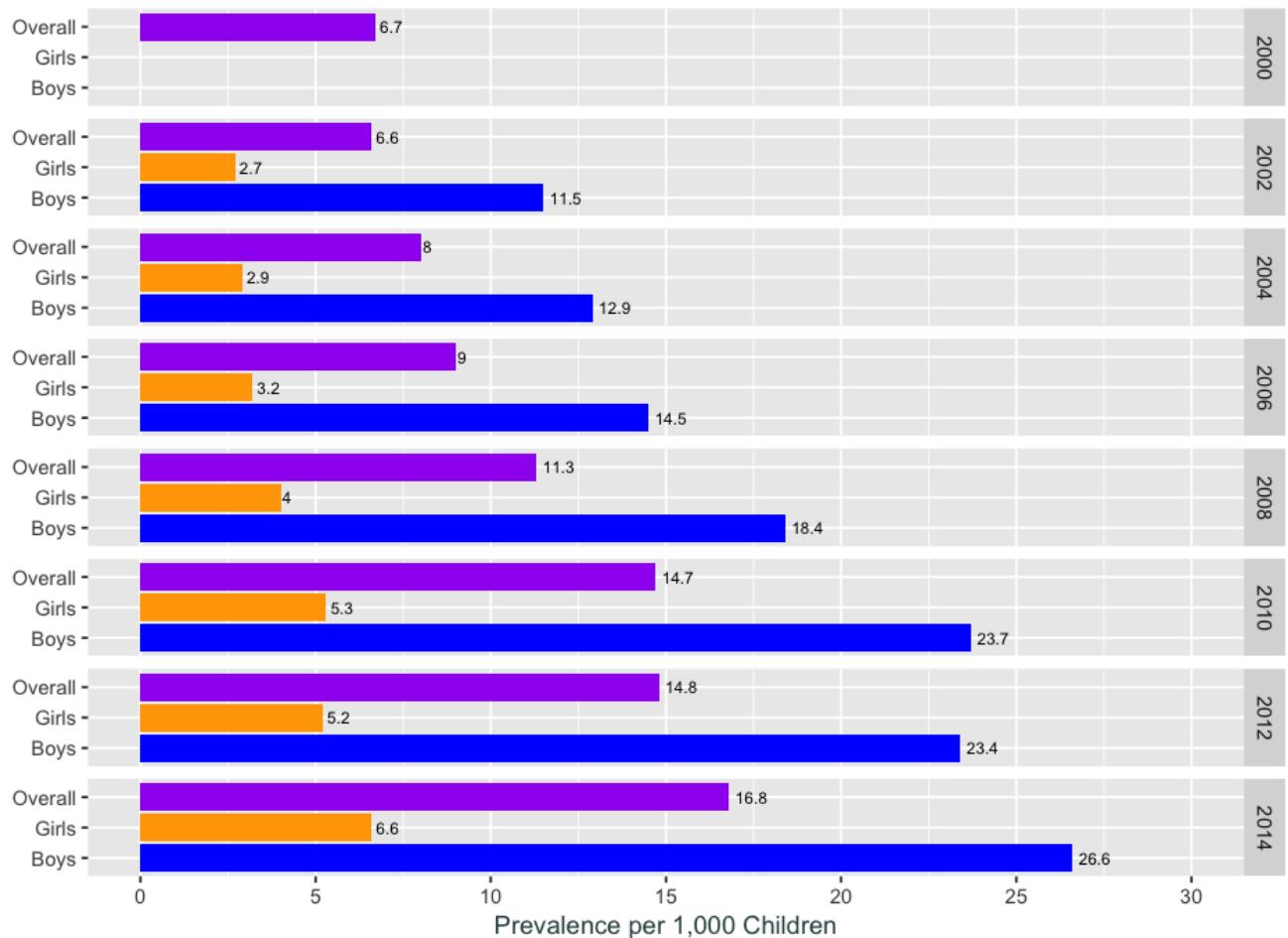
```
In [1073]: # Adjust in-line plot size to M x N  
options(repr.plot.width=8, repr.plot.height=6)
```

```
In [1074]: ggplot(ASD_National_ADDM_Reshaped_All, aes(Sex.Group, Prevalence)) +
  geom_col(aes(fill = Sex.Group, colours = )) + # Use column chart
  geom_text(aes(label = Prevalence), vjust = +0.5, hjust = -0.2, size = 2.5) +
  scale_y_continuous(name = "Prevalence per 1,000 Children",
                     breaks = seq(0, 30, 5),
                     limits=c(0, 30)) +
  scale_x_discrete(name = "") +
  scale_fill_manual("Sex Group:", values = c("Overall" = "purple",
                                             "Boys" = "blue",
                                             "Girls" = "orange")) +
  ggtile("Prevalence Estimates by Sex [ Source: ADDM ] [ Year: ALL ]") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey"),
        legend.position = 'none') +
  coord_flip() + # Rotate chart
  facet_grid(facets = Year ~ .)
```

Warning message:

"Removed 2 rows containing missing values (position\_stack)." Warning message:  
"Removed 2 rows containing missing values (geom\_text)."

**Prevalence Estimates by Sex [ Source: ADDM ] [ Year: ALL ]**

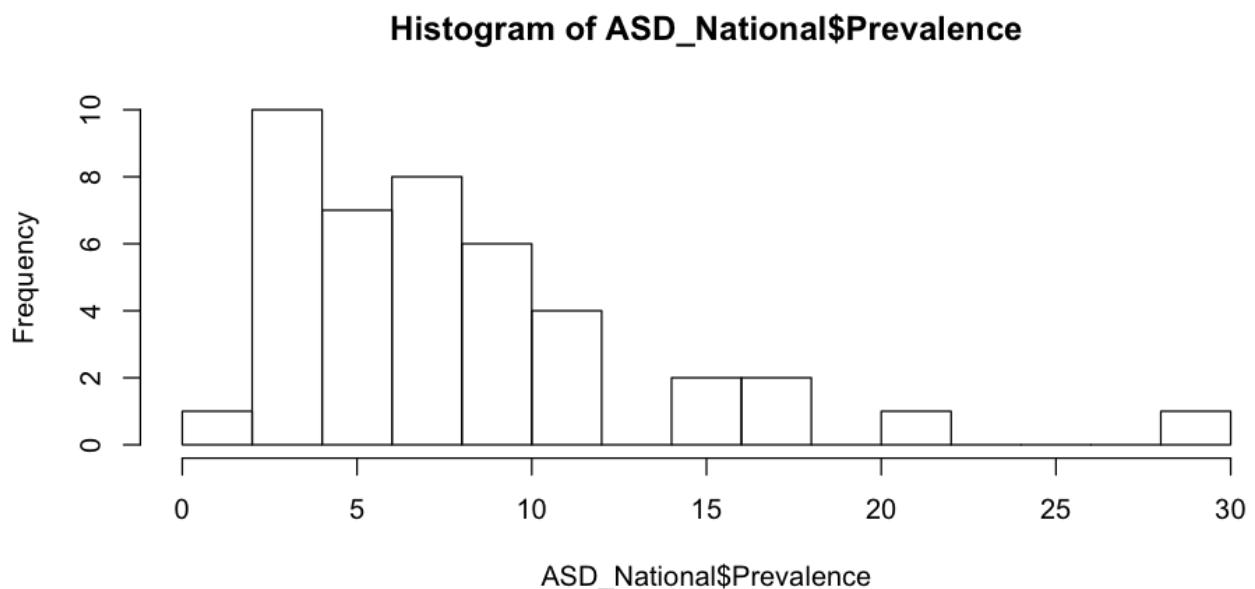


## Data Visualisation (Enhanced) - Histogram (distribution of binned continuous variable)

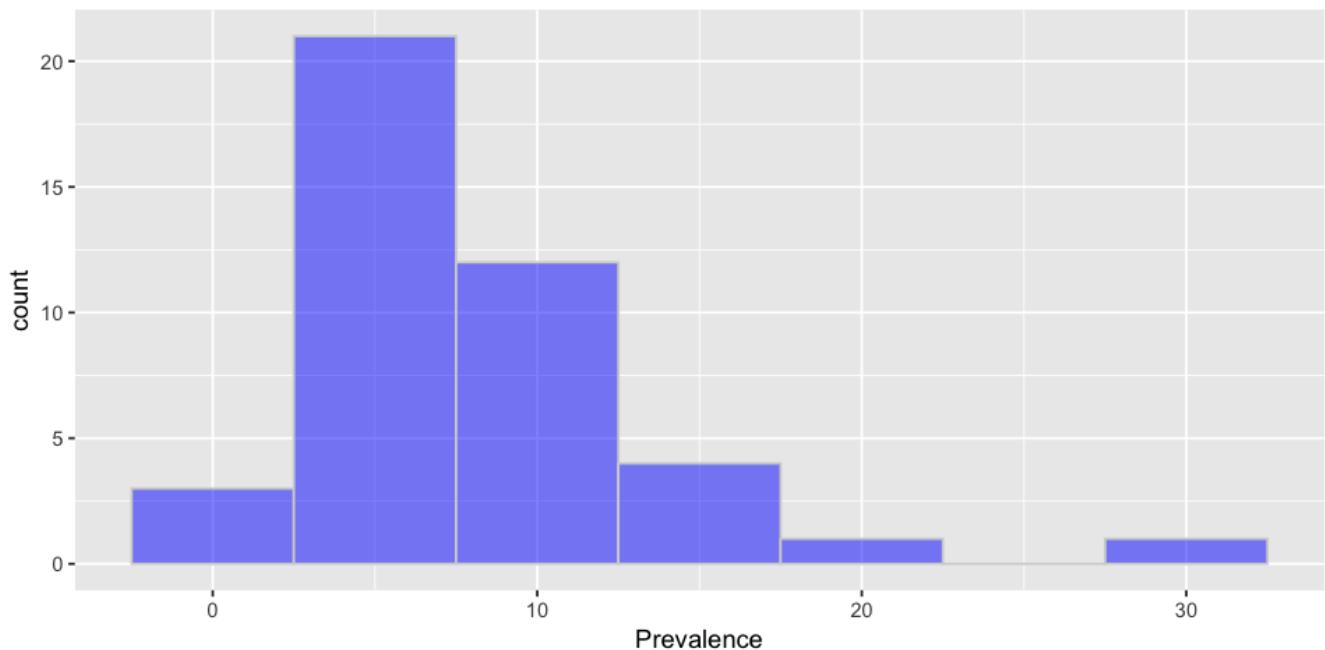
```
In [1075]: # Adjust in-line plot size to M x N  
options(repr.plot.width=8, repr.plot.height=4)
```

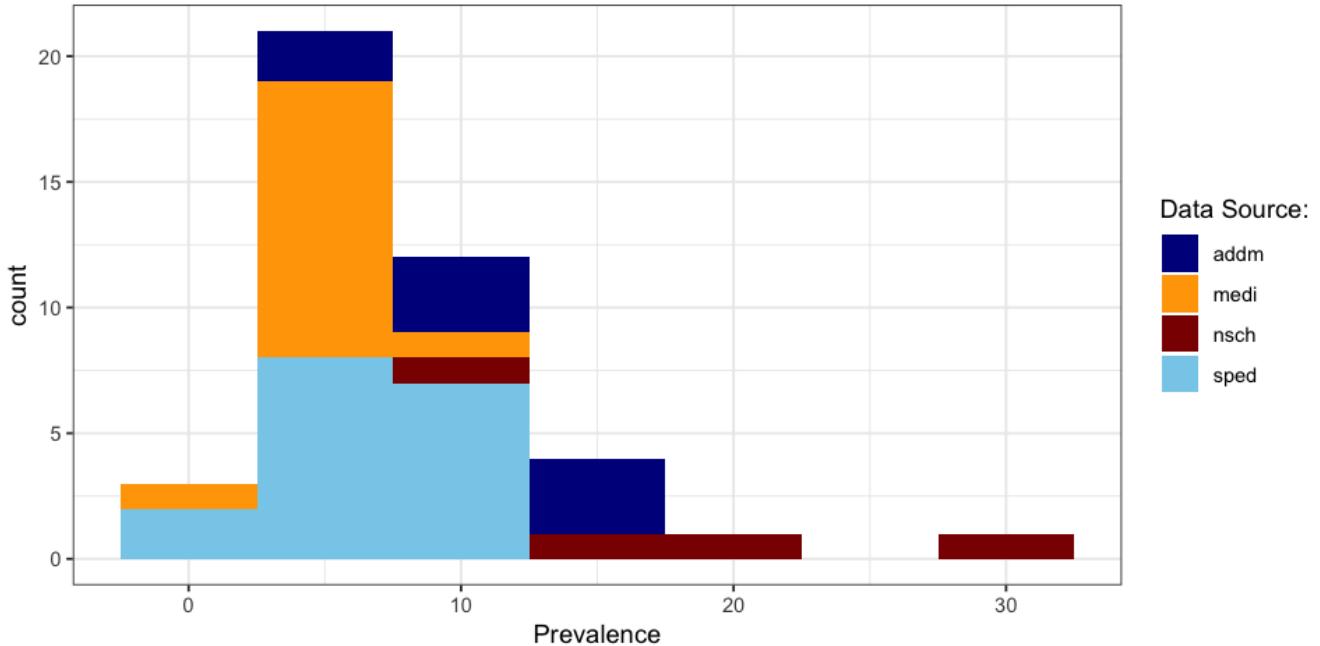
```
In [1076]: # Create histogram using R graphics  
hist(ASD_National$Prevalence, breaks = 10)
```



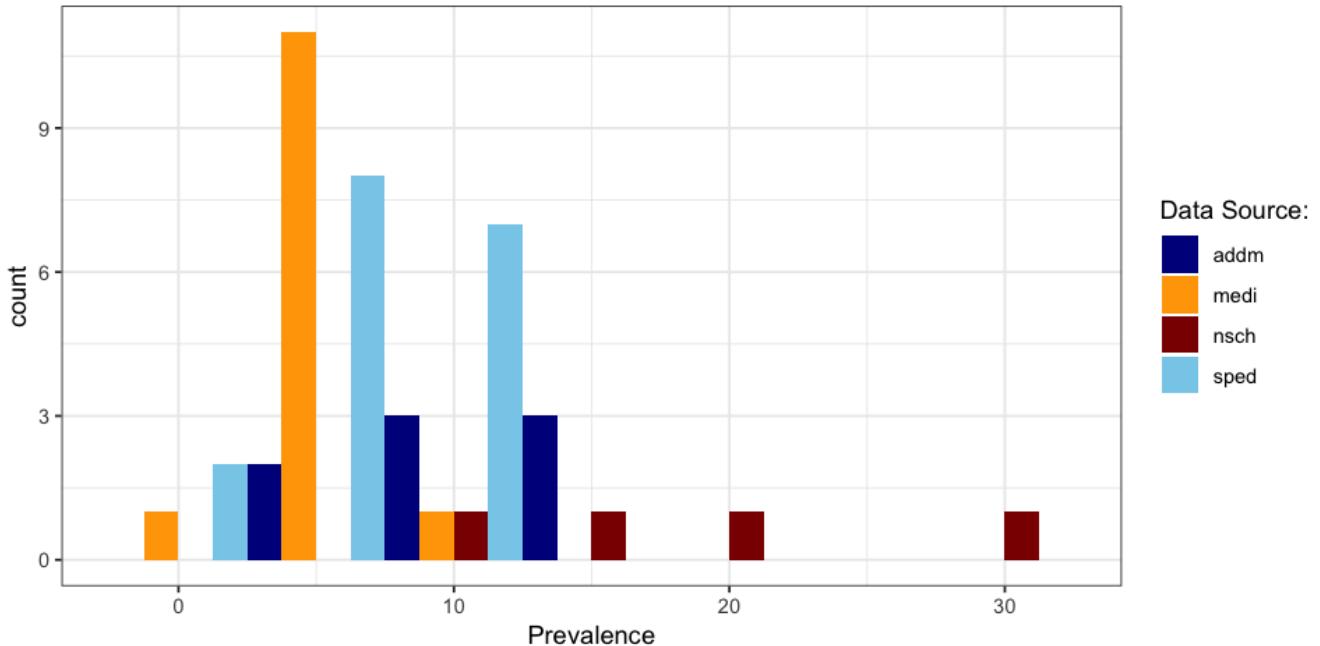
```
In [1077]: # Create histogram using ggplot2  
ggplot(ASD_National, aes(x=Prevalence)) +  
  geom_histogram(binwidth = 5, fill = "blue", color = "lightgrey", alpha=0.5)
```



```
In [1078]: # Use color to differentiate sub-group data (Data Source)
ggplot(ASD_National, aes(x=Prevalence, fill = Source)) +
  geom_histogram(binwidth = 5) +
  theme_bw() + theme(legend.position="right") +
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue"))
```

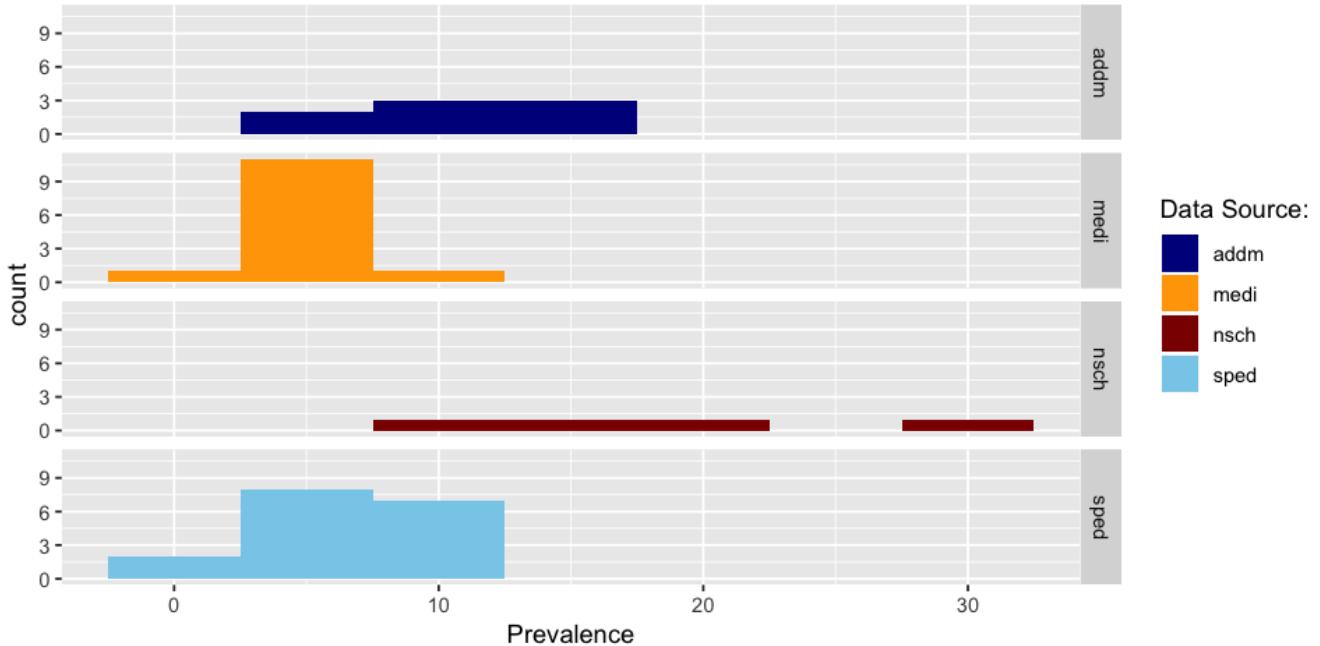


```
In [1079]: # Plot sub-group data side by side, using position="dodge"
ggplot(ASD_National, aes(x=Prevalence, fill = Source)) +
  geom_histogram(binwidth = 5, position="dodge") +
  theme_bw() + theme(legend.position="right") +
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue"))
```

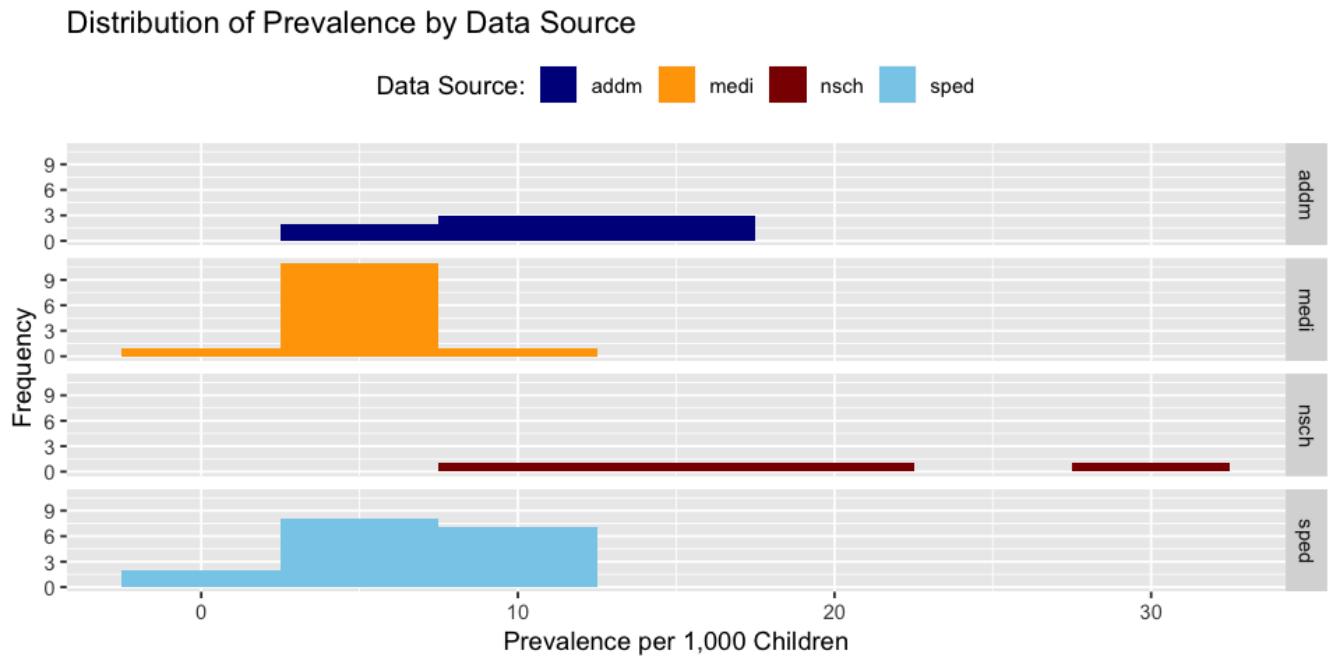


```
In [1080]: # Split plots using facet_grid()
```

```
ggplot(ASD_National, aes(x=Prevalence, fill = Source)) +  
  geom_histogram(binwidth = 5) +  
  theme(legend.position="right") +  
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",  
                                              "medi" = "orange",  
                                              "nsch" = "darkred",  
                                              "sped" = "skyblue")) +  
  facet_grid(facets = Source ~ .)
```



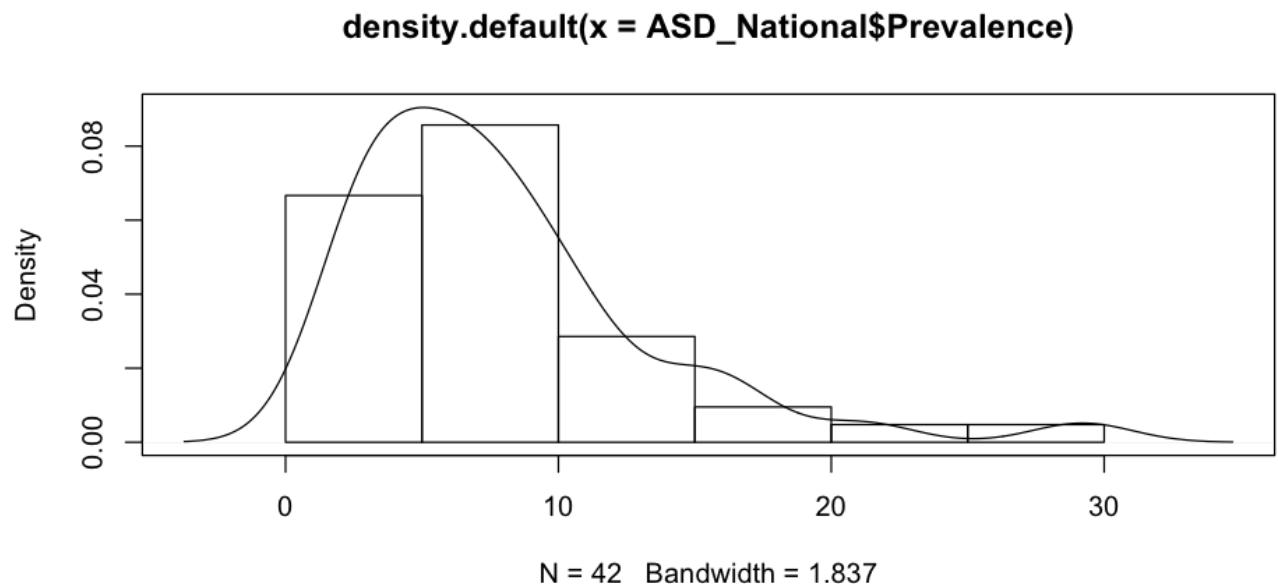
```
In [1081]: # Add title and caption using ggplot2
ggplot(ASD_National, aes(x=Prevalence, fill = Source)) +
  geom_histogram(binwidth = 5) +
  theme(legend.position="top") +
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue")) +
  labs(x="Prevalence per 1,000 Children",
       y="Frequency",
       title="Distribution of Prevalence by Data Source") +
  facet_grid(facets = Source ~ .)
```



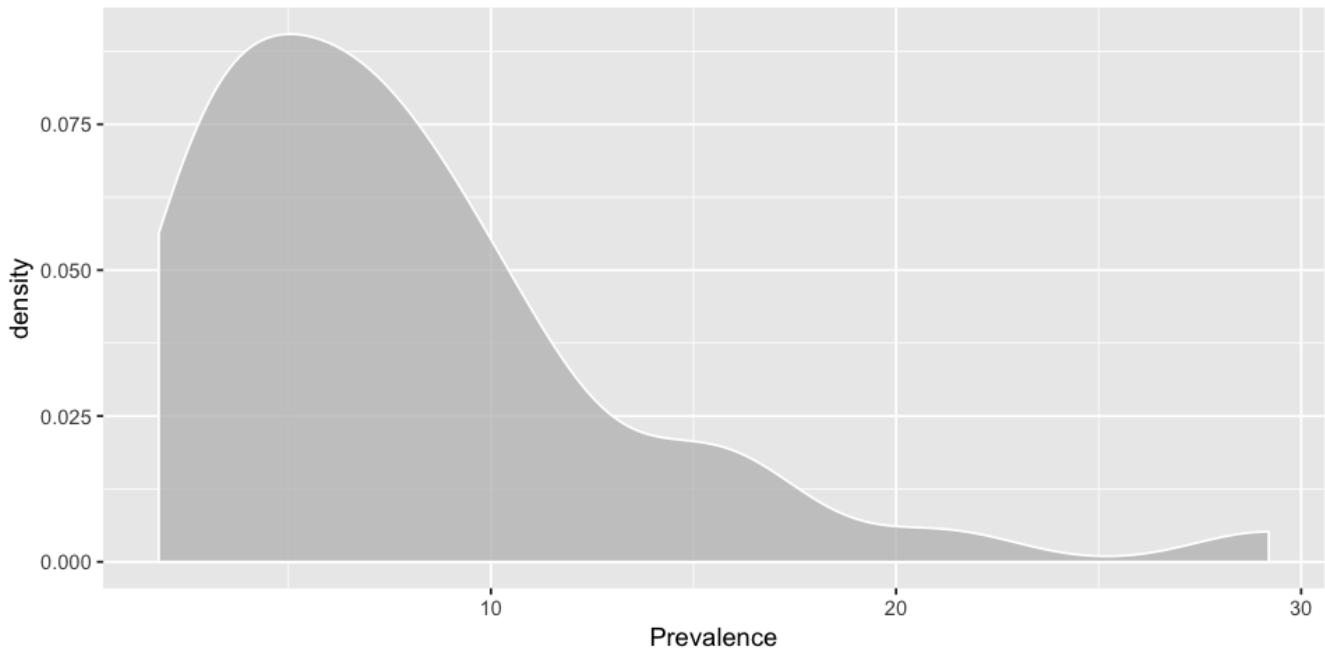
### Data Visualisation (Enhanced) - Density plot (distribution for continuous variable normalized to 100% area under curve)

```
In [1082]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

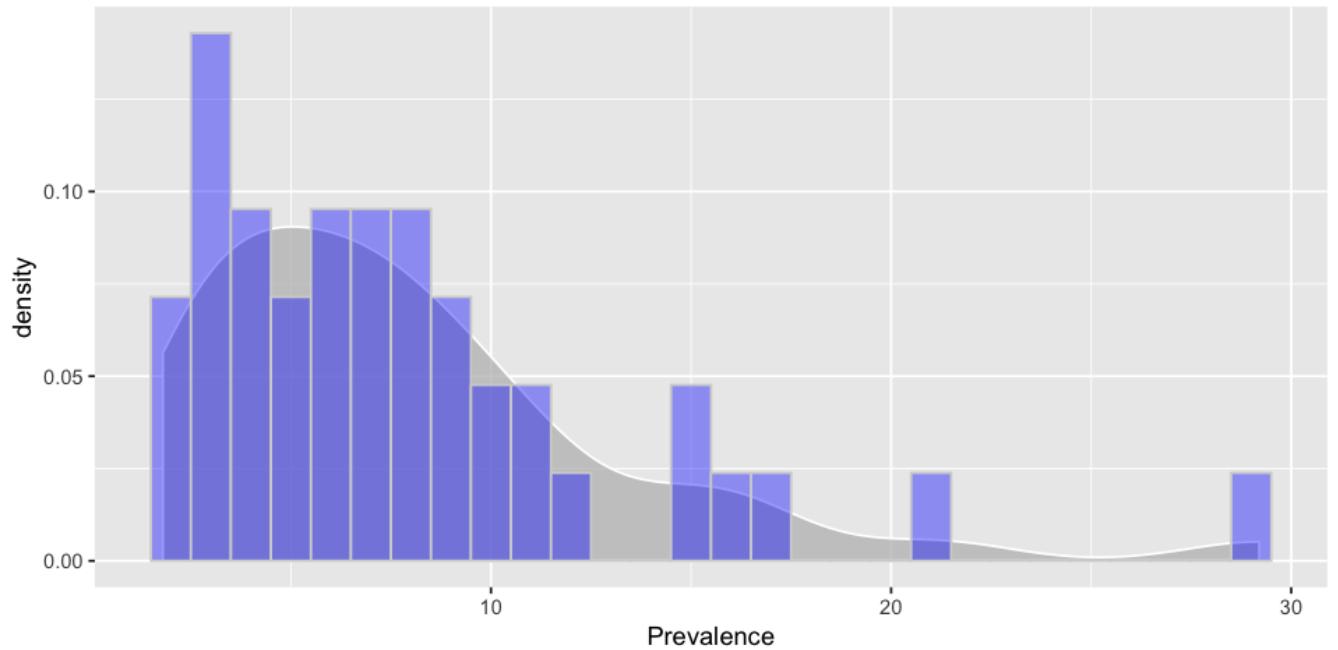
```
In [1083]: # Create plot using R graphics  
plot(density(ASD_National$Prevalence))  
# Optionally, overlay histogram  
hist(ASD_National$Prevalence, probability = TRUE, add = TRUE)
```



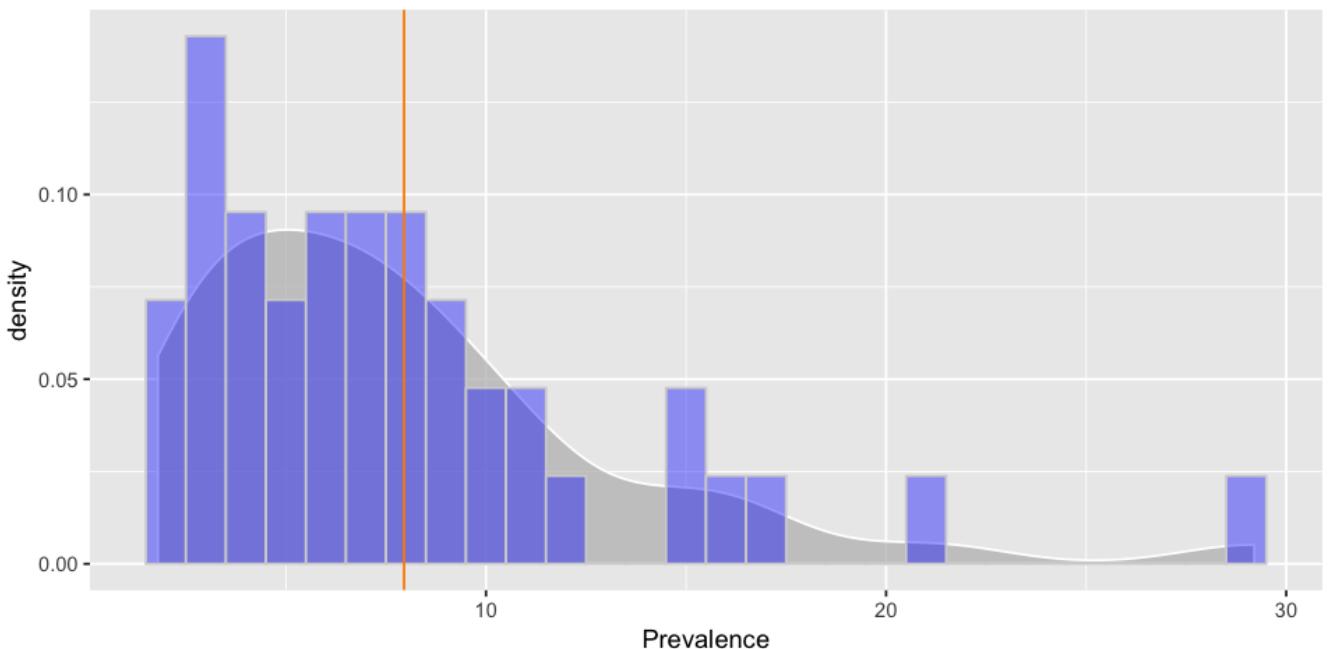
```
In [1084]: # Create plot using ggplot2
p <- ggplot(ASD_National) +
  geom_density(aes(x=Prevalence), fill = "grey", color = "white", alpha=0.75)
p # Show
```



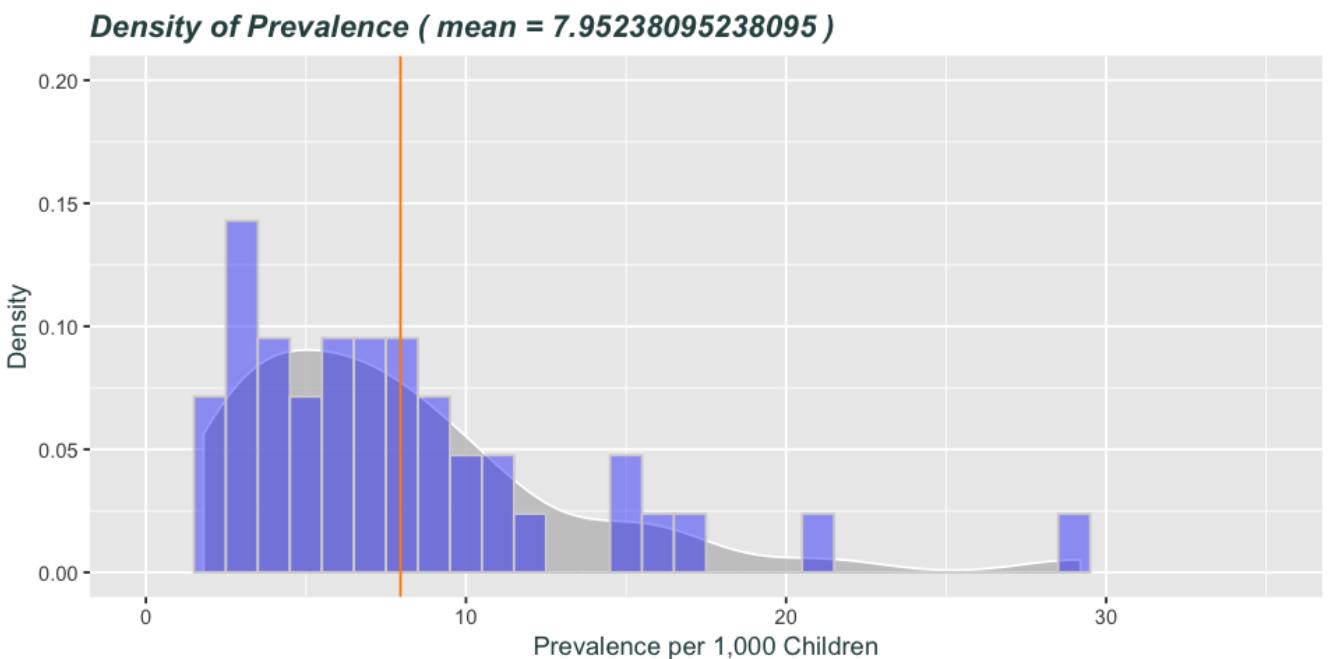
```
In [1085]: # Optionally, overlay histogram  
p <- p + geom_histogram(aes(x = Prevalence, y = ..density..), binwidth = 1, fill  
p # Show
```



```
In [1086]: # Optionally, overlay Prevalence mean  
p <- p + geom_vline(aes(xintercept = mean(ASD_National$Prevalence)), colour="darkblue")  
p # Show
```

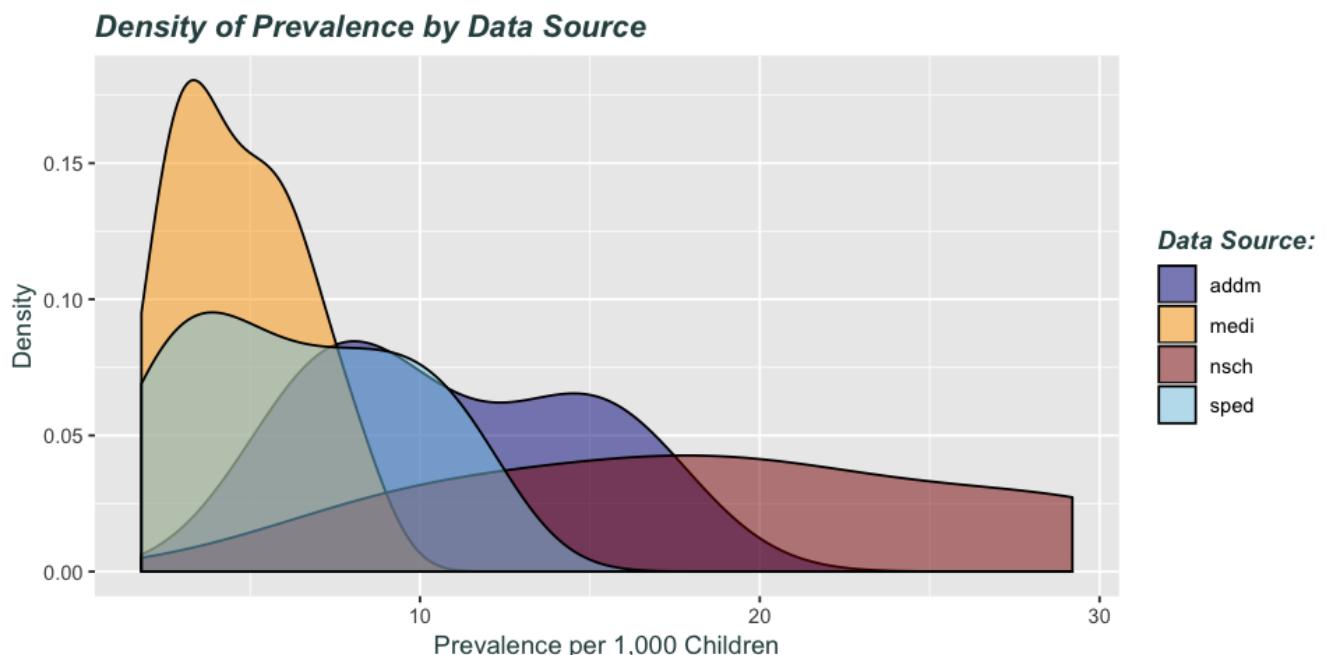


```
In [1087]: # Lastly, add other captions  
p <- p + coord_cartesian(xlim=c(0, 35), ylim=c(0, 0.2)) +  
  labs(x="Prevalence per 1,000 Children", y="Density",  
       title=paste("Density of Prevalence ( mean =", mean(ASD_National$Prevalence),  
       theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),  
             axis.title = element_text(face = 'plain', color = "darkslategrey"))  
p # Show
```



< Prevelance distribution by Data Source >

```
In [1088]: # Prevelance distribution by Data Source
ggplot(ASD_National) + geom_density(aes(x = Prevalence, fill = Source), alpha = 0.5)
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue")) +
  labs(x = "Prevalence per 1,000 Children",
       y = "Density",
       title = "Density of Prevalence by Data Source") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey"))
```



< Prevelance distribution by Data Source with split >

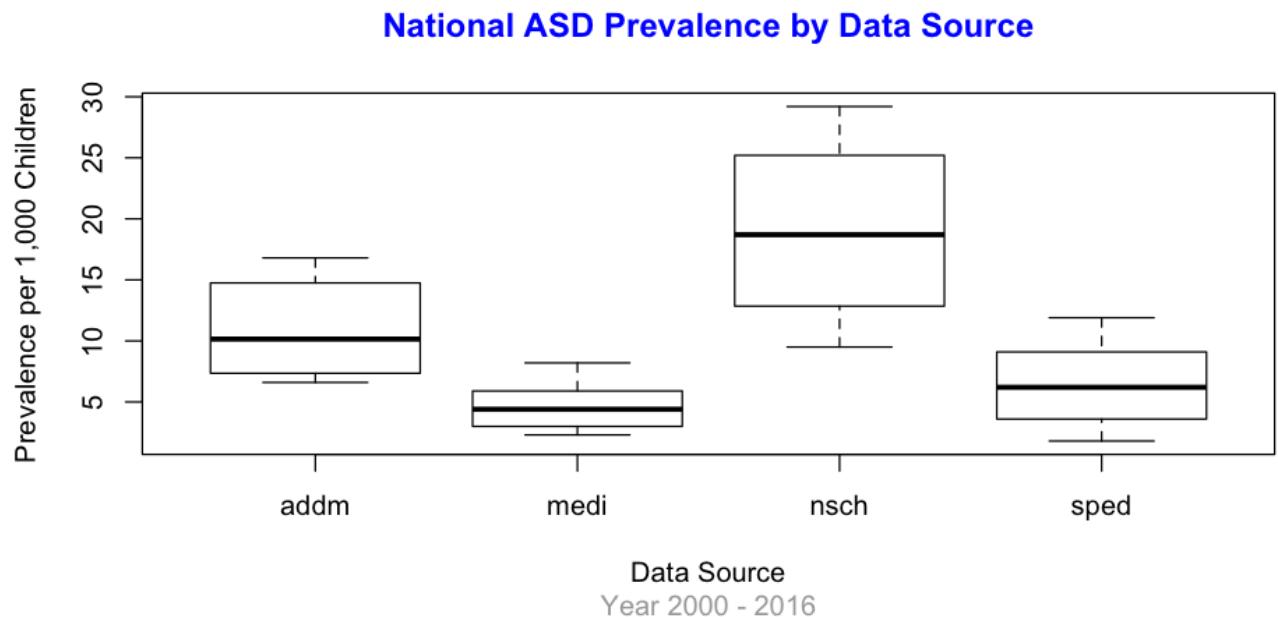
```
In [1089]: # Prevelance distribution by Data Source with split
ggplot(ASD_National) + geom_density(aes(x = Prevalence, fill = Source), colour =
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue")) +
  labs(x="Prevalence per 1,000 Children",
       y="Density",
       title="Density of Prevalence by Data Source") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey")) +
  facet_wrap(~Source)
```



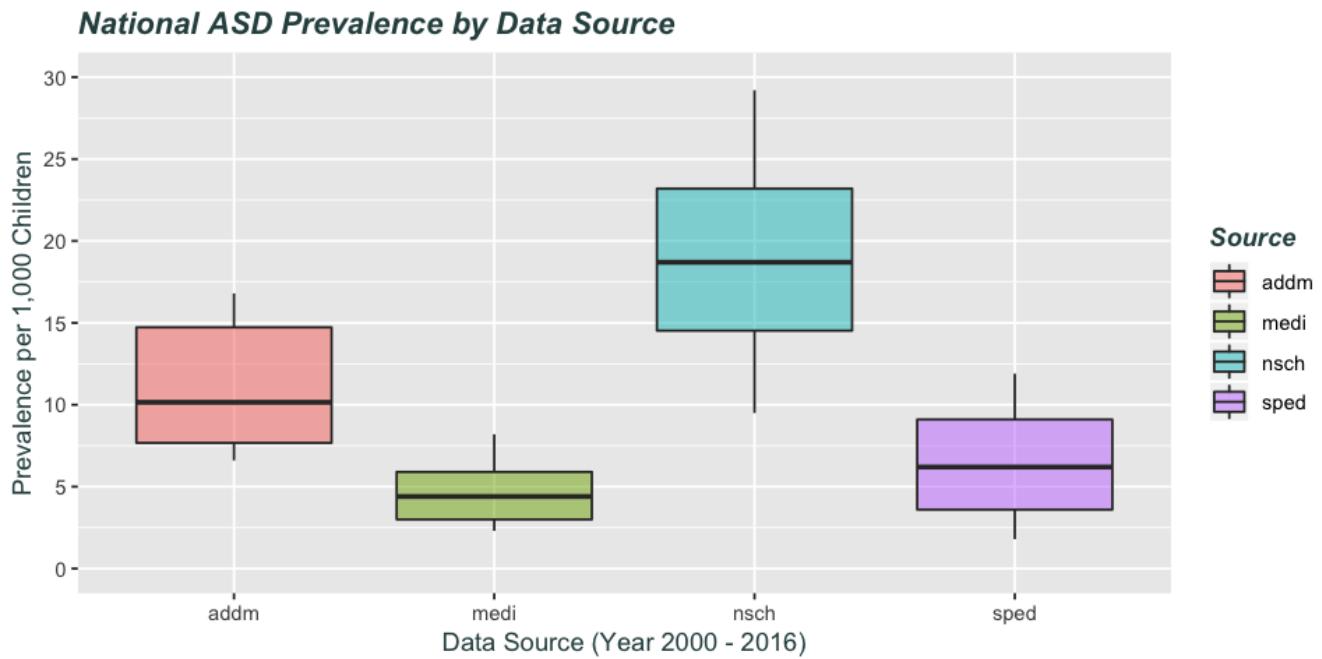
## Data Visualisation (Enhanced) - Box plot

```
In [1090]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

```
In [1091]: # Create plot using R graphics
# Create 'Prevalence' box plots break by 'Source'
boxplot(ASD_National$Prevalence ~ ASD_National$Source,
        main = "National ASD Prevalence by Data Source",
        xlab = "Data Source",
        ylab = "Prevalence per 1,000 Children",
        sub = "Year 2000 - 2016",
        col.main="blue", col.lab="black", col.sub="darkgrey")
```



```
In [1092]: # Create box plot using ggplot2
ggplot(ASD_National, aes(x = Source, y = Prevalence, fill = Source)) +
  geom_boxplot(alpha = 0.5) +
  scale_y_continuous(name = "Prevalence per 1,000 Children",
                     breaks = seq(0, 30, 5),
                     limits=c(0, 30)) +
  scale_x_discrete(name = "Data Source (Year 2000 - 2016)") +
  ggtitle("National ASD Prevalence by Data Source") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey"))
```

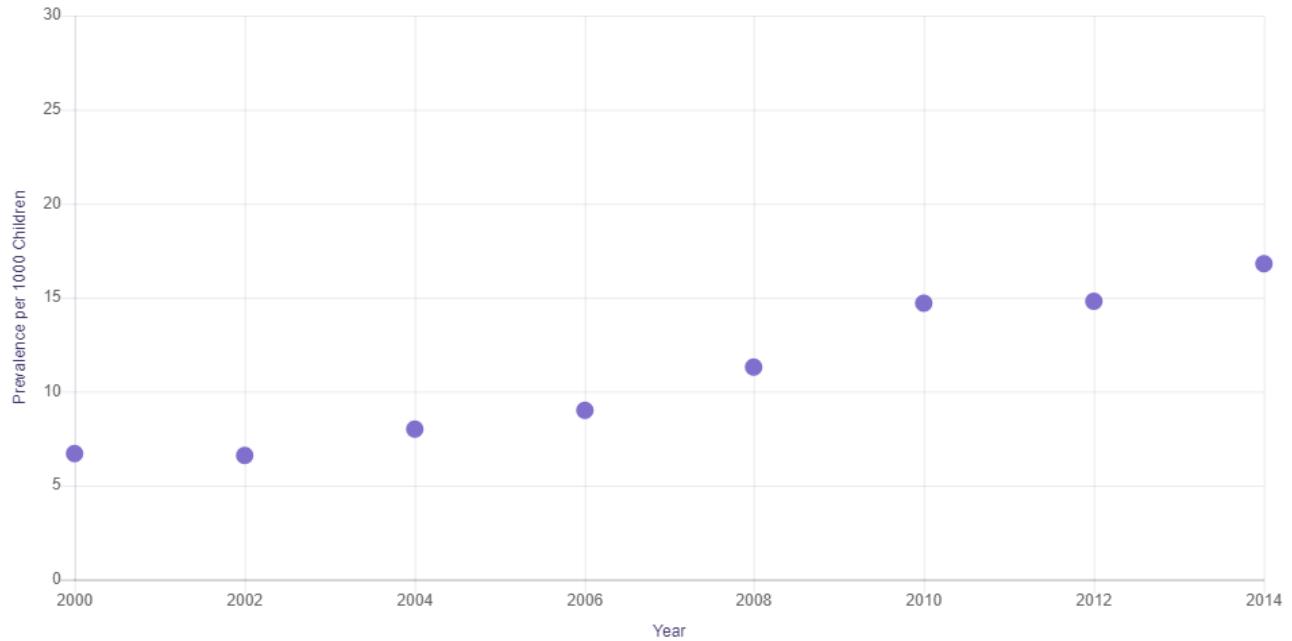


## Data Visualisation (Enhanced) - Line chart

**Data Visualisation (Enhanced) - [ CDC ] REPORTED PREVALENCE HAS CHANGED OVER TIME**

### Prevalence Estimates Over Time

Using data set: ADDM Network\* ▾ Show prevalence for: U.S. or Total† ▾



Note: Hover your mouse over data points above to show prevalence by year.

\*ADDM Network data only represent a selection of sites within states (but not entire states) that were funded during each project cycle; therefore, data are not available for the entire United States.

\*\*ADDM estimate = the total for all sites combined.

†NSCH data are not comparable over time as data collection methods changed. See technical notes for further details.

‡For NSCH data, data are suppressed when the width of the confidence interval exceeds 1.2 times the point estimate. This is the same approach that is recommended by NSCH [here](#) and our point estimates (and suppressed data points) match those on childhealthdata.org for 2016-2017.

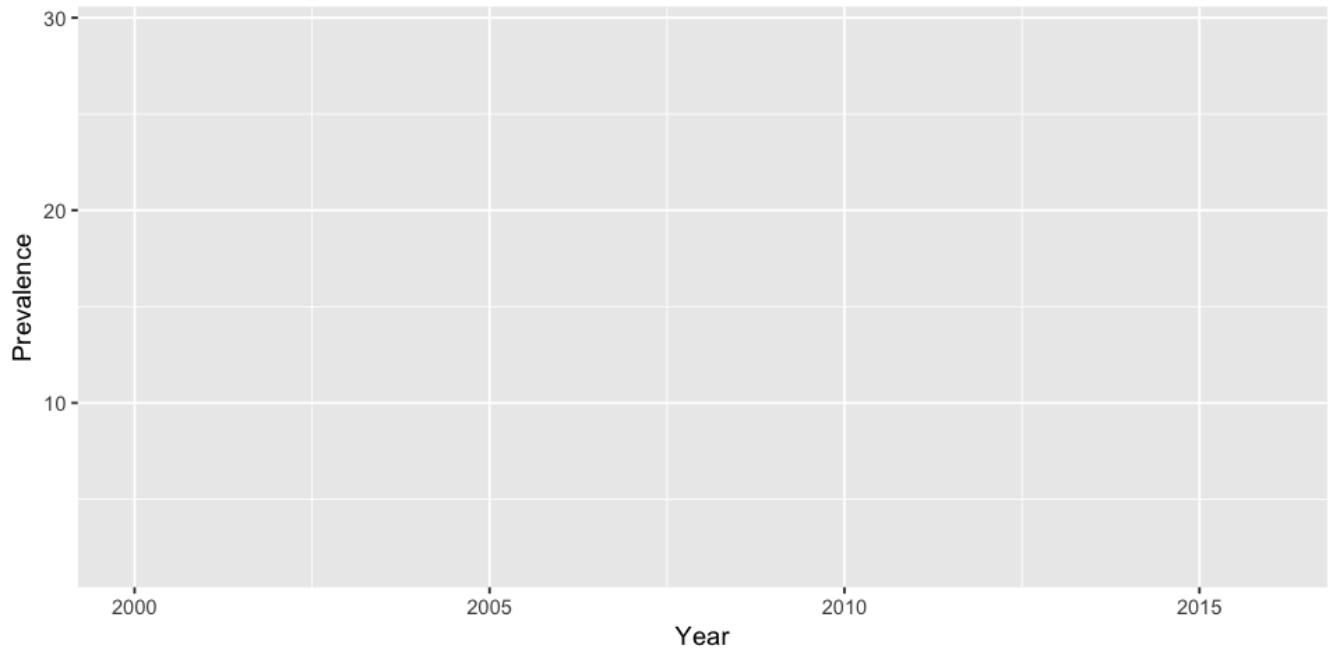
+++If NSCH 2016 data are selected, combined 2016-2017 estimates are shown.

## Data Visualisation (Enhanced) - [ R ] REPORTED PREVALENCE HAS CHANGED OVER TIME [Source: ALL]

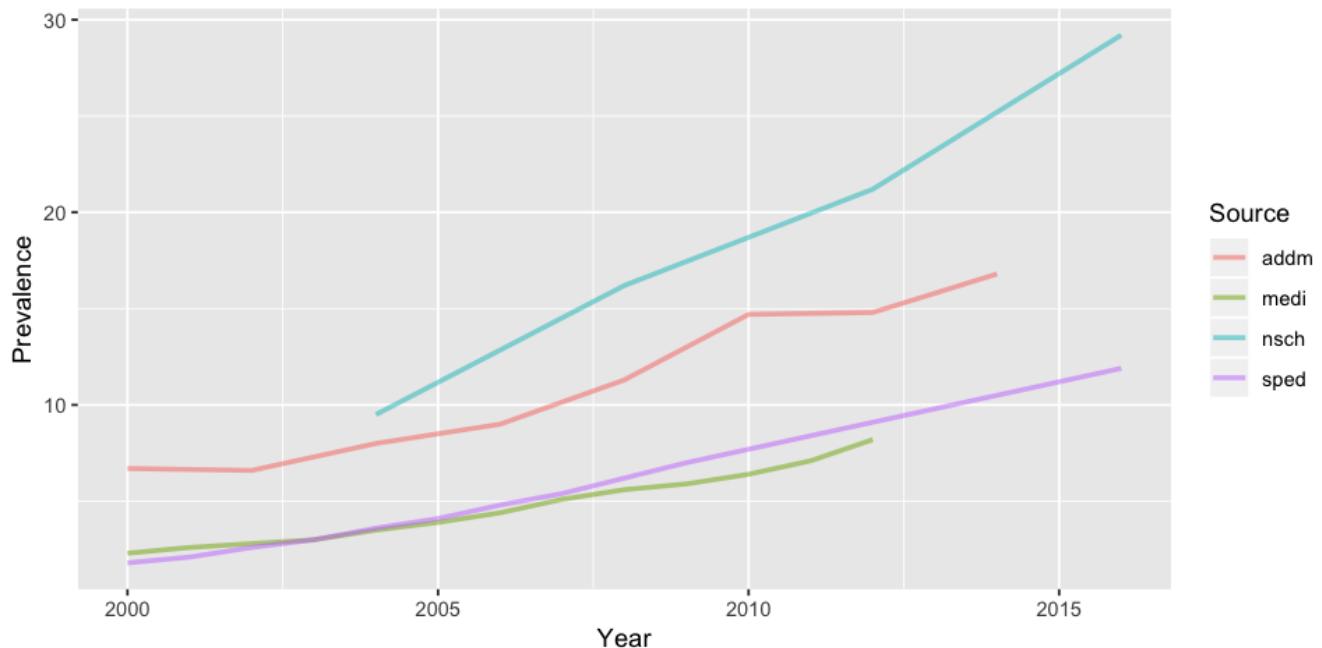
```
In [1093]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

In [1094]:

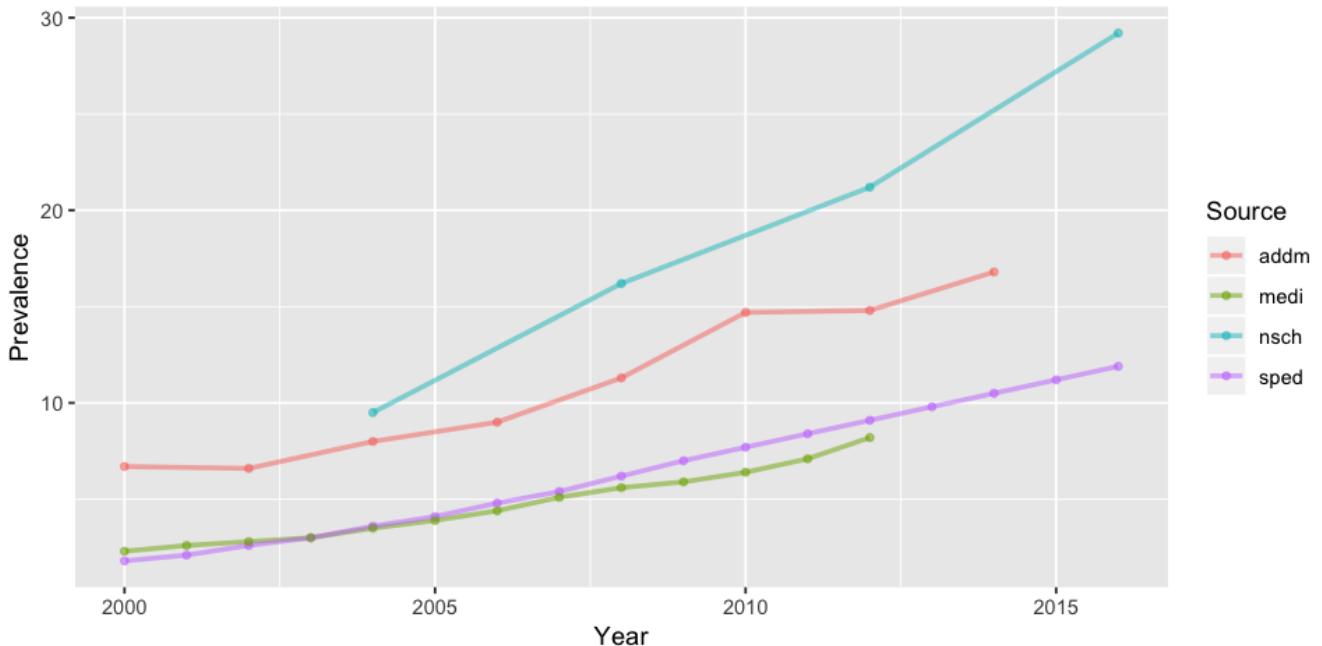
```
# -----  
# Build chart/plot layer by layer  
# -----  
  
# Define a ggplot graphic object; provide data and x y for use  
p <- ggplot(ASD_National, aes(x = Year, y = Prevalence))  
# Show plot  
p
```



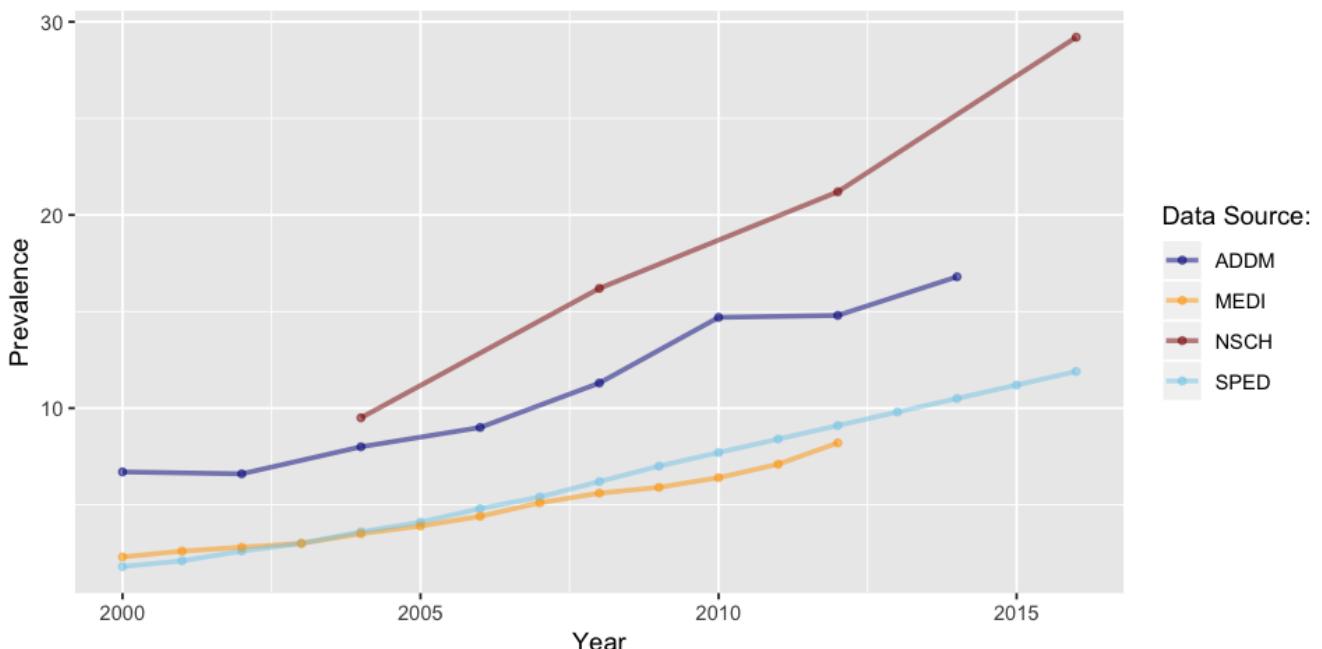
```
In [1095]: # Select (add) line chart type:  
p <- p + geom_line(aes(color = Source),  
                     linetype = "solid", # http://sape.inf.usi.ch/quick-reference/  
                     size=1,  
                     alpha=0.5)  
# Show plot  
p
```



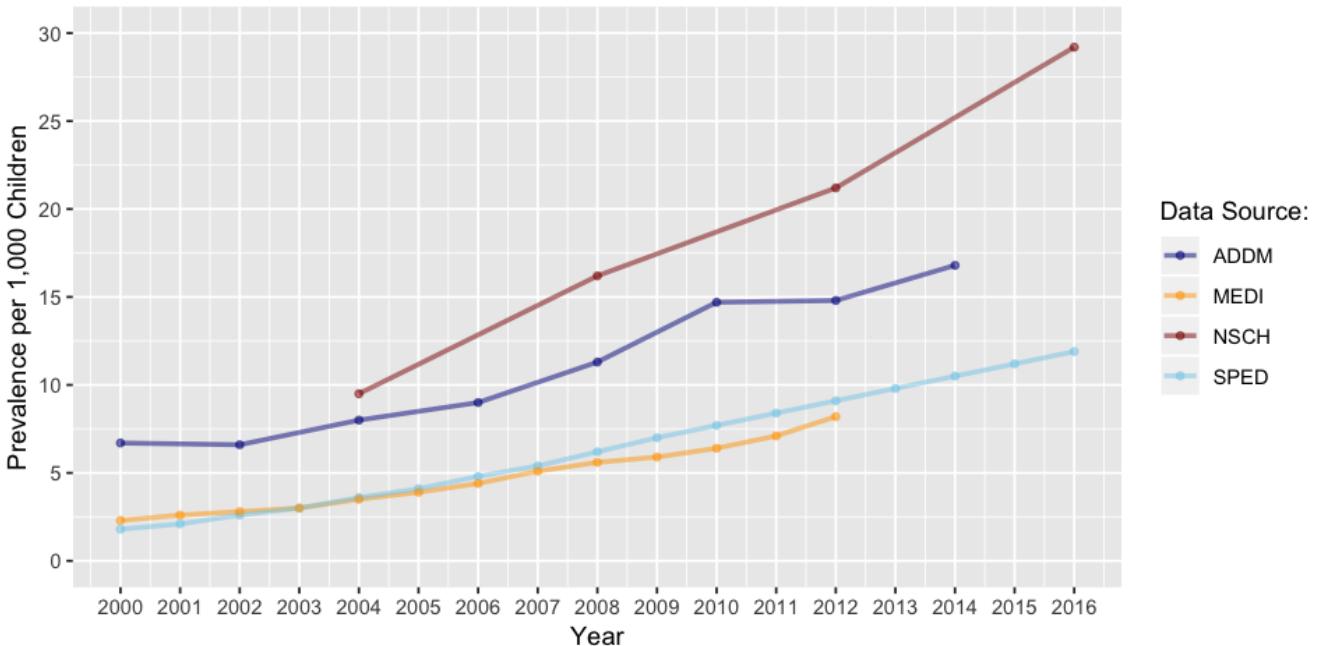
```
In [1096]: # Select (add) points to chart:  
p <- p + geom_point(aes(color = Source),  
                      size=2,  
                      shape=20,  
                      alpha=0.5)  
# Show plot  
p
```



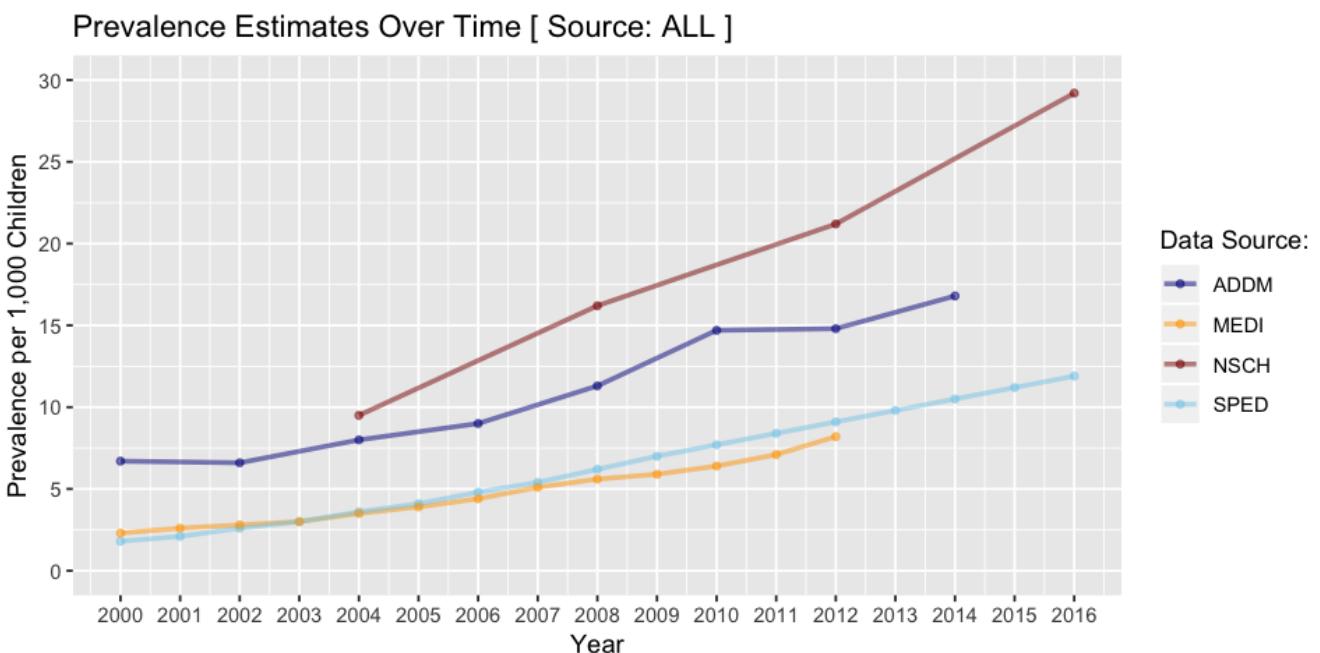
```
In [1097]: # Customize line color and legend name:  
p <- p + scale_color_manual("Data Source:",  
                             labels = c('ADDM', 'MEDI', 'NSCH', 'SPED'),  
                             values = c("addm" = "darkblue",  
                                       "medi" = "orange",  
                                       "nsch" = "darkred",  
                                       "sped" = "skyblue"))  
# Show plot  
p
```



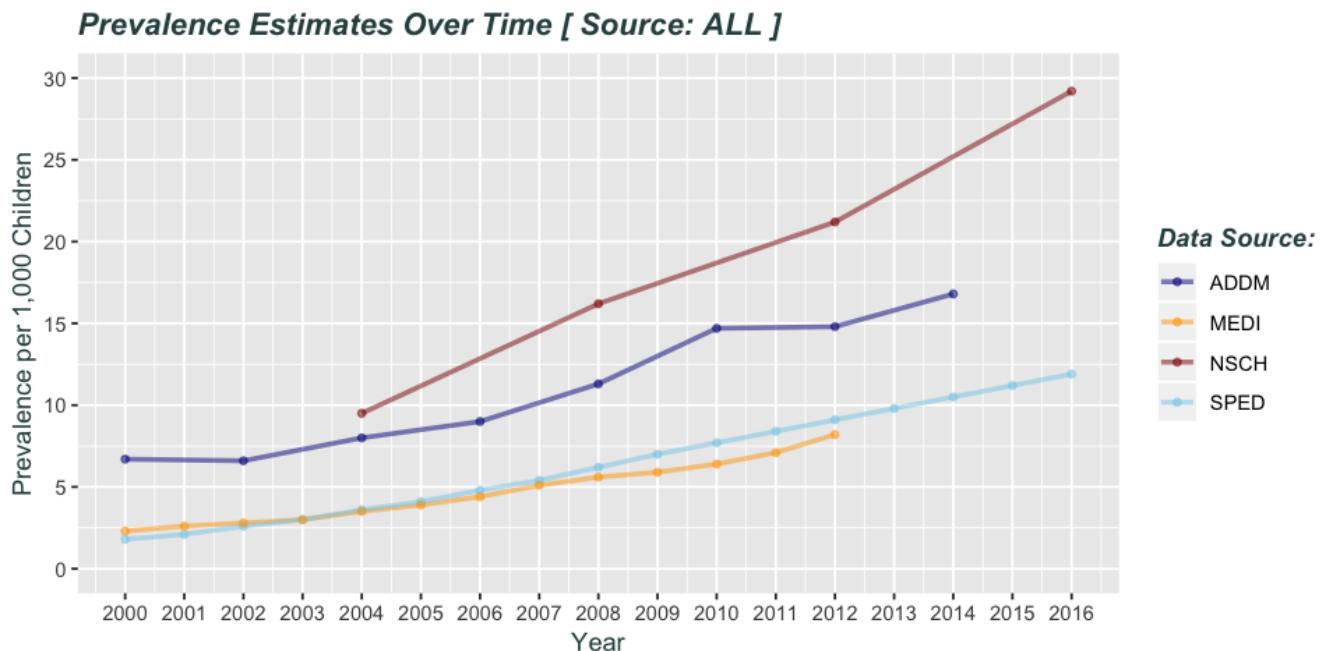
```
In [1098]: # Adjust x and y axis, scale, limit and labels:
p <- p + scale_y_continuous(name = "Prevalence per 1,000 Children",
                             breaks = seq(0, 30, 5),
                             limits=c(0, 30)) +
  scale_x_continuous(name = "Year",
                     breaks = seq(2000, 2016, 1),
                     limits = c(2000, 2016))
# Show plot
p
```



```
In [1099]: # Customise chart title:
p <- p + ggtitle("Prevalence Estimates Over Time [ Source: ALL ]")
# Show plot
p
```



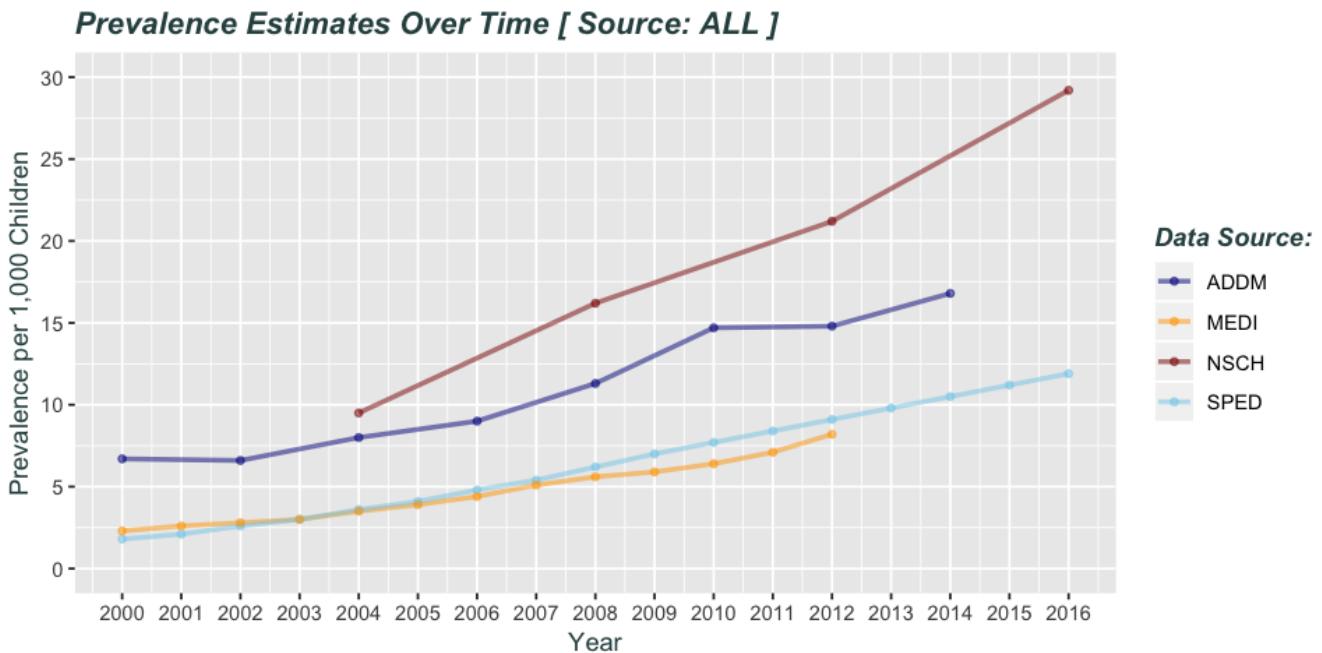
```
In [1100]: # Customise chart title and axis labels:  
p <- p + theme(title = element_text(face = 'bold.italic', color = "darkslategrey",  
                  axis.title = element_text(face = 'plain', color = "darkslategrey"))  
# Show plot  
p
```



**Consolidate above code into one chunk:**

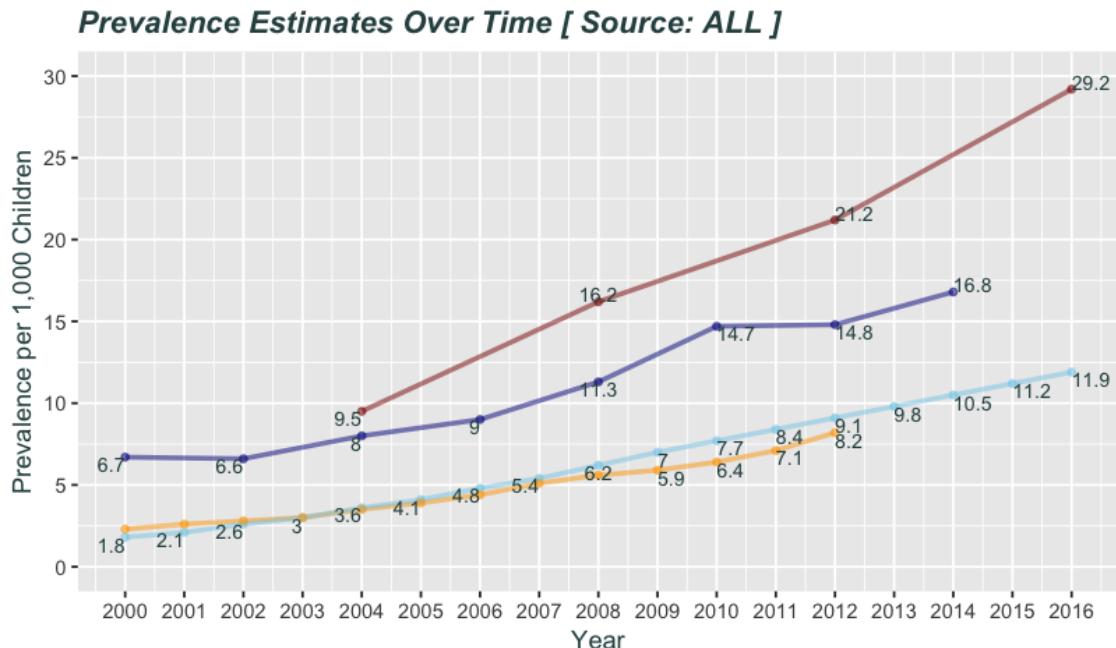
In [1101]:

```
# -----  
# Consolidate above code into one chunk  
# -----  
p <- ggplot(ASD_National, aes(x = Year, y = Prevalence)) +  
  geom_line(aes(color = Source),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(color = Source),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  scale_color_manual("Data Source:",  
                     labels = c('ADDM', 'MEDI', 'NSCH', 'SPED'),  
                     values = c("addm" = "darkblue",  
                               "medi" = "orange",  
                               "nsch" = "darkred",  
                               "sped" = "skyblue")) +  
  scale_y_continuous(name = "Prevalence per 1,000 Children",  
                     breaks = seq(0, 30, 5),  
                     limits=c(0, 30)) +  
  scale_x_continuous(name = "Year",  
                     breaks = seq(2000, 2016, 1),  
                     limits = c(2000, 2016)) +  
  ggtitle("Prevalence Estimates Over Time [ Source: ALL ]") +  
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),  
        axis.title = element_text(face = 'plain', color = "darkslategrey"))  
# Show plot  
p
```



Optionally, display data values/labels:

```
In [1102]: # Optionally, display data values/labels
p + geom_text(aes(label = round(Prevalence, 1)), # Values are rounded for display
              vjust = "outward",
              #           nudge_y = 0.2, # optionally life the text
              hjust = "outward",
              check_overlap = TRUE,
              size = 3, # size of textual data label
              col = 'darkslategrey')
```



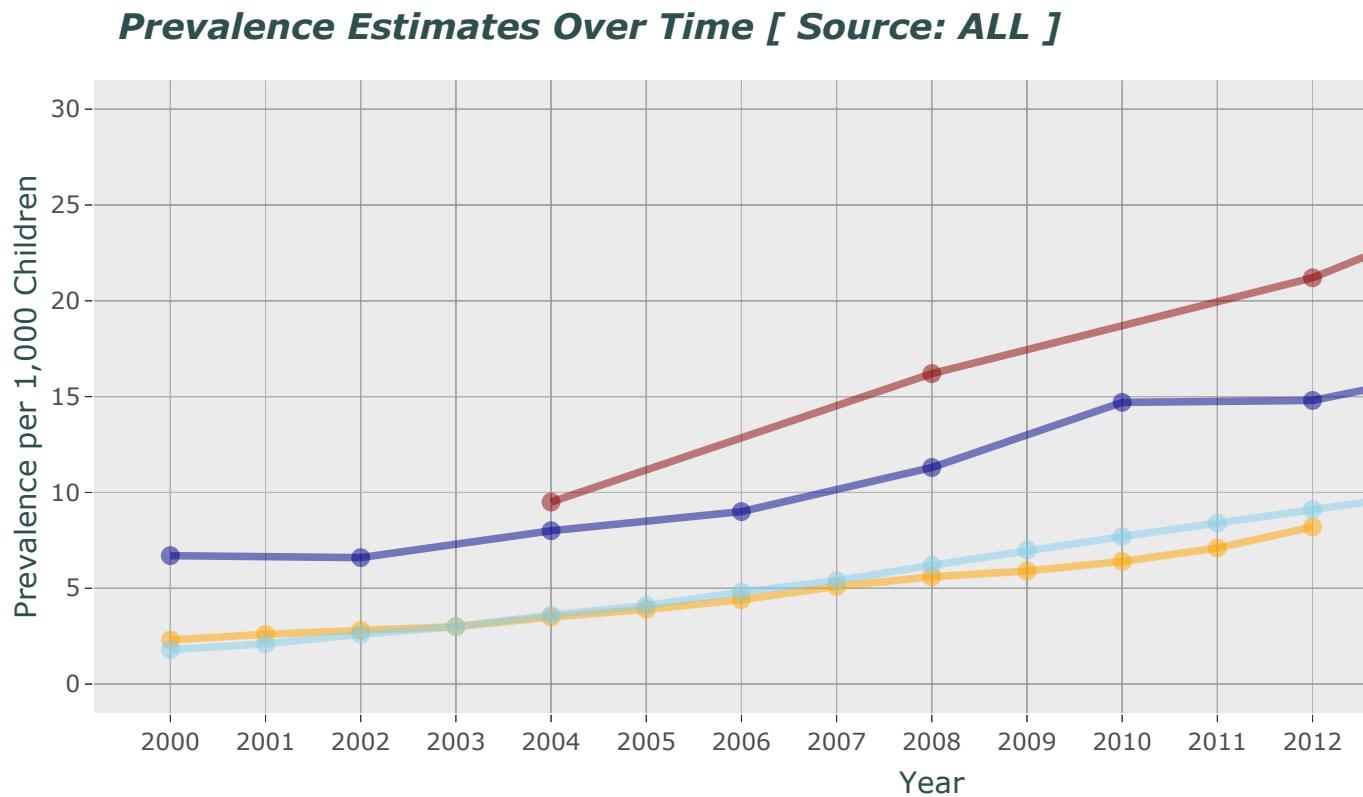
## Data Visualisation (Enhanced) - Dynamic Visualisation with plotly

```
In [1103]: if(!require(plotly)){install.packages("plotly")}
library(plotly)
```

Create ployly graph object from ggplot graph object:

```
In [1104]: p_dynamic <- p
p_dynamic <- ggplotly(p_dynamic)
p_dynamic
```

```
In [1105]: p_dynamic
```



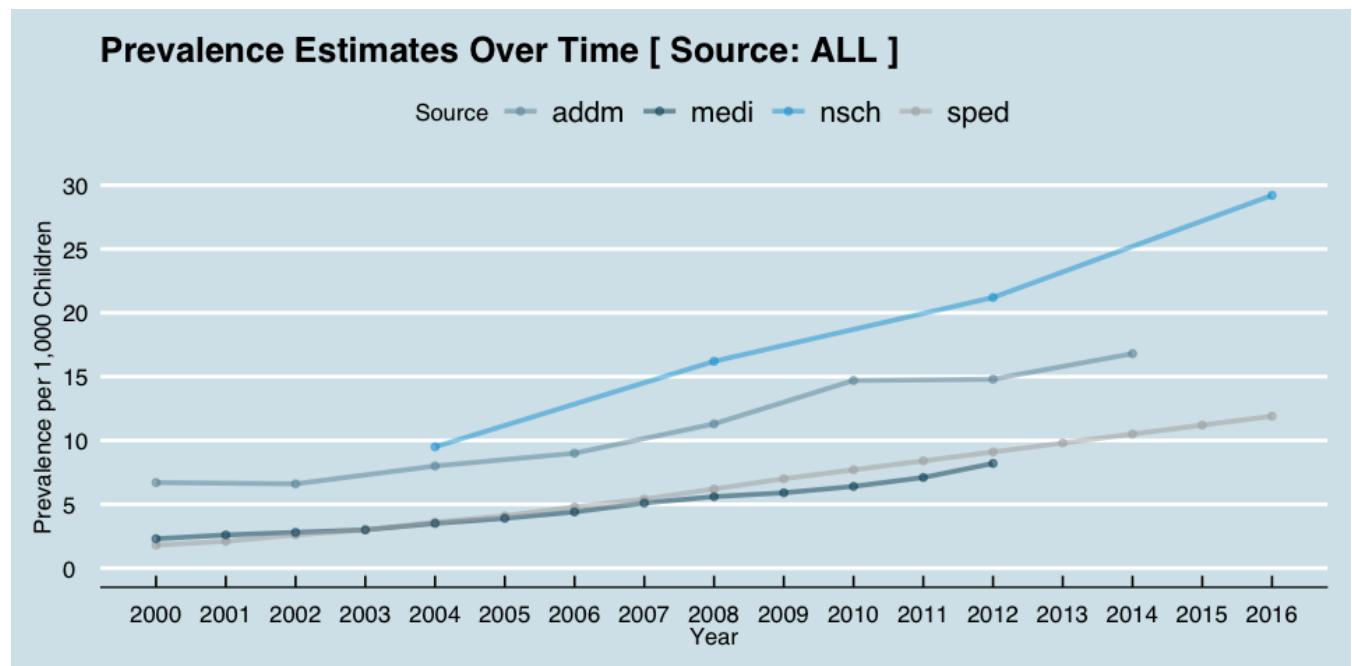
### Data Visualisation (Enhanced) - Use themes as aesthetic template

```
In [1106]: if(!require(ggthemes)){install.packages("ggthemes")}  
library(ggthemes)
```

Theme of the Economist magazine:

```
In [1107]: # Theme of the economist magazine:  
p + theme_economist() + scale_colour_economist()
```

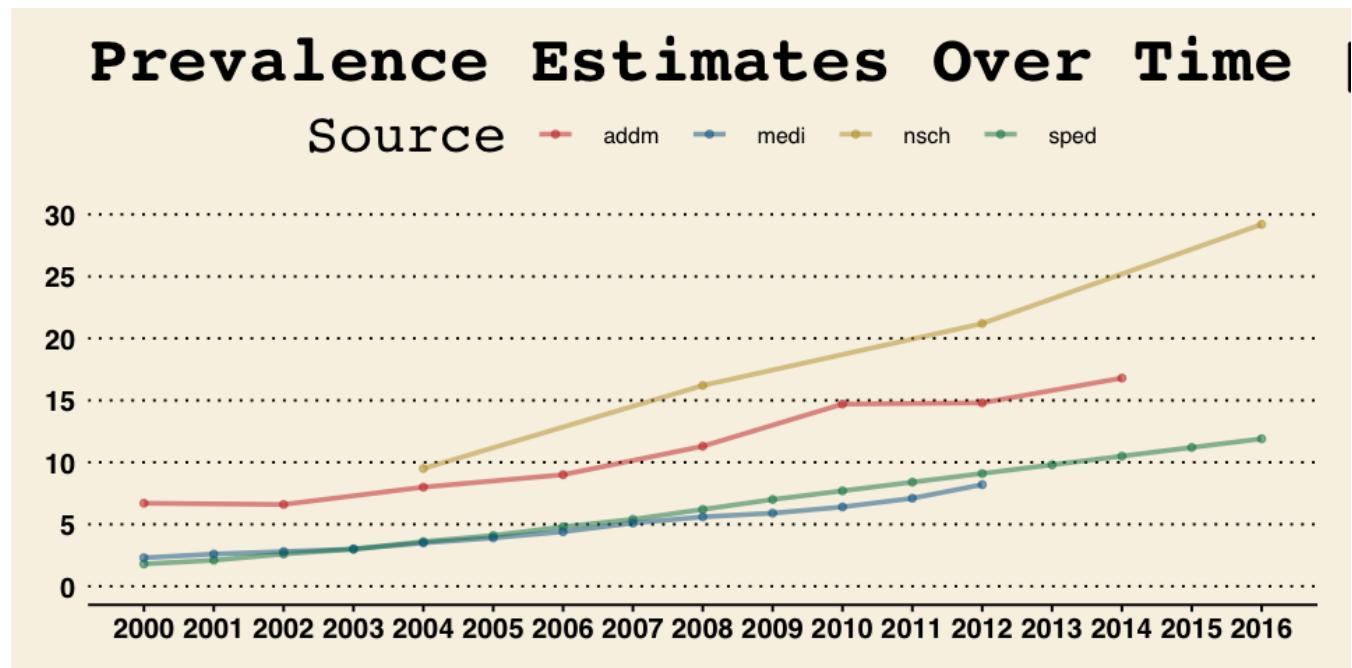
Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.



#### Theme of the Wall Street Journal:

```
In [1108]: # Theme of the Wall Street Journal:  
p + theme_wsj() + scale_colour_wsj("colors6")
```

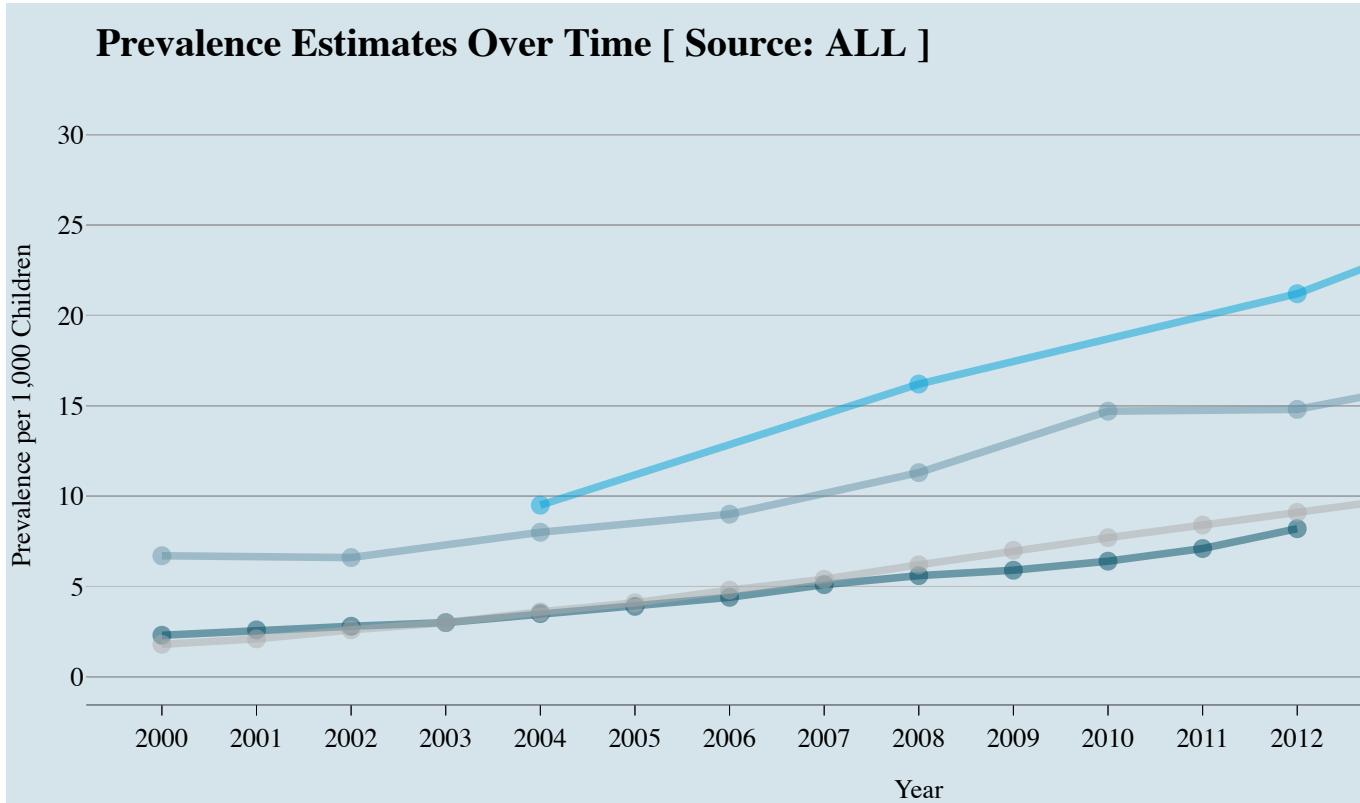
Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.



#### Dynamic chart with theme of the economist magazine:

```
In [1109]: # Dynamic chart with theme of the economist magazine:  
p_dynamic <- p + theme_economist() + scale_colour_economist()  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.



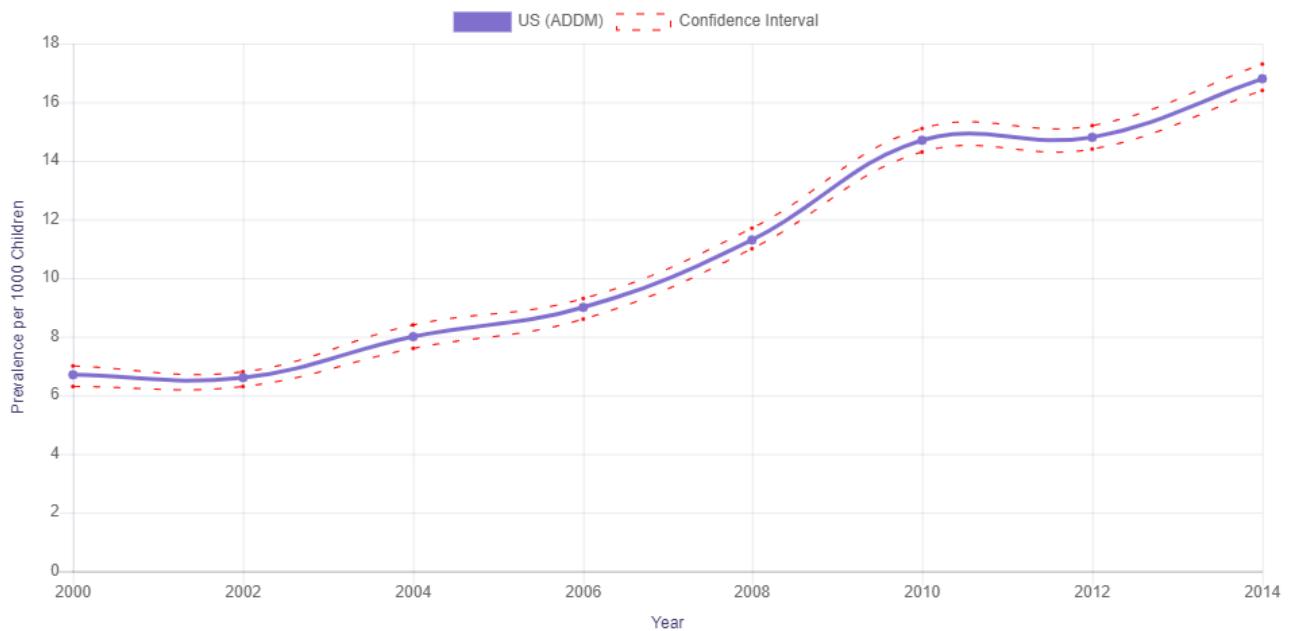
Data Visualisation (Enhanced) - [ CDC ] ADDM Network estimates for overall ASD prevalence in US over time [ Source: ADDM ] over [ Year ]

## 2014 ADDM NETWORK DATA

In this section, explore the most recent ADDM data, both overall and among certain demographic groups by study area.

### ADDM Network estimates for overall ASD prevalence in US over time

with confidence interval



\*ADDM data do not represent the entire state, only a selection of sites within the state.

\*\*ADDM estimate = the total for all sites combined.

<sup>†</sup>NSCH data are not comparable over time as data collection methods changed and the data are not provided here. See technical notes for further details.

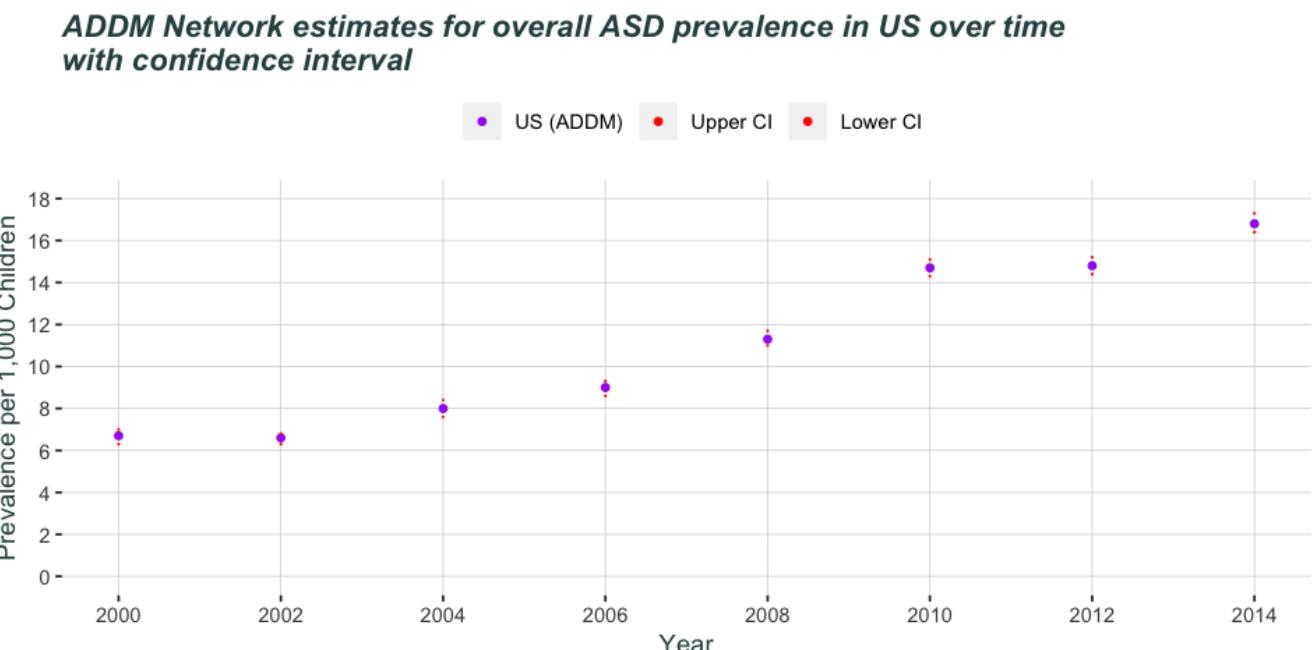
## Data Visualisation (Enhanced) - [ R ] ADDM Network estimates for overall ASD prevalence in US over time [ Source: ADDM ] over [ Year ]

```
In [1110]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

```
In [1111]: # Filter only data of ADDM
ASD_National_ADDM <- subset(ASD_National, Source == 'addm')
```

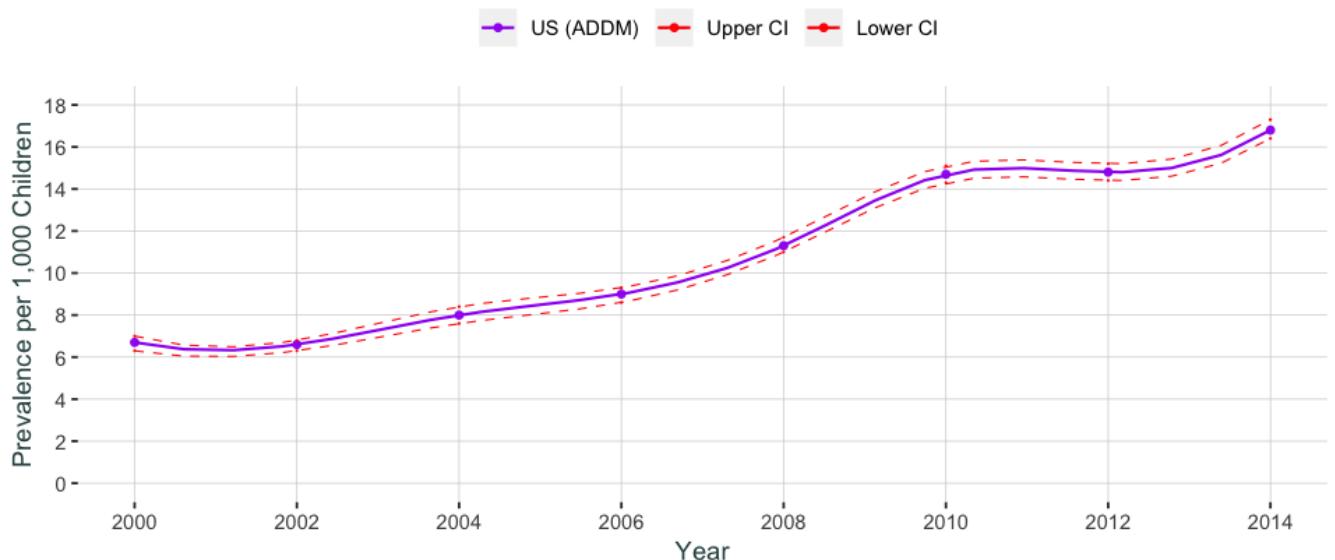
In [1112]:

```
# -----  
# [addm] ADDM Network estimates for overall ASD prevalence in US over time  
# -----  
  
# Color:  
# 'ADDM_Average' "purple"  
  
p <- ggplot(ASD_National_ADDM, aes(x = Year, y = Prevalence)) +  
  geom_point(aes(y = Prevalence, color = 'ADDM_Average'), # Name for manual colour map  
             size=2,  
             shape=20,  
             alpha=0.95) +  
  # Add point for Upper.CI  
  geom_point(aes(y = Upper.CI, color = 'ADDM_U_CI'), # Name for manual colour map  
             size=0.1,  
             shape=20,  
             alpha=0.95) +  
  # Add point for Lower.CI  
  geom_point(aes(y = Lower.CI, color = 'ADDM_L_CI'), # Name for manual colour map  
             size=0.1,  
             shape=20,  
             alpha=0.95) +  
  scale_colour_manual(name="",  
                      labels = c("US (ADDM)", "Upper CI", "Lower CI"), # Names shown  
                      values = c(ADDM_Average="purple", ADDM_U_CI="red", ADDM_L_CI="blue"))  
  # Add title, axis label, and axis scale  
p <- p + scale_y_continuous(name = "Prevalence per 1,000 Children",  
                            breaks = seq(0, 18, 2),  
                            limits=c(0, 18)) +  
  scale_x_continuous(name = "Year",  
                     breaks = seq(2000, 2014, 2),  
                     limits = c(2000, 2014)) +  
  ggtitle("ADDM Network estimates for overall ASD prevalence in US over time\\nwith confidence interval")  
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),  
        axis.title = element_text(face = 'plain', color = "darkslategrey"),  
        panel.background = element_blank(), # Remove chart background colour  
        legend.position = 'top',  
        panel.grid.major = element_line(size = 0.2, linetype = 'solid', colour = "#cccccc"))  
  # Show plot  
p
```



```
In [1113]: # Add smooth curve to go through date points, using interpolation with splines:
# https://stackoverflow.com/questions/35205795/plotting-smooth-line-through-all-d
spline_ADDM_Prevalence <- as.data.frame(spline(ASD_National_ADDM$Year, ASD_Nation
spline_ADDM_Prevalence_U_CI <- as.data.frame(spline(ASD_National_ADDM$Year, ASD_N
spline_ADDM_Prevalence_L_CI <- as.data.frame(spline(ASD_National_ADDM$Year, ASD_N
# Show plot
p + geom_line(data = spline_ADDM_Prevalence, aes(x = x, y = y, color = 'ADDM_Aver
geom_line(data = spline_ADDM_Prevalence_U_CI, aes(x = x, y = y, color = 'ADDM_U
geom_line(data = spline_ADDM_Prevalence_L_CI, aes(x = x, y = y, color = 'ADDM_L
```

**ADDM Network estimates for overall ASD prevalence in US over time  
with confidence interval**



## Data Visualisation (Enhanced) - [ R ] REPORTED PREVALENCE VARIES BY SEX [ Source: ADDM ] over [ Year ]

```
In [1114]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

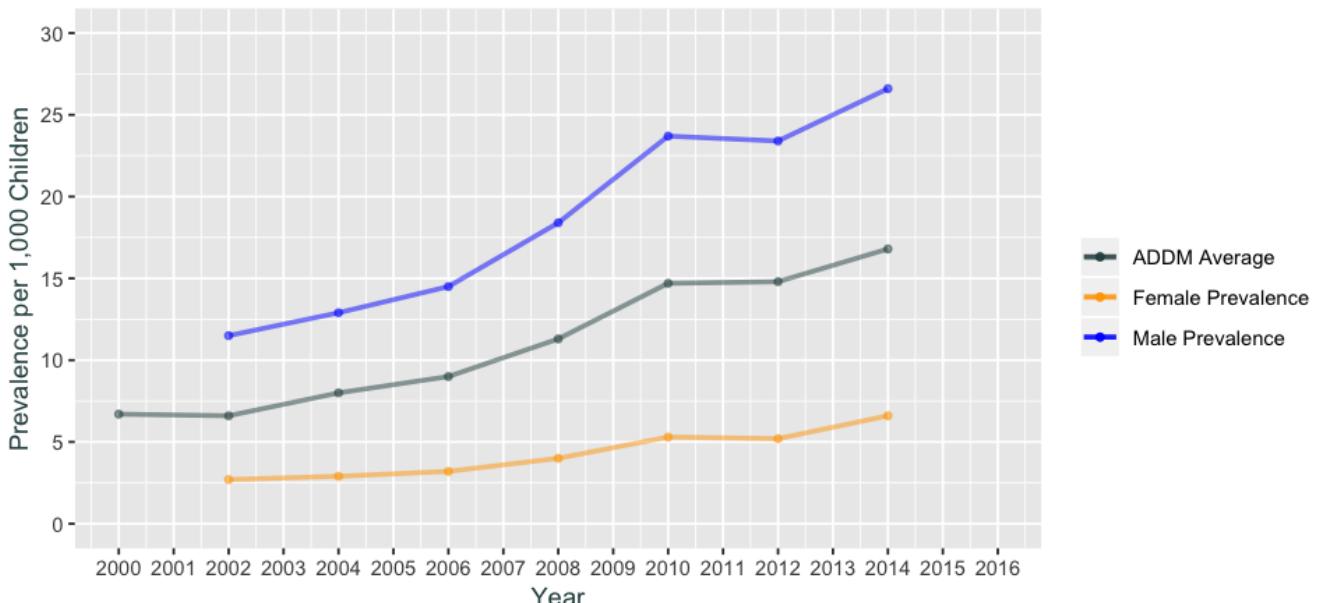
In [1115]:

```
# -----  
# [addm] < Prevalence Varies by Sex >  
# -----  
  
# Color:  
# 'ADDM_Average' "darkslategrey"  
# 'Female_Prevalence' "orange"  
# 'Male_Prevalence' "blue"  
  
p <- ggplot(ASD_National_ADDM, aes(x = Year, y = Prevalence)) +  
  geom_line(aes(y = Prevalence, colour = 'ADDM_Average'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Prevalence, color = 'ADDM_Average'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  # Add line for Female  
  geom_line(aes(y = Female.Prevalence, colour = 'Female_Prevalence'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Female.Prevalence, color = 'Female_Prevalence'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  # Add line for Male  
  geom_line(aes(y = Male.Prevalence, colour = 'Male_Prevalence'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Male.Prevalence, color = 'Male_Prevalence'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  scale_colour_manual(name="",  
                     labels = c("ADDM Average", "Female Prevalence", "Male Preva"),  
                     values = c(ADDM_Average="darkslategrey", Female_Prevalence= # Add title, axis label, and axis scale  
p <- p + scale_y_continuous(name = "Prevalence per 1,000 Children",  
                            breaks = seq(0, 30, 5),  
                            limits=c(0, 30)) +  
  scale_x_continuous(name = "Year",  
                     breaks = seq(2000, 2016, 1),  
                     limits = c(2000, 2016)) +  
  ggtitle("Prevalence Estimates by Sex [ Source: ADDM ]") +  
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),  
        axis.title = element_text(face = 'plain', color = "darkslategrey"))  
# Show plot  
p
```

Warning message:

"Removed 1 rows containing missing values (geom\_path)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."Warning message:  
"Removed 1 rows containing missing values (geom\_path)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."

### Prevalence Estimates by Sex [ Source: ADDM ]



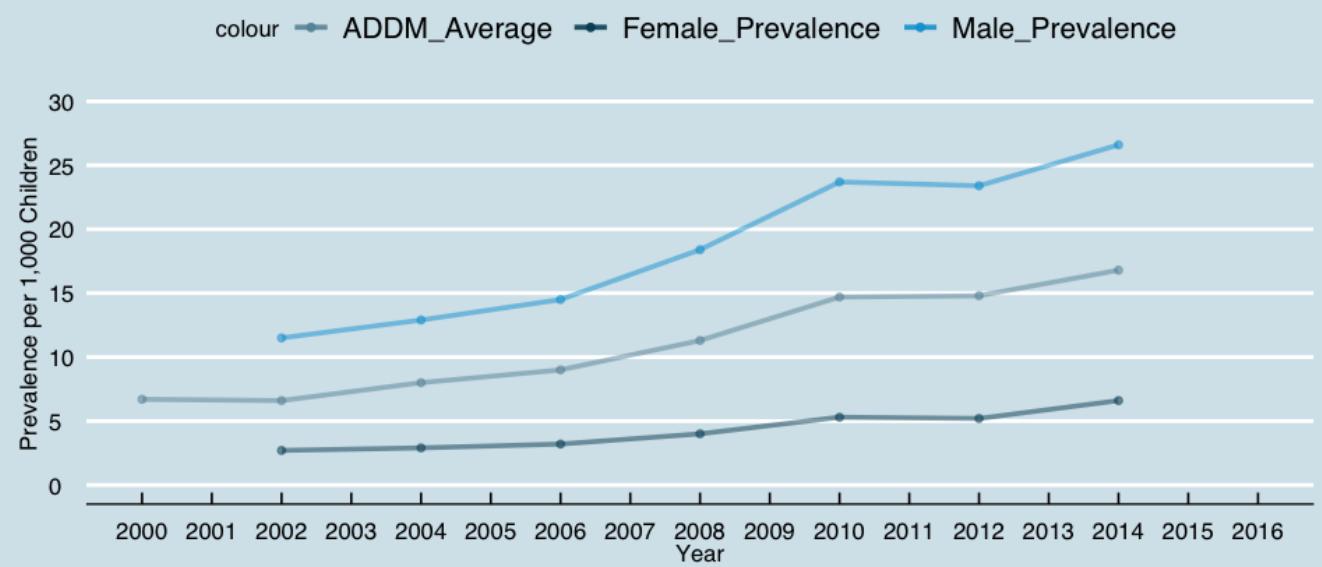
```
In [1116]: # Apply theme
p + theme_economist() + scale_colour_economist() # p + theme_wsj() + scale_colour
```

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.

Warning message:

"Removed 1 rows containing missing values (geom\_path)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."Warning message:  
"Removed 1 rows containing missing values (geom\_path)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."

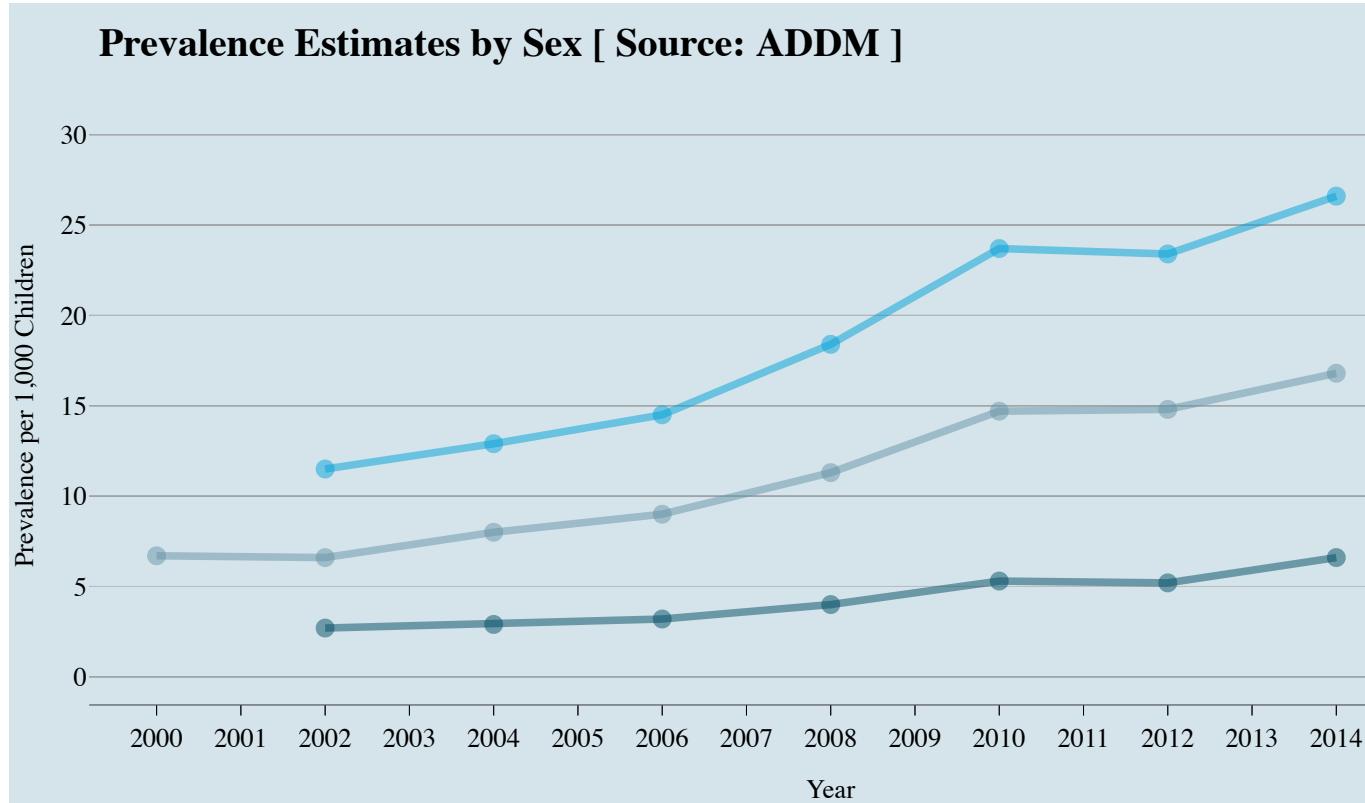
### Prevalence Estimates by Sex [ Source: ADDM ]



```
In [1117]: # Dynamic chart:
```

```
p_dynamic <- p + theme_economist() + scale_colour_economist()  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.



### Quiz:

Add 95% Confidence Interval to above plot (Use ggplot)

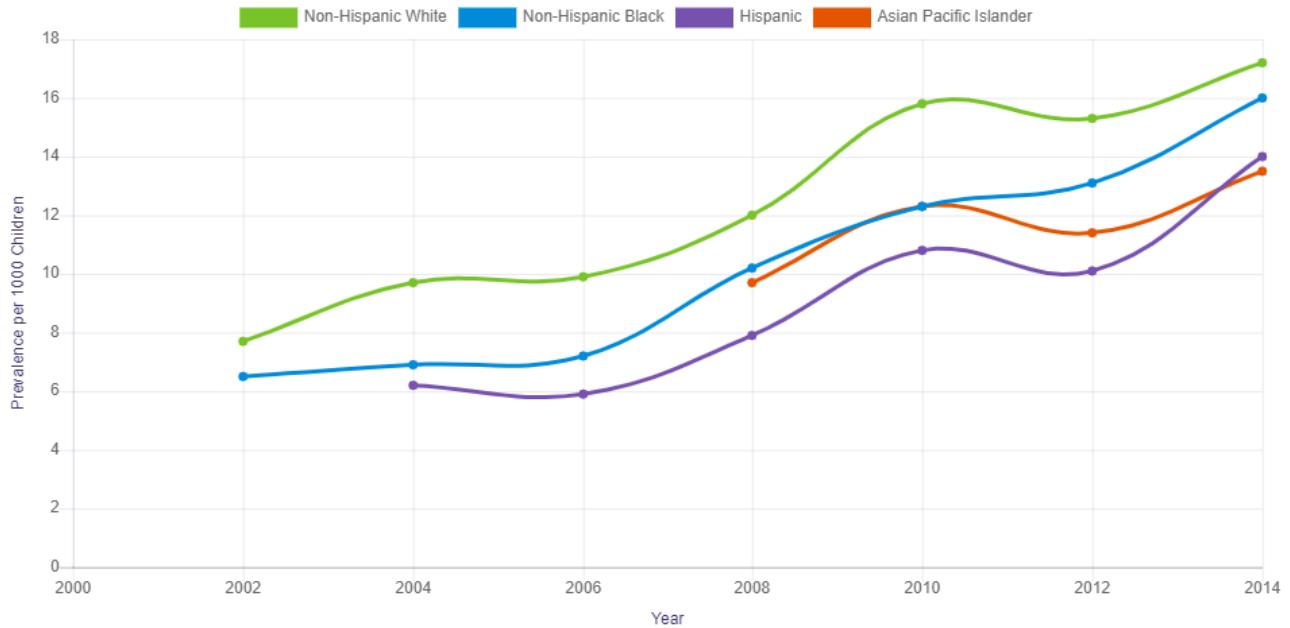
```
In [1118]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

**Data Visualisation (Enhanced) - [ CDC ] REPORTED PREVALENCE VARIES BY RACE AND ETHNICITY**

### Prevalence Estimates by Race/Ethnicity

Show ADDM prevalence estimates\* by race/ethnicity for: U.S. or Total† ▾



Note: Click the icons and racial/ethnic groups above the chart to hide or unhide data. Hover your mouse over data points to show prevalence by year.

\*ADDM data do not represent the entire state, only a selection of sites within the state.

†ADDM estimate = the total for all sites combined.

## Data Visualisation (Enhanced) - [ R ] REPORTED PREVALENCE VARIES BY RACE AND ETHNICITY [ Source: ADDM ] With Average

```
In [1119]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

In [1120]:

```
# -----
# [addm] < Prevalence Varies by Race and Ethnicity >
# -----  
  
# Color:  
# 'ADDM_Average' "darkslategrey"  
# 'Asian_Pacific_Islander' "darkred"  
# 'Hispanic' "darkorchid3"  
# 'Non_Hispanic_Black' "deepskyblue3"  
# 'Non_Hispanic_White' "chartreuse3"  
  
p <- ggplot(ASD_National_ADDM, aes(x = Year, y = Prevalence)) +  
  geom_line(aes(y = Prevalence, colour = 'ADDM_Average'),  
            linetype = "dotted", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Prevalence, color = 'ADDM_Average'),  
             size=2,  
             shape=20,  
             alpha=0) +  
  # Add line for Asian.or.Pacific.Islander.Prevalence  
  geom_line(aes(y = Asian.or.Pacific.Islander.Prevalence, colour = 'Asian_Pacific'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Asian.or.Pacific.Islander.Prevalence, colour = 'Asian_Pacific'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  # Add line for Hispanic.Prevalence  
  geom_line(aes(y = Hispanic.Prevalence, colour = 'Hispanic'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Hispanic.Prevalence, colour = 'Hispanic'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  # Add line for Non.hispanic.black.Prevalence  
  geom_line(aes(y = Non.hispanic.black.Prevalence, colour = 'Non_Hispanic_Black'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Non.hispanic.black.Prevalence, colour = 'Non_Hispanic_Black'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  # Add line for Non.hispanic.white.Prevalence  
  geom_line(aes(y = Non.hispanic.white.Prevalence, colour = 'Non_Hispanic_White'),  
            linetype = "solid", # http://sape.inf.usi.ch/quick-reference/ggplot2  
            size=1,  
            alpha=0.5) +  
  geom_point(aes(y = Non.hispanic.white.Prevalence, colour = 'Non_Hispanic_White'),  
             size=2,  
             shape=20,  
             alpha=0.5) +  
  scale_colour_manual(name="",  
                     labels = c("ADDM Average",  
                               "Asian/Pacific Islander",  
                               "Hispanic",  
                               "Non-Hispanic Black",  
                               "Non-Hispanic White"),
```

```

values = c(ADDM_Average="darkslategrey",
          Asian_Pacific_Islander ="darkred",
          Hispanic ="darkorchid3",
          Non_Hispanic_Black ="deepskyblue3",
          Non_Hispanic_White ="chartreuse3"))

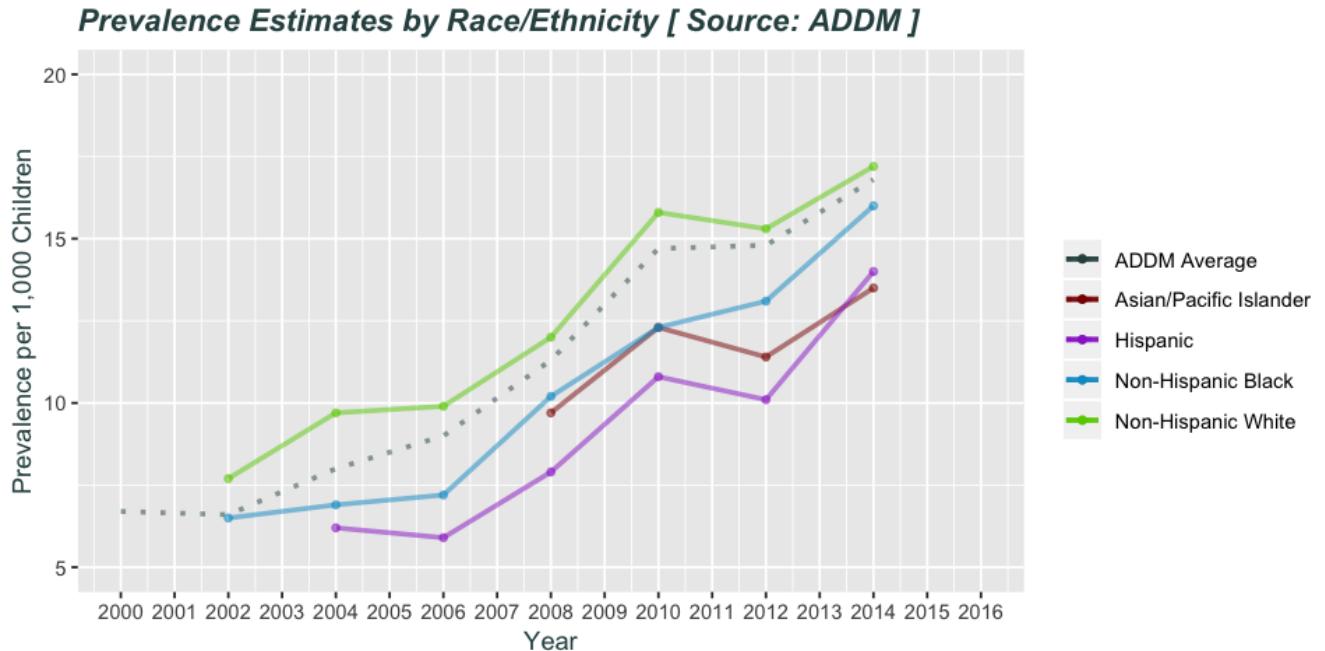
# Add title, axis label, and axis scale
p <- p + scale_y_continuous(name = "Prevalence per 1,000 Children",
                             breaks = seq(5, 20, 5),
                             limits=c(5, 20)) +
  scale_x_continuous(name = "Year",
                     breaks = seq(2000, 2016, 1),
                     limits = c(2000, 2016)) +
  ggtitle("Prevalence Estimates by Race/Ethnicity [ Source: ADDM ]") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey"))

# Show plot
p

```

Warning message:

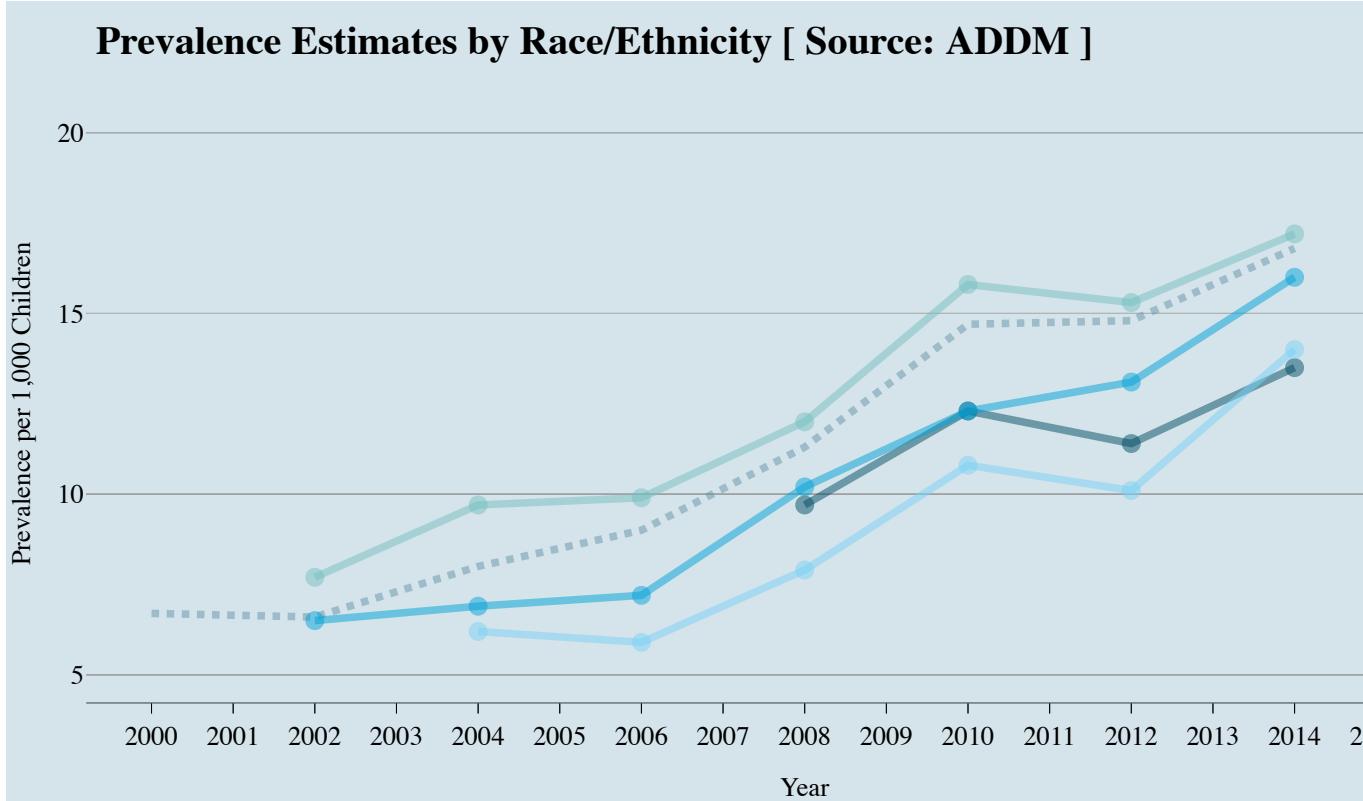
"Removed 4 rows containing missing values (geom\_path)."Warning message:  
"Removed 4 rows containing missing values (geom\_point)."Warning message:  
"Removed 2 rows containing missing values (geom\_path)."Warning message:  
"Removed 2 rows containing missing values (geom\_point)."Warning message:  
"Removed 1 rows containing missing values (geom\_path)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."Warning message:  
"Removed 1 rows containing missing values (geom\_path)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."Warning message:  
"Removed 1 rows containing missing values (geom\_point)."



```
In [1121]: # Apply theme
# p + theme_economist() + scale_colour_economist() # p + theme_wsj() + scale_col
```

```
In [1122]: # Dynamic chart:  
p_dynamic <- p + theme_economist() + scale_colour_economist()  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.



### Quiz:

Change above zig-zag lines to spline/smooth lines.

Hints: Refer to [ADDM Network estimates](#) for overall ASD prevalence in US over time.

```
In [1123]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

0

```
In [1124]: # -----
# Dataset: US. State Level Children ASD Prevalence
# -----  
  
ASD_State      <- read.csv("../dataset/ADV_ASD_State.csv", stringsAsFactors = FALSE)  
  
# Obtain number of rows and number of columns/features/variables  
dim(ASD_State)  
# Obtain overview (data structure/types)  
str(ASD_State)
```

1692 48

## Data Visualisation (Enhanced) - US. State Level Data Pre-Process data

### Pre-Process data: Missing data

```
In [1125]: # Count missing values in dataframe:  
sum(is.na(ASD_State)) # No missing data recognised by R (NA)  
# Define several offending strings  
na_strings <- c("", "No data", "NA", "N A", "N / A", "N/A", "N/ A", "Not Available")  
# Replace these defined missing values to R's internal NA  
ASD_State = replace_with_na_all(ASD_State, condition = -.x %in% na_strings)  
# Count missing values in dataframe:  
sum(is.na(ASD_State))
```

14454

28992

### Remove invalid unicode char/string: \x92

```
In [1126]: # Remove invalid unicode char/string: \x92  
ASD_State$Source_Full1[ASD_State$Source_Full1 == "National Survey of Children\x92]
```

Delete/Drop variable by index: column from 14 to 26, 29, and 30

```
In [1127]: cbind(names(ASD State), c(1:length(names(ASD State))))
```

|              |       |    |
|--------------|-------|----|
|              | State | 1  |
| Denominator  |       | 2  |
| Prevalence   |       | 3  |
| Lower.Cl     |       | 4  |
| Upper.Cl     |       | 5  |
| Year         |       | 6  |
| Source       |       | 7  |
| Source_Full1 |       | 8  |
| State_Full1  |       | 9  |
| State_Full2  |       | 10 |
| erator_ASD   |       | 11 |
| or_NonASD    |       | 12 |
| Proportion   |       | 13 |

```
In [1128]: # Delete/Drop variable by index: column from 14 to 26, 29, and 30  
# names(ASD_State)  
ASD State <- ASD State[ -c(14:26, 29, 30) ]
```

## Create new variables

```
In [1129]: # Create one new variable: Source_UC as uppercase of Source  
ASD_State$Source_UC <- toupper(ASD_State$Source)  
# Create one new variable: Source_Full3 by combining Source_UC and Source_Full1  
ASD_State$Source_Full3 <- paste(ASD_State$Source_UC, ASD_State$Source_Full1)
```

## Convert to correct data types

```
In [1130]: str(ASD.State)
```

```
Classes 'tbl_df', 'tbl' and 'data.frame':       1692 obs. of  35 variables:
 $ State                      : chr  "AZ" "GA" "MD" "NJ" ...
 $ Denominator                : int  45322 43593 21532 29714 24535 230
65 35472 45113 36472 11020 ...
 $ Prevalence                  : num  6.5 6.5 5.5 9.9 6.3 4.5 3.3 6.2
6.9 5.9 ...
 $ Lower.CI                    : num  5.8 5.8 4.6 8.9 5.4 3.7 2.7 5.5
6.1 4.6 ...
 $ Upper.CI                    : num  7.3 7.3 6.6 11.1 7.4 5.5 3.9 7 7.
8 7.5 ...
 $ Year                        : int  2000 2000 2000 2000 2000 2000 200
2 2002 2002 2002 ...
 $ Source                      : chr  "addm" "addm" "addm" "addm" ...
 $ Source_Full1                : chr  "Autism & Developmental Disabilit
ies Monitoring Network" "Autism & Developmental Disabilities Monitoring Networ
k" "Autism & Developmental Disabilities Monitoring Network" "Autism & Developme
ntal Disabilities Monitoring Network" ...
 $ State_Full1                 : chr  "Arizona" "Georgia" "Maryland" "N
ew Jersey" ...
```

```
In [1131]: # cbind(names(ASD.State), c(1:length(names(ASD.State))))
```

## Convert variables to numeric

```
In [1132]: # Convert Prevalence and CIs from categorical/chr to numeric
ix <- 13:33 # define an index
ASD_State[ix] <- lapply(ASD_State[ix], as.numeric)
```

## Convert variables to categorical/factor

```
In [1133]: # Convert Source from categorical/chr to categorical/factor
ix <- c(1, 7, 8, 9, 10, 34, 35) # define an index
ASD_State[ix] <- lapply(ASD_State[ix], as.factor)

# Create new ordered factor Year_Factor from Year
ASD_State$Year_Factor <- factor(ASD_State$Year, ordered = TRUE)
```

```
In [1134]: # Display unique values (levels) of a factor categorical
lapply(select_if(ASD_State, is.factor), levels)
```

### \$State

```
'AK'  'AL'  'AR'  'AZ'  'CA'  'CO'  'CT'  'DC'  'DE'  'FL'  'GA'  'HI'  'IA'  'ID'  'IL'  'IN'  'KS'
'KY'  'LA'  'MA'  'MD'  'ME'  'MI'  'MN'  'MO'  'MS'  'MT'  'NC'  'ND'  'NE'  'NH'  'NJ'  'NM'
'NV'  'NY'  'OH'  'OK'  'OR'  'PA'  'RI'  'SC'  'SD'  'TN'  'TX'  'UT'  'VA'  'VT'  'WA'  'WI'
'WV'  'WY'
```

### \$Source

```
'addm'  'medi'  'nsch'  'sped'
```

### \$Source\_Full1

```
'Autism & Developmental Disabilities Monitoring Network'  'Medicaid'
'National Survey of Children\'s Health'  'Special Education Child Count'
```

### \$State\_Full1

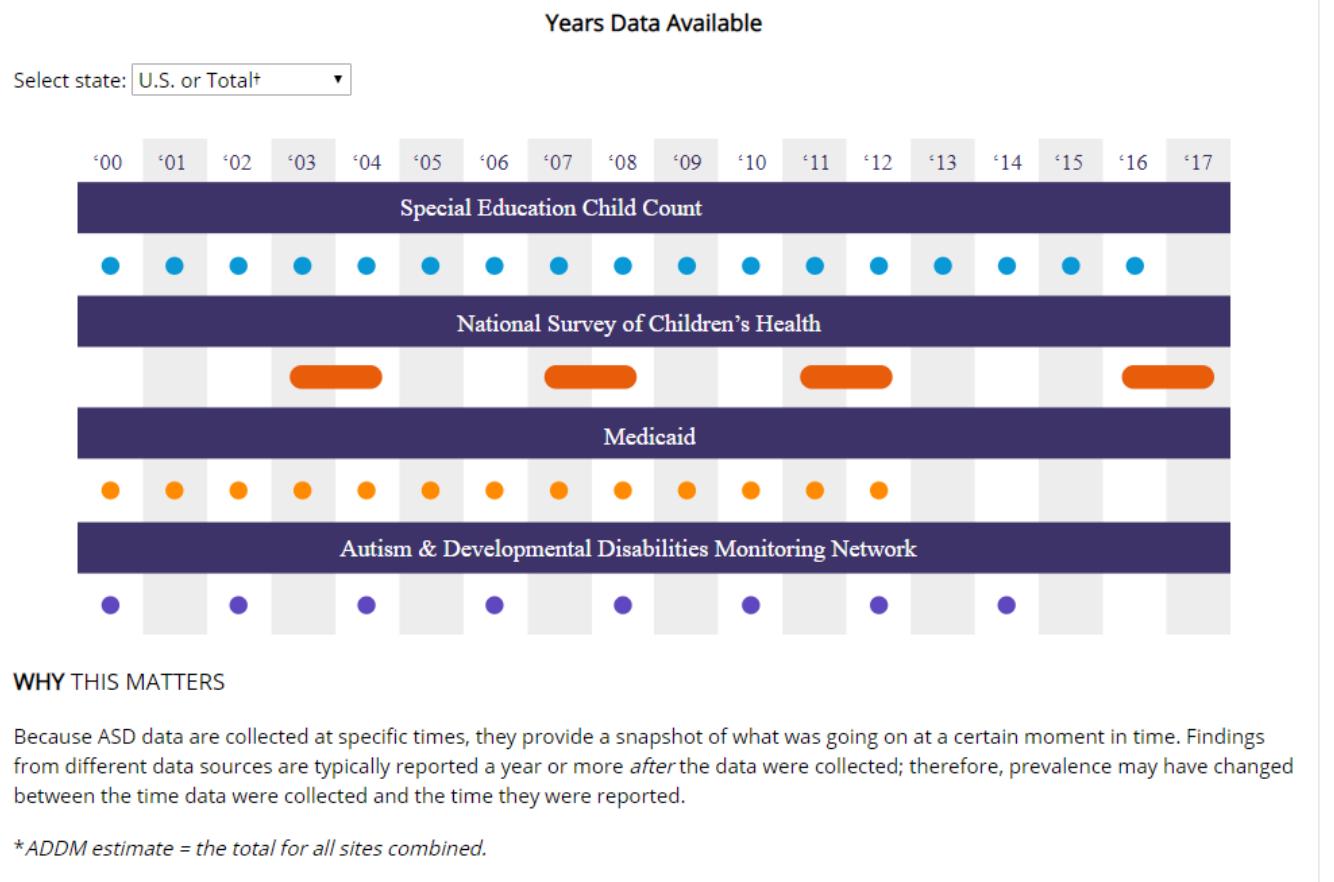
```
'Alabama'  'Alaska'  'Arizona'  'Arkansas'  'California'  'Colorado'  'Connecticut'  'Delaware'
'District of Columbia'  'Florida'  'Georgia'  'Hawaii'  'Idaho'  'Illinois'  'Indiana'  'Iowa'  'Kansas'
'Kentucky'  'Louisiana'  'Maine'  'Maryland'  'Massachusetts'  'Michigan'  'Minnesota'  'Mississippi'
'Missouri'  'Montana'  'Nebraska'  'Nevada'  'New Hampshire'  'New Jersey'  'New Mexico'
```

**Optionally, export the processed dataframe data to CSV file.**

```
In [1135]: write.csv(ASD_State, file = "../dataset/ADV_ASD_State_R.csv", row.names = FALSE)
```

```
In [1136]: # Read back in above saved file:
# ASD_State <- read.csv("../dataset/ADV_ASD_State_R.csv")
# ASD_State$Year_Factor <- factor(ASD_State$Year_Factor, ordered = TRUE) # Conver
```

## Data Visualisation (Enhanced) - US. State Level Data Visualisation



Above chart shows at data source level, we'd also like to know State level data availability. How?

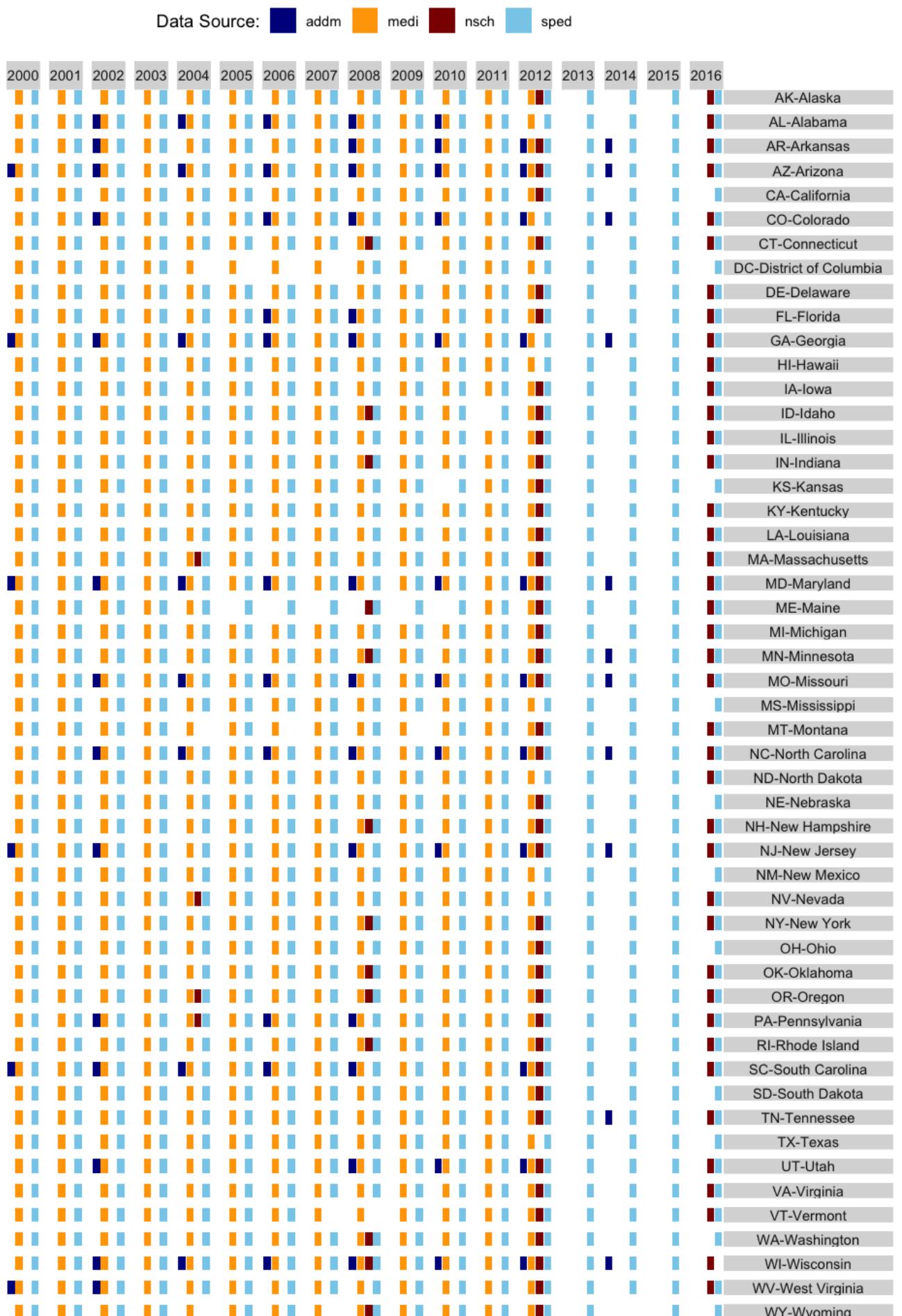
Data Visualisation (Enhanced) - [ R ] Explore the Data [ Years Data Available by State ]

```
In [1137]: # Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=12)
```

```
In [1138]: # -----
# [State] < Years Data Available by State >
# -----
p <- ggplot(ASD_State, aes(x = Source, fill = Source)) +
  geom_bar() + theme(axis.text.x=element_blank(), # Hide axis
                     axis.ticks.x=element_blank(), # Hide axis
                     axis.text.y=element_blank(), # Hide axis
                     axis.ticks.y=element_blank(), # Hide axis
                     panel.background = element_blank(), # Remove panel background
                     legend.position="top",
                     strip.text.y = element_text(angle=0) # Rotate text to horizontal
  ) +
  scale_fill_manual("Data Source:", values = c("addm" = "darkblue",
                                              "medi" = "orange",
                                              "nsch" = "darkred",
                                              "sped" = "skyblue")) +
  facet_grid(facets = State_Full2 ~ Year) +
  labs(x="", y="", title="Years Data Available by State") # layers of graphics
```

```
In [1139]: # Below plot may run for a while  
# Show plot  
p
```

## Years Data Available by State



Filter and create dataframe of different data sources, for easy data access

```
In [1140]: # Filter and create dataframe of different data sources, for easy data access
ASD_State_ADDM <- subset(ASD_State, Source == 'addm')
ASD_State_MEDI <- subset(ASD_State, Source == 'medi')
ASD_State_NSCH <- subset(ASD_State, Source == 'nsch')
ASD_State_SPED <- subset(ASD_State, Source == 'sped')
```

## Data Visualisation (Enhanced) - [ R ] Explore the Data Years Data Available by State [ Source: ADDM ]

```
In [1141]: # Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=6)
```

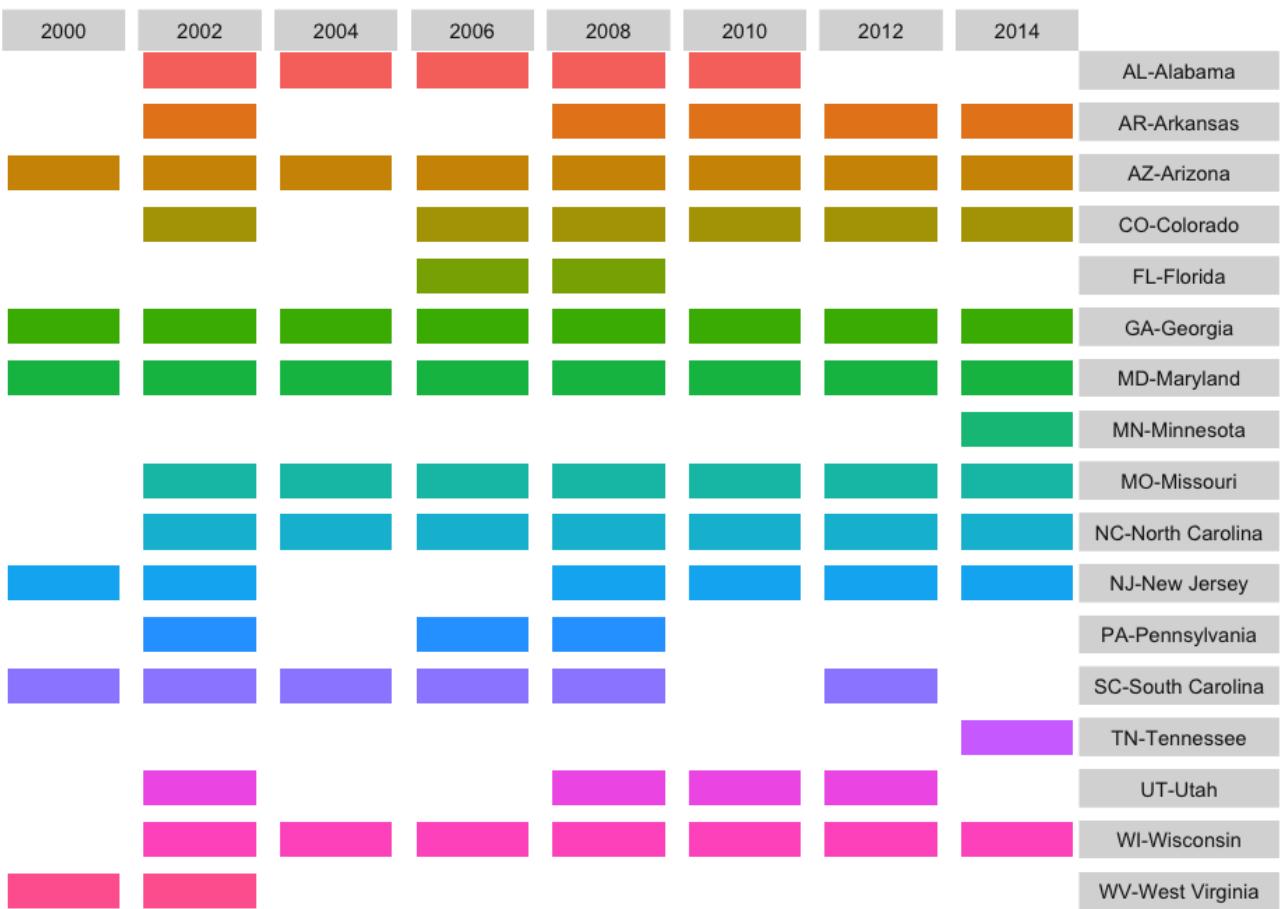
### Years Data Available by State [ Source: ADDM ]

```
In [1142]: # Years Data Available by State [ Source: ADDM ]
p <- ggplot(ASD_State_ADDM, aes(x = 1, fill = State_Full2)) +
  geom_bar() + theme(axis.text.x=element_blank(), # Hide axis
                      axis.ticks.x=element_blank(), # Hide axis
                      axis.text.y=element_blank(), # Hide axis
                      axis.ticks.y=element_blank(), # Hide axis
                      panel.background = element_blank(), # Remove panel background
                      legend.position="none",
                      strip.text.y = element_text(angle=0) # Rotate text to horizontal
  ) +
  facet_grid(facets = State_Full2 ~ Year_Factor) +
  labs(x="", y="", title="Years Data Available by State [ Source: ADDM ]") # layout
```

```
In [1143]: # Show plot
```

p

### Years Data Available by State [ Source: ADDM ]



## Quiz:

Create Years Data Available by State [ Source: XXXX ] for other three data sources:

```
In [1144]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

## Data Visualisation (Enhanced) - [ R ] REPORTED PREVALENCE VARIES BY GEOGRAPHIC LOCATION (States) Prevalence Estimates by State [ Source: ADDM ]

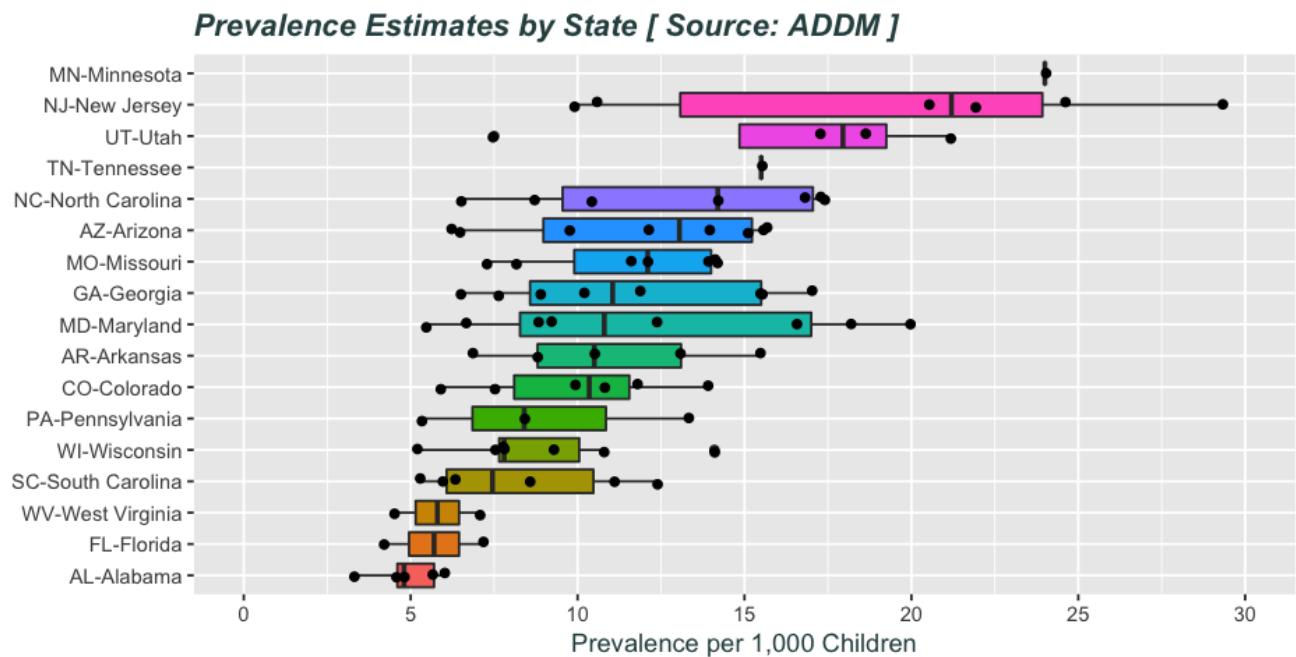
```
In [1145]: # Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

Visualise: Prevalence Estimates by State [ Source: ADDM ]

```
In [1146]: # Prevalence Estimates by State [ Source: ADDM ] , aggregated for different years
p <- ggplot(ASD_State_ADDM, aes(x = reorder(State_Full2, Prevalence, FUN = median,
                                             y = Prevalence)) +
  geom_boxplot(aes(fill = reorder(State_Full2, Prevalence, FUN = median))) + # fill
  scale_fill_discrete(guide = guide_legend(title = "US. States")) + # Legend Name
  # geom_boxplot(fill = 'darkslategrey', alpha = 0.2) +
  scale_y_continuous(name = "Prevalence per 1,000 Children",
                     breaks = seq(0, 30, 5),
                     limits=c(0, 30)) +
  scale_x_discrete(name = "") +
  ggtitle("Prevalence Estimates by State [ Source: ADDM ]") +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
        axis.title = element_text(face = 'plain', color = "darkslategrey"),
        legend.position = 'none') +
  coord_flip() + # Rotate chart
  geom_jitter(position=position_jitter(0.1)) # Add actual data points
```

```
In [1147]: # Show plot
```

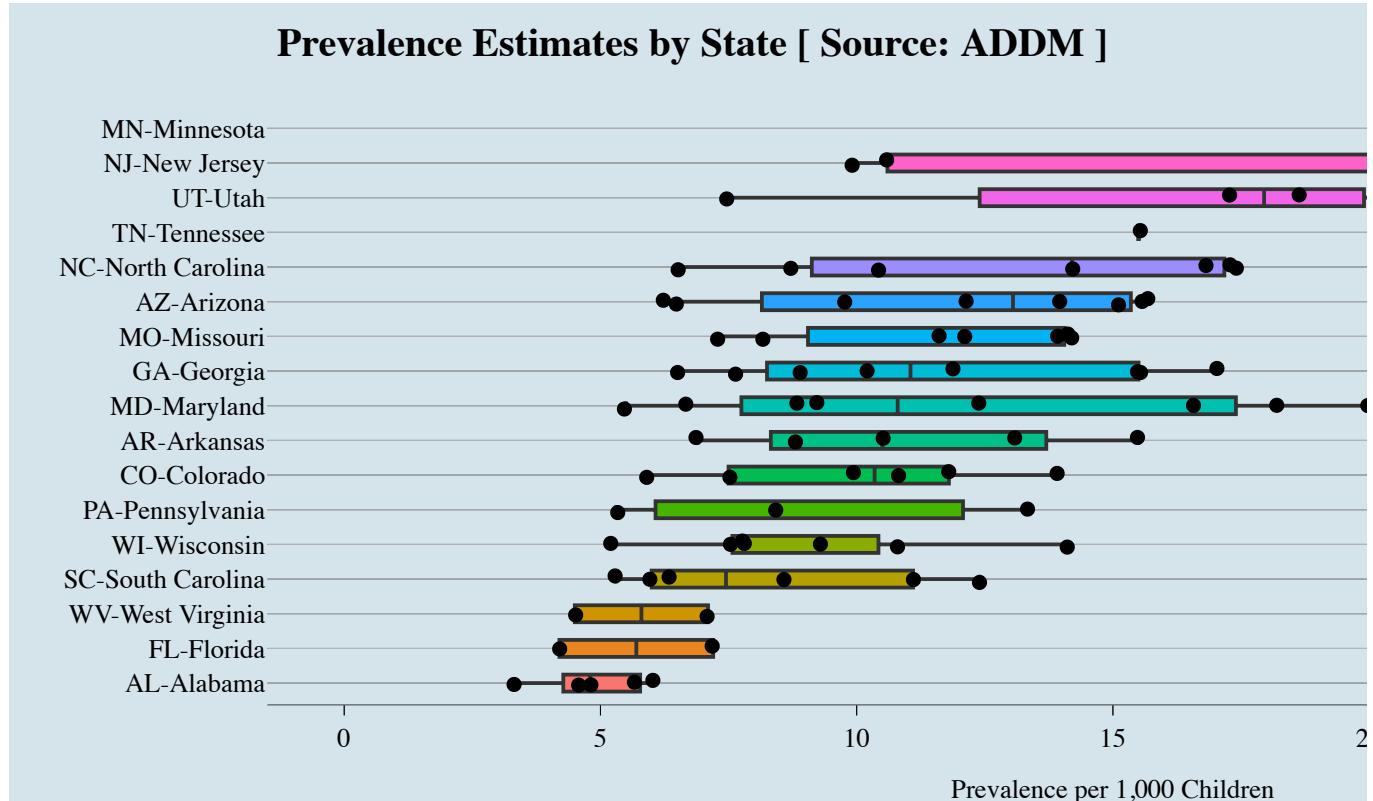
```
p
```



```
In [1148]: # Theme of the economist magazine:
```

```
# p + theme_economist() + scale_colour_economist() + theme(legend.position = 'non
```

```
In [1149]: # Dynamic chart  
p_dynamic <- p + theme_economist() + scale_colour_economist() + theme(legend.position="none")  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```



### Quiz:

Create Prevalence Estimates by State [ Source: XXXX ] for other three data sources:

```
In [1150]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

### Data Visualisation (Enhanced) - [ R ] US. State Level No. Children Surveyed by State [ Source: ADDM ] [Year 2014]

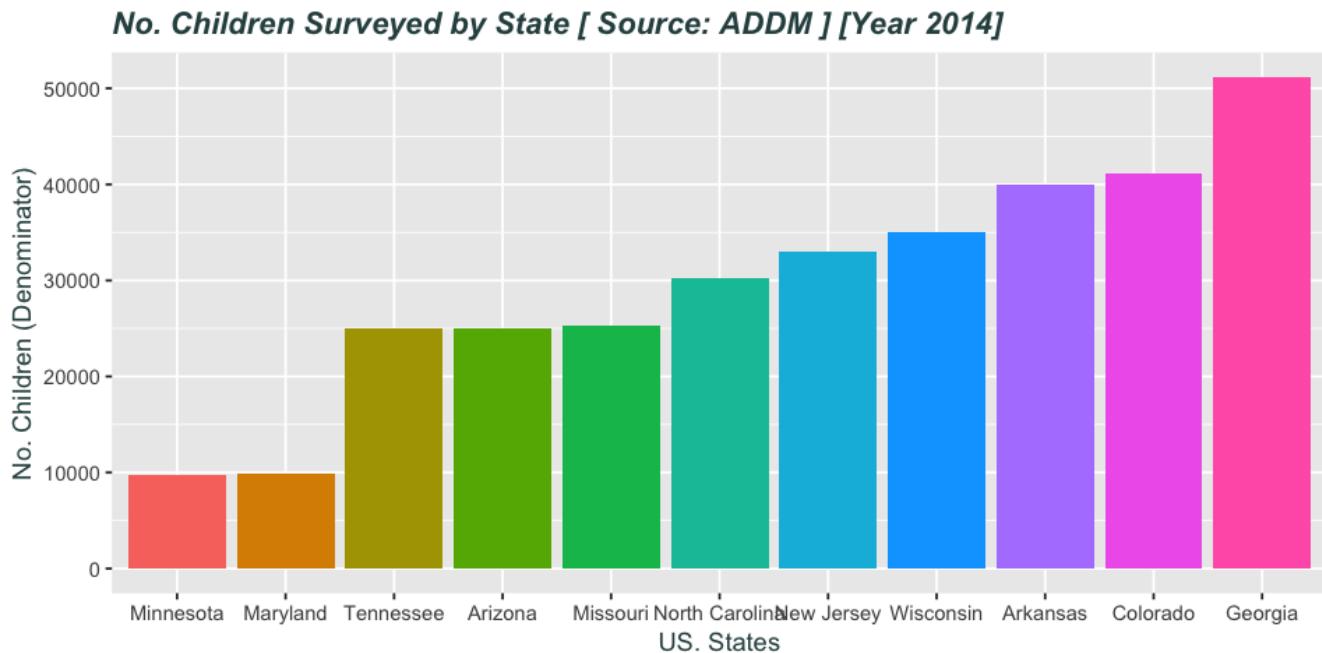
```
In [1151]: # Adjust in-line plot size to M x N  
options(repr.plot.width=8, repr.plot.height=4)
```

Visualise: No. Children Surveyed by State [ Source: ADDM ] [Year 2014]

```
In [1152]: # All State Prevalence data with: Source == 'addm' & Year == 2014
# filter using dataframe: ASD_State_ADDM
ASD_State_Subset <- subset(ASD_State_ADDM, Year == 2014)
# or filer using dataframe: ASD_State
ASD_State_Subset <- subset(ASD_State, Source == 'addm' & Year == 2014)
```

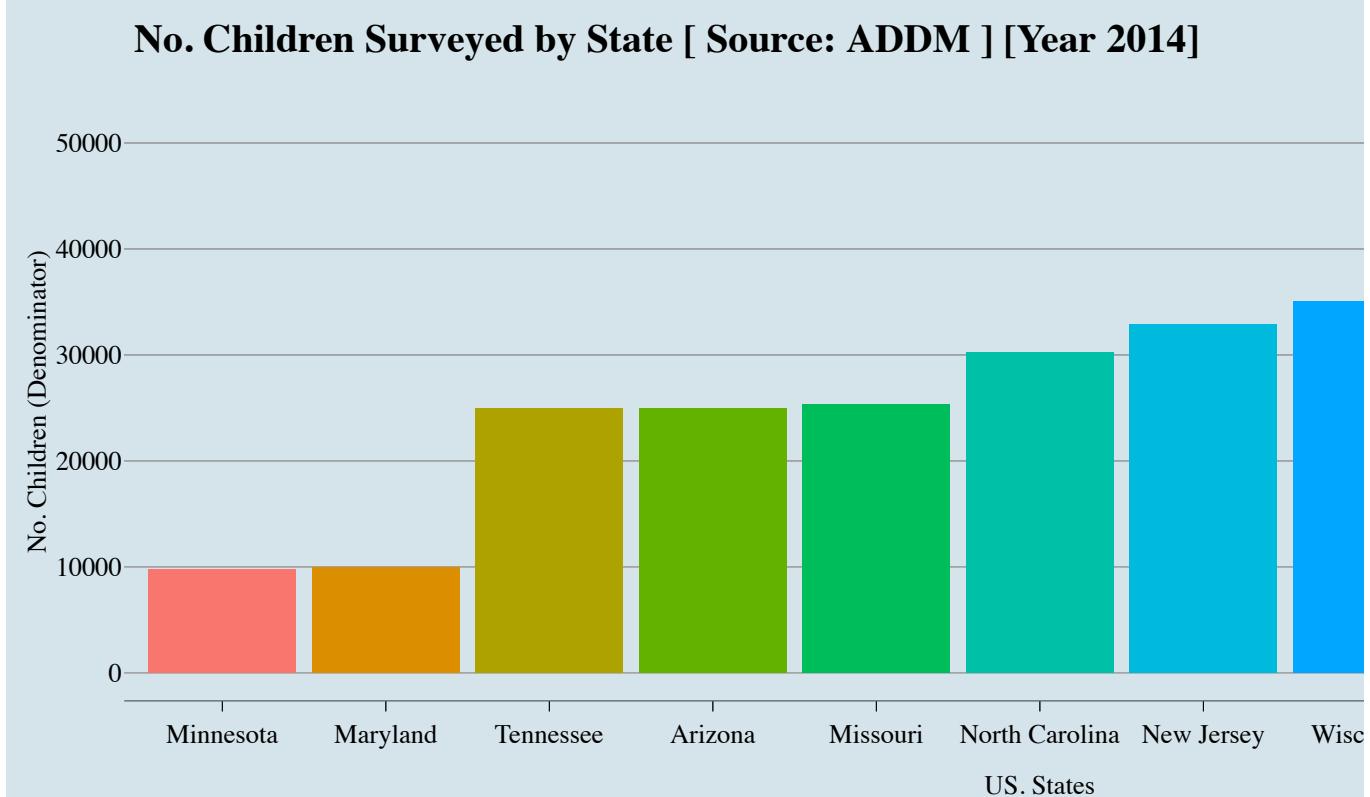
```
In [1153]: # Bar plot/chart for < No. Children surveyed by State [ADDM] [Year 2014] >
p <- ggplot(ASD_State_Subset, aes(x = reorder(State_Full1, Denominator, FUN = median),
y = Denominator)) +
  geom_bar(stat="identity", aes(fill = reorder(State_Full1, Denominator, FUN = median)),
  scale_fill_discrete(guide = guide_legend(title = "US. States")) + # Legend Name
  scale_x_discrete(name = "US. States") +
  scale_y_continuous(name = "No. Children (Denominator)") +
  ggtitle("No. Children Surveyed by State [ Source: ADDM ] [Year 2014]") +
  # geom_text(aes(label=Denominator), vjust=1.6, color="darkslategrey", size=3.5) +
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),
  axis.title = element_text(face = 'plain', color = "darkslategrey"),
  legend.position="none")
```

```
In [1154]: # Show plot
p
```



```
In [1155]: # Theme of the economist magazine:
# p + theme_economist() + scale_colour_economist() + theme(legend.position = 'none')
```

```
In [1156]: # Dynamic chart  
p_dynamic <- p + theme_economist() + scale_colour_economist() + theme(legend.position = "none")  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```



### Quiz:

Create No. Children Surveyed by State [ Source: XXXX ] [Year CCYY] for other data sources & years:

```
In [1157]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

### Quiz:

Create No. ASD Children by State [ Source: XXXX ] [Year CCYY] for other data sources & years:

Hint: Use variable: ASD\_State\_ADDM\$Numerator\_ASD

```
In [1158]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

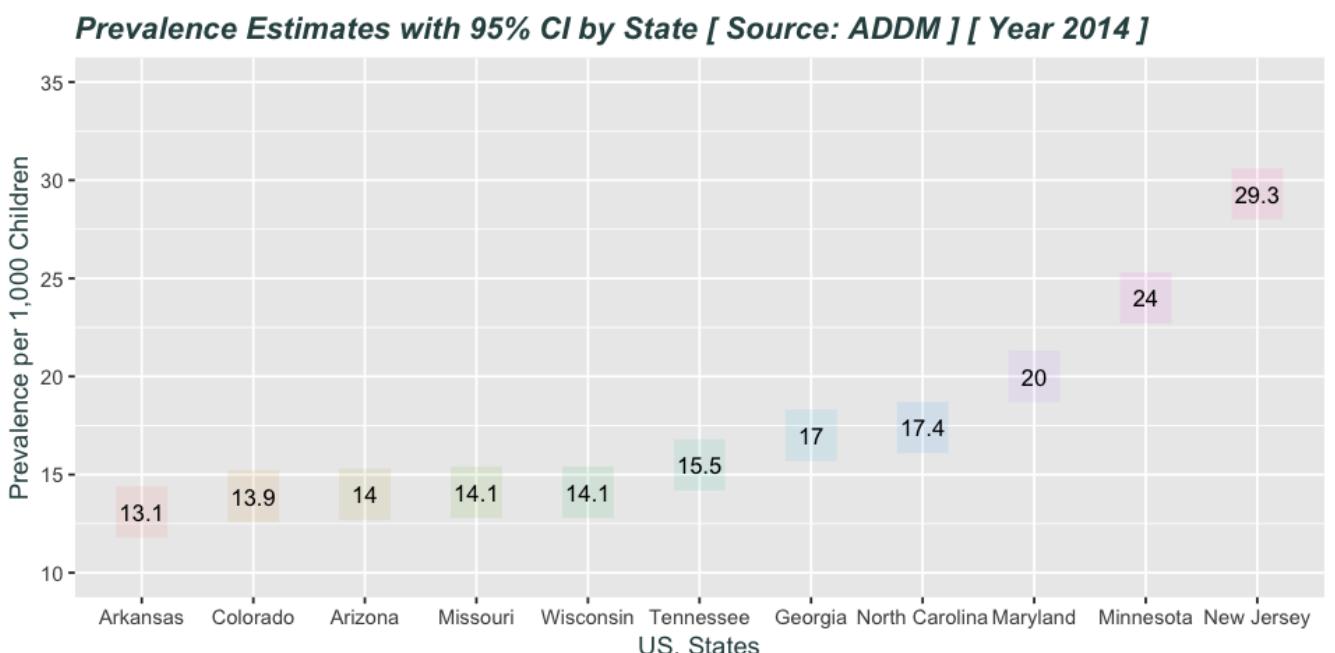
## Data Visualisation (Enhanced) - [ R ] US. State Level Prevalence Estimates with 95% CI by State [ Source: ADDM ] [ Year 2014 ]

```
In [1159]: # Adjust in-line plot size to M x N  
# options(repr.plot.width=8, repr.plot.height=4)
```

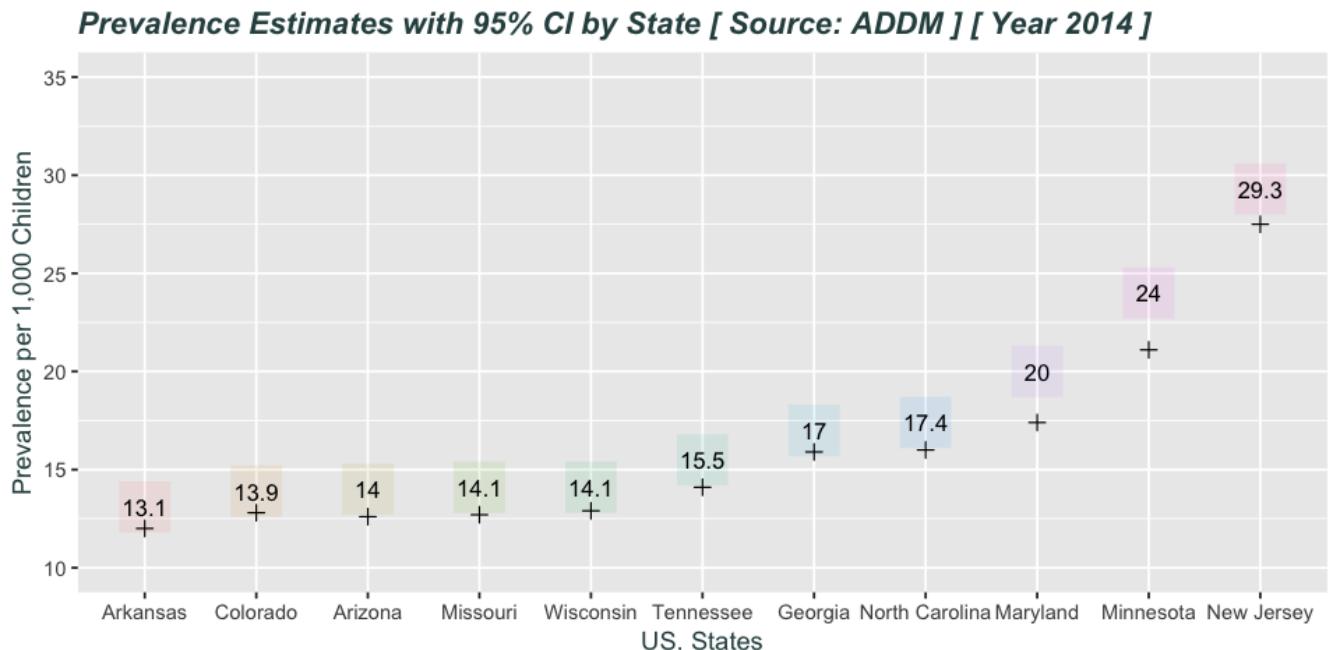
Visualise: Prevalence Estimates with 95% CI by State [ Source: ADDM ] [ Year 2014 ]

```
In [1160]: # ASD_State_Subset <- subset(ASD_State_ADDM, Year == 2014)  
# or  
# ASD_State_Subset <- subset(ASD_State, Source == 'addm' & Year == 2014)  
  
# Point plot/chart  
p = ggplot(ASD_State_Subset, aes(x = reorder(State_Full1, Prevalence, median),  
                                  y = Prevalence)) +  
  geom_point(stat="identity", aes(colour = reorder(State_Full1, Prevalence, median)),  
             scale_colour_discrete(guide = guide_legend(title = "US. States")) + # Legend Na  
             scale_y_continuous(name = "Prevalence per 1,000 Children",  
                                breaks = seq(10, 35, 5),  
                                limits=c(10, 35)) +  
             scale_x_discrete(name = "US. States") +  
  ggtitle("Prevalence Estimates with 95% CI by State [ Source: ADDM ] [ Year 2014 ]")  
  theme(title = element_text(face = 'bold.italic', color = "darkslategrey"),  
        axis.title = element_text(face = 'plain', color = "darkslategrey"),  
        legend.position = 'none') +  
  geom_text(aes(label=Prevalence), hjust=0.5, color="black", size=3.5) # Show da
```

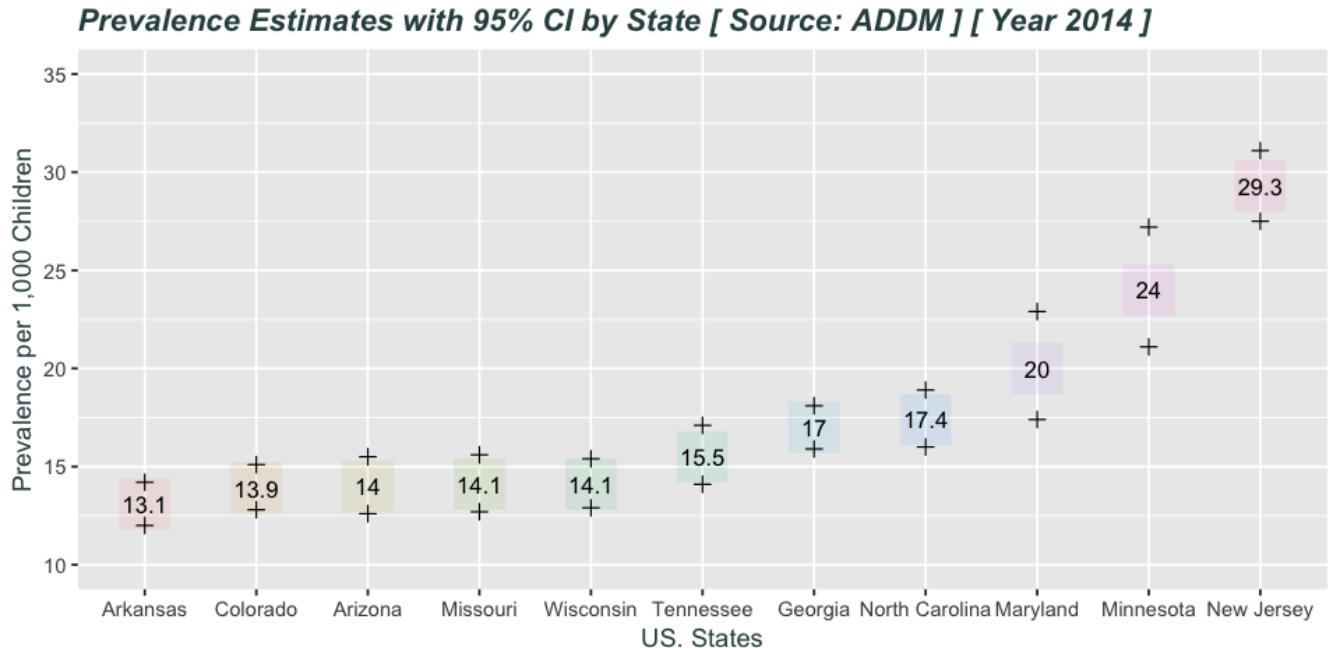
```
In [1161]: # Show plot  
p
```



```
In [1162]: # Add Lower.CI
p = p + geom_point(data = ASD_State_Subset, aes(x = reorder(State_Full1, Prevalence),
                                                shape=Source # point shape
), size = 2 # point size
) +
  # geom_text(aes(label=Lower.CI), hjust=-0.1, vjust=3, color="darkslategrey",
  # scale_shape_manual(values=3) # manual define point shape
# Show plot
p
```



```
In [1163]: # Add Upper.CI
p = p + geom_point(data = ASD_State_Subset, aes(x = reorder(State_Full1, Prevalence),
                                                shape=Source # point shape
), size = 2 # point size
)
# geom_text(aes(label=Upper.CI), hjust=-0.1, vjust=-3, color="darkslategrey", size=3)
# Show plot
p
```

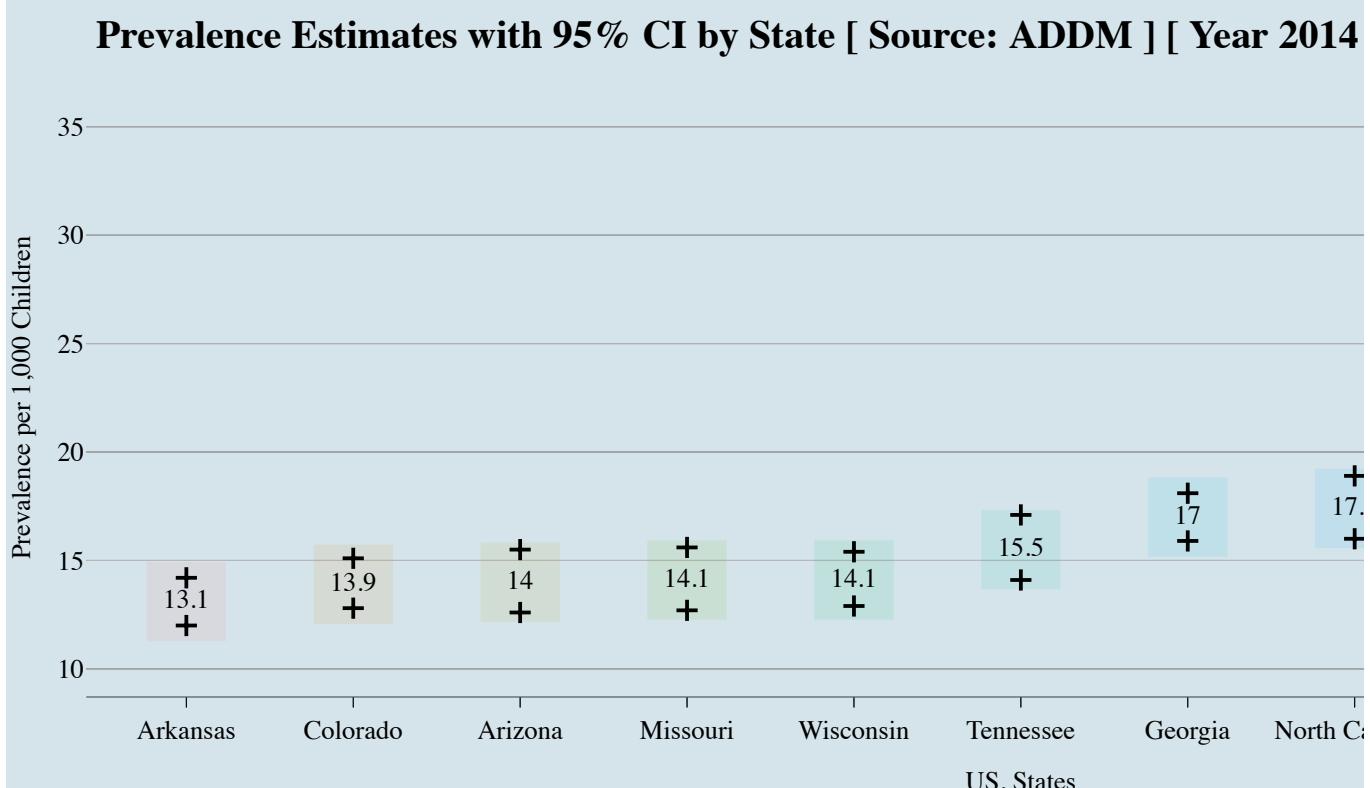


```
In [1164]: # theme of the economist magazine:
# p + theme_economist() + scale_colour_economist() + scale_colour_discrete(guide="none")
```

```
In [1165]: # Dynamic chart  
p_dynamic <- p + theme_economist() + scale_colour_economist() + scale_colour_disc  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.



### Quiz:

Create Prevalence Estimates with 95% CI by State [ Source: ADDM ] [Year CCYY] for other data sources & years:

```
In [1166]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

### Data Visualisation (Enhanced) - [ R ] US. State Level Prevalence Estimates over Year [ Source: ADDM ] [ State: AZ-Arizona ]

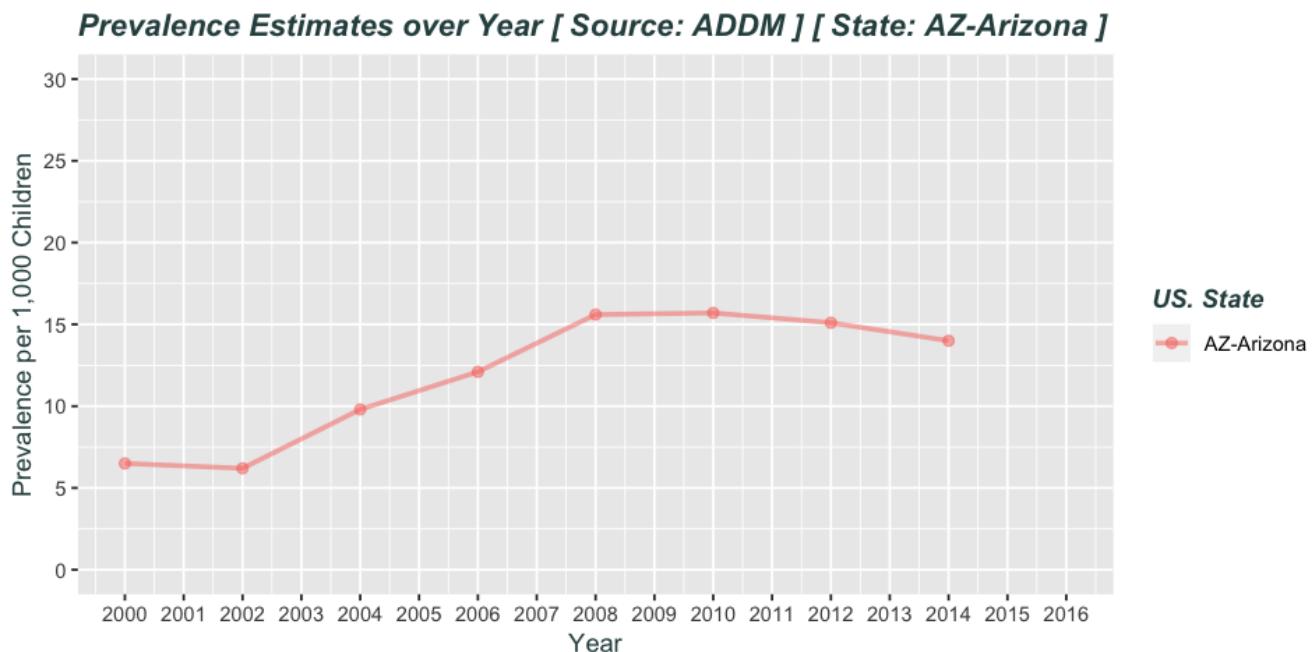
```
In [1167]: # Adjust in-line plot size to M x N  
# options(repr.plot.width=8, repr.plot.height=4)
```

Visualise: Prevalence Estimates over Year [ Source: ADDM ] [ State: AZ-Arizona ]

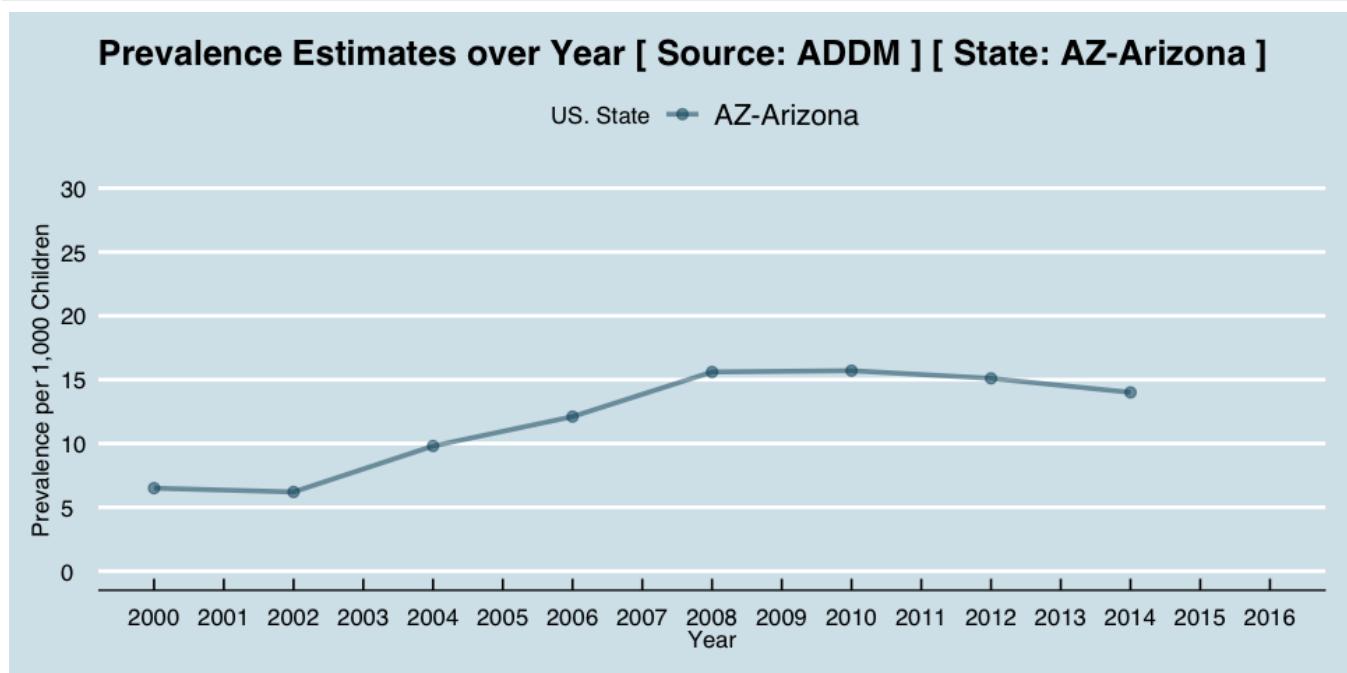
```
In [1168]: # All year/time Prevalence data with: Source_UC == 'ADDM' & State_Full2 == 'AZ-Ar
ASD_State_Subset <- subset(ASD_State, Source_UC == 'ADDM' & State_Full2 == 'AZ-Ar

# Line plot/chart for < State ASD Prevalence [ADDM] [AZ-Arizona] >
p <- ggplot(ASD_State_Subset, aes(x = Year, y = Prevalence))
# Select (add) line chart type:
p <- p + geom_line(aes(color = State_Full2),
                     linetype = "solid", # http://sape.inf.usi.ch/quick-reference/
                     size=1,
                     alpha=0.5)
# Select (add) points to chart:
p <- p + geom_point(aes(color = State_Full2),
                     size=3,
                     shape=20,
                     alpha=0.5)
# Customize legend name:
p <- p + labs(color = "US. State")
# Adjust x and y axis, scale, limit and labels:
p <- p + scale_y_continuous(name = "Prevalence per 1,000 Children",
                             breaks = seq(0, 30, 5),
                             limits=c(0, 30)) +
  scale_x_continuous(name = "Year",
                     breaks = seq(2000, 2016, 1),
                     limits = c(2000, 2016))
# Customize chart title:
p <- p + ggtitle("Prevalence Estimates over Year [ Source: ADDM ] [ State: AZ-Ari
# Customize chart title and axis labels:
p <- p + theme(title = element_text(face = 'bold.italic', color = "darkslategrey"
                                         axis.title = element_text(face = 'plain', color = "darkslategrey")
```

```
In [1169]: # Show plot
p
```



```
In [1170]: # Theme of the economist magazine:  
p + theme_economist() + scale_colour_economist()
```

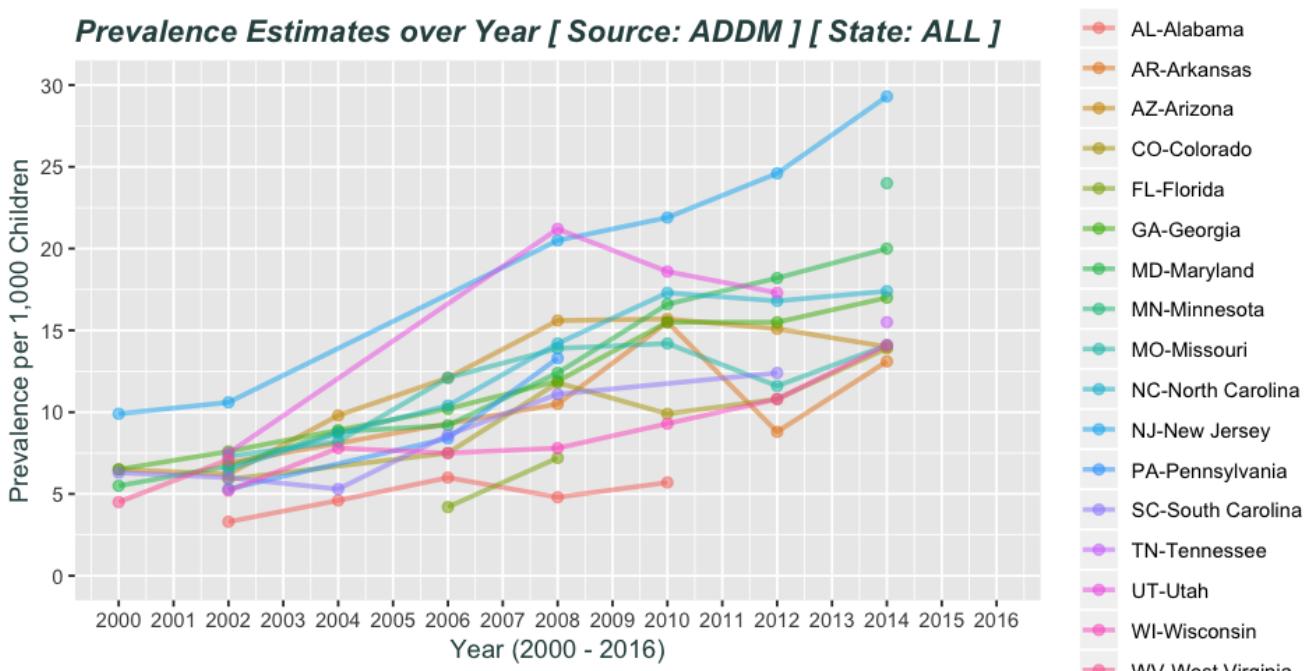


### Data Visualisation (Enhanced) - [ R ] US. State Level Prevalence Estimates over Year [ Source: ADDM ] [ State: ALL ]

```
In [1171]: # Adjust in-line plot size to M x N  
# options(repr.plot.width=8, repr.plot.height=4)
```

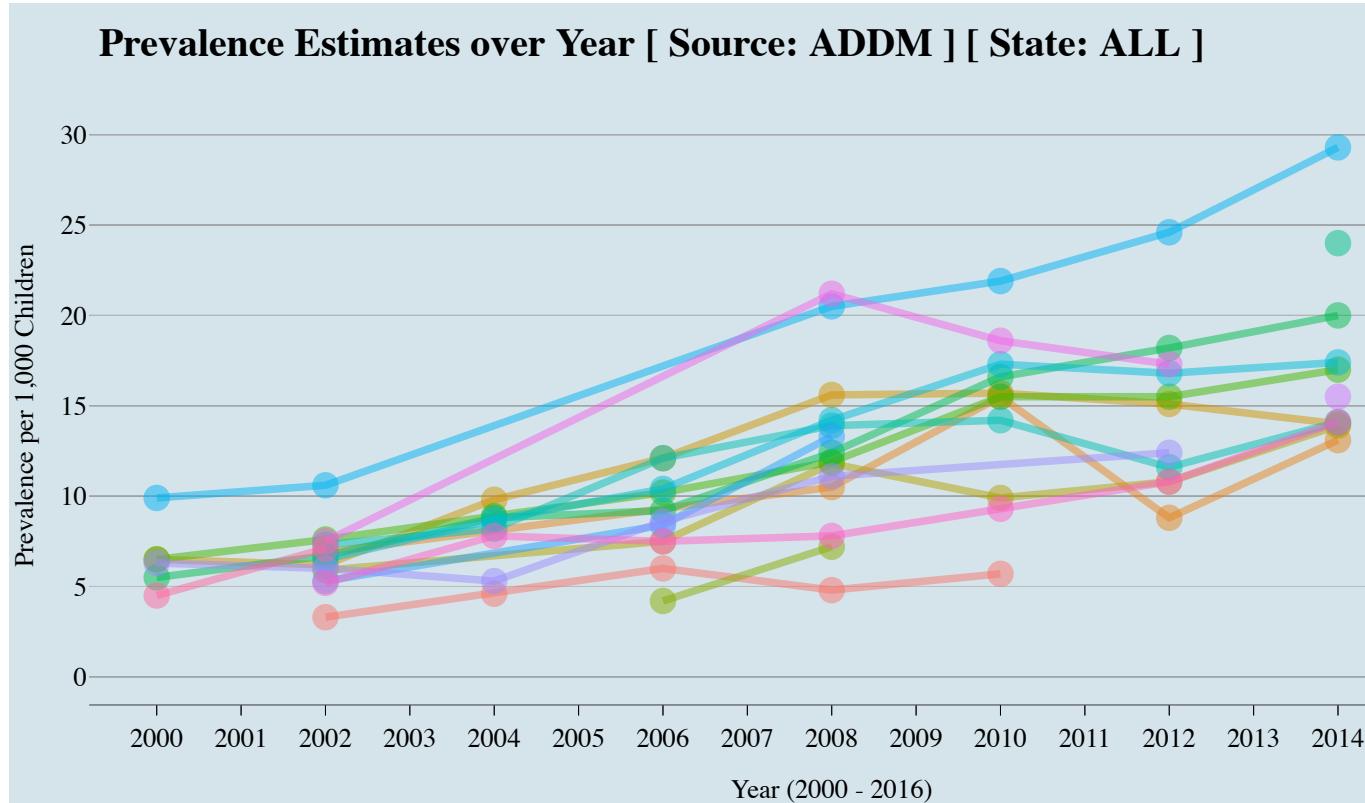
Visualise: Prevalence Estimates over Year [ Source: ADDM ] [ State: ALL ]

```
In [1173]: # Show plot
```



```
In [1174]: # Dynamic chart
p_dynamic <- p + theme_economist() + scale_colour_economist() + scale_colour_disc
p_dynamic <- ggplotly(p_dynamic)
p_dynamic
```

Scale for 'colour' is already present. Adding another scale for 'colour', which will replace the existing scale.

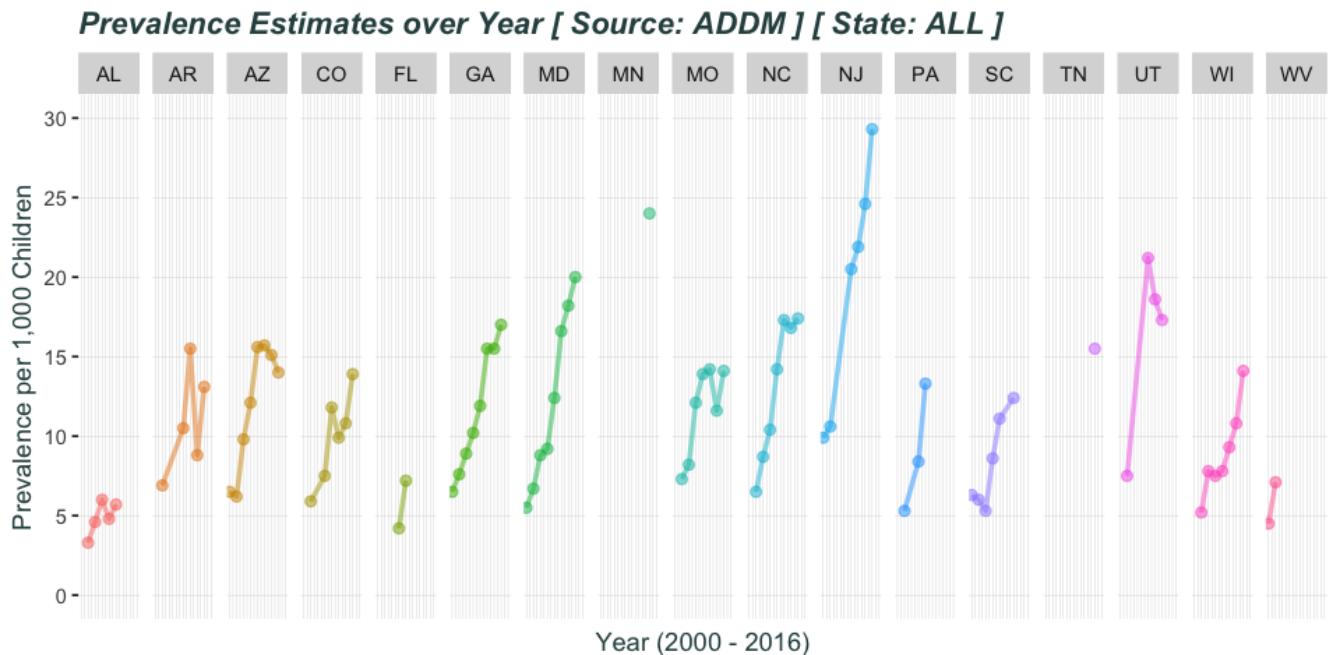


Split chart by state

```
In [1175]: # Show plot in facet_grid
p + facet_grid(facets = . ~ State) +
  theme(legend.position = "none", # Hide legend
        axis.text.x=element_blank(), # Hide axis
        axis.ticks.x=element_blank(), # Hide axis
        panel.background = element_blank(), # Remove panel background
        panel.grid.major = element_line(size = 0.1, linetype = 1, colour = "lightgrey")
)
```

geom\_path: Each group consists of only one observation. Do you need to adjust the group aesthetic?

geom\_path: Each group consists of only one observation. Do you need to adjust the group aesthetic?



## Data Visualisation (Enhanced) - Plotting on Map

```
In [1176]: # -----
# EDA - Visualisation on map
# -----
if(!require(usmap)){install.packages("usmap")}
library(usmap) # usmap: Mapping the US
```

## Data Visualisation (Enhanced) - Plotting on Map [ CDC ] REPORTED PREVALENCE VARIES BY GEOGRAPHIC LOCATION

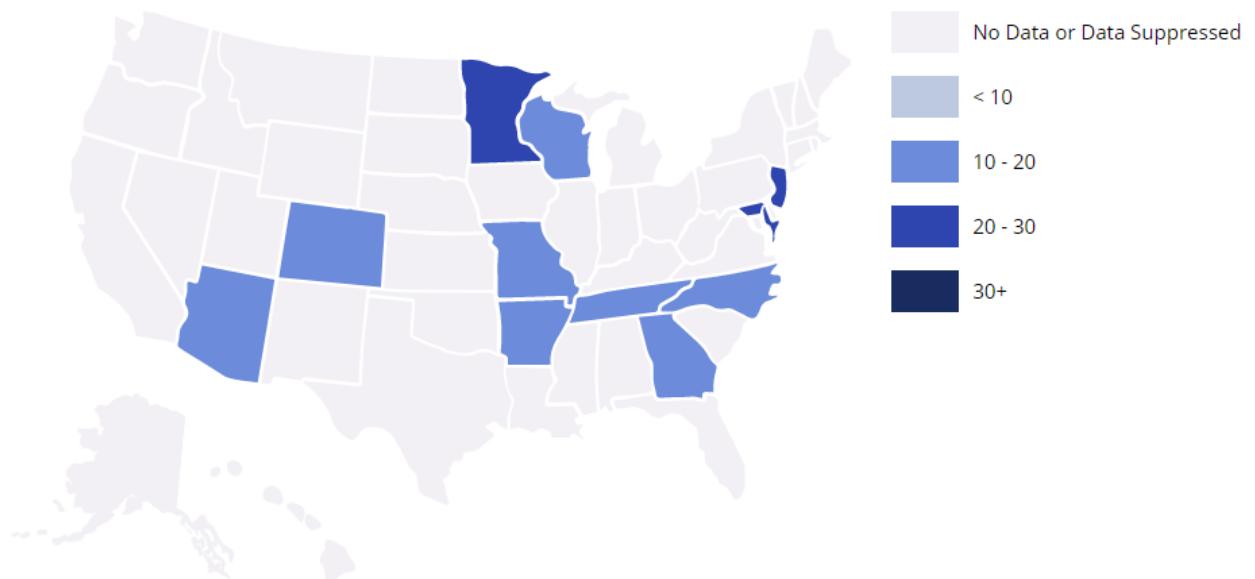
### Prevalence Estimates by Geographic Area

Using data set: ADDM Network\*

Show prevalence for: 2014 ▾

Prevalence by State

Prevalence per 1,000 Children:



\*ADDM data do not represent the entire state, only a selection of sites within the state.

†If NSCH 2016 data are selected, combined 2016-2017 estimates are shown.

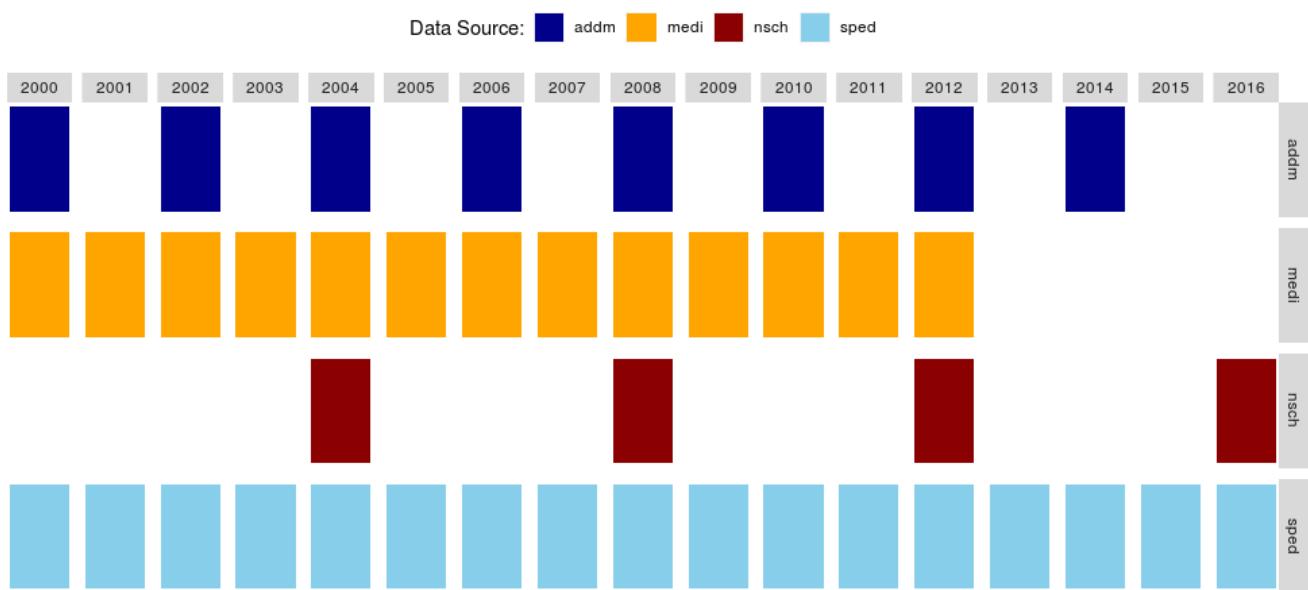
††For NSCH data, data are suppressed when the width of the confidence interval exceeds 1.2 times the point estimate. This is the same approach that is recommended by NSCH [here](#) and our point estimates (and suppressed data points) match those on childhealthdata.org for 2016-2017.

## Data Visualisation (Enhanced) - Plotting on Map [ R ] REPORTED PREVALENCE VARIES BY GEOGRAPHIC LOCATION

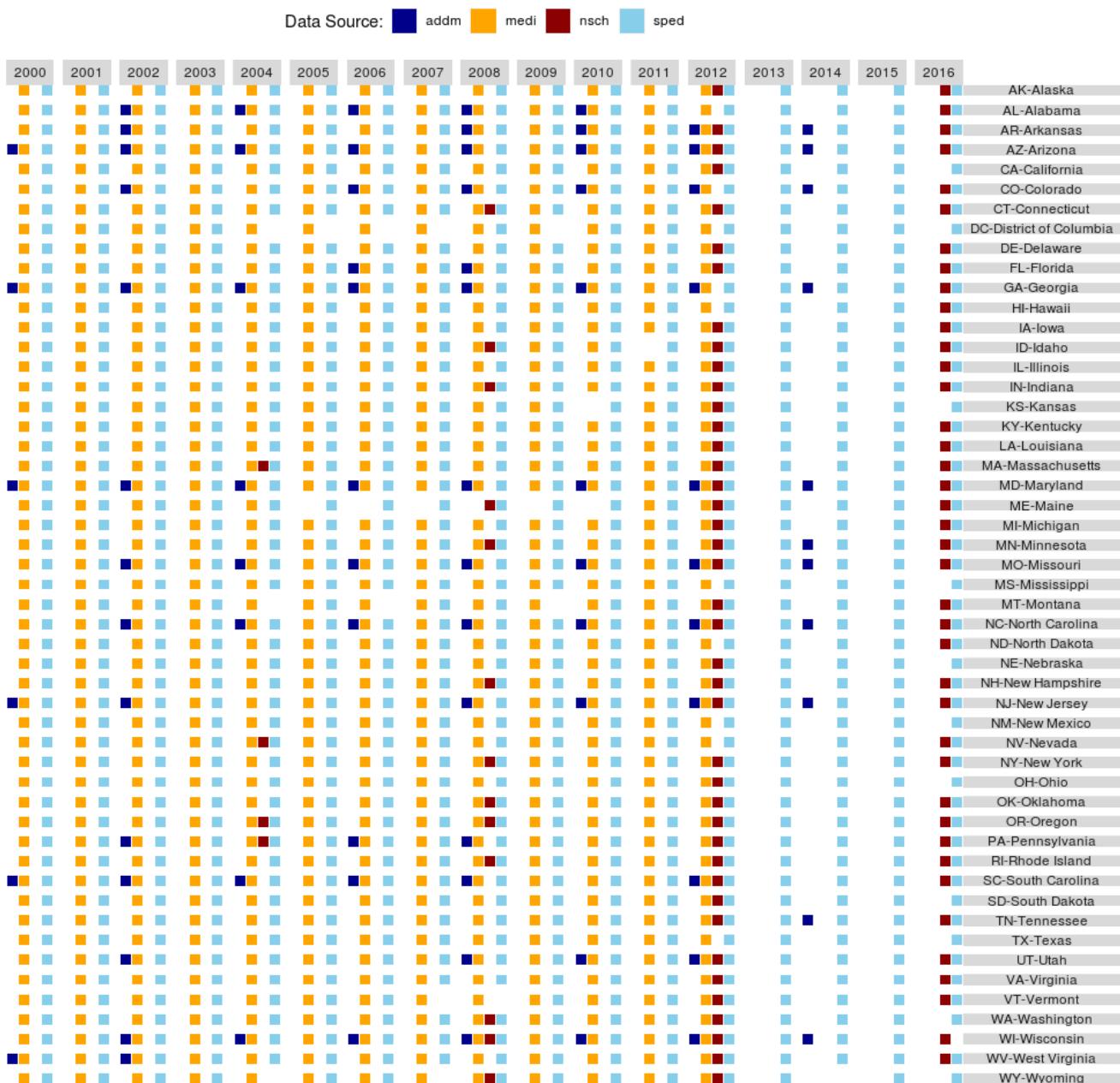
### Let's review data availability by data Sources & Years:

- ASD\_State\_ADDM in Years: 2000, 2002, 2004, 2006, 2008, 2010, 2012, 2014
- ASD\_State\_MEDI in Years: 2000 ~ 2012
- ASD\_State\_NSCH in Years: 2004, 2008, 2012, 2016
- ASD\_State\_SPED in Years: 2000 ~ 2016

### Years Data Available



### Years Data Available by State



## Data Visualisation (Enhanced) - Plotting on Map [ R ] REPORTED PREVALENCE VARIES BY GEOGRAPHIC LOCATION [ Source: ADDM ] [ Year: 2014 ]

```
In [1177]: # Adjust in-line plot size to M x N  
# options(repr.plot.width=8, repr.plot.height=4)
```

**Prepare US State level data:** [ Source: ADDM ] [ Year: 2014 ]

```
In [1178]: # Prepare data - addm 2014  
Map_Data_Source = 'addm' # Available values lowercase: 'addm', 'medi', 'nsch', 's  
Map_Data_Value = 'Prevalence' # variable must be numeric, variable name in 'quota'  
  
# Uncomment below to use Prevalence of different groups:  
# Map_Data_Value = 'Male.Prevalence' # variable must be numeric, variable name in  
# Map_Data_Value = 'Female.Prevalence' # variable must be numeric, variable name  
# Map_Data_Value = 'Asian.or.Pacific.Islander.Prevalence' # variable must be nume  
  
Map_Data_Year = 2014 # must be integer  
ASD_State_Subset = subset(ASD_State, Source == Map_Data_Source & Year == Map_Data_Year)
```

**The usmap package/function requires input data to have a column of state, or fips.** (case sensitive)

- state: Name of US state
- fips: FIPS code for either a US state

<https://cran.r-project.org/web/packages/usmap/vignettes/mapping.html> (<https://cran.r-project.org/web/packages/usmap/vignettes/mapping.html>)

<https://cran.r-project.org/web/packages/usmap/usmap.pdf> (<https://cran.r-project.org/web/packages/usmap/usmap.pdf>).

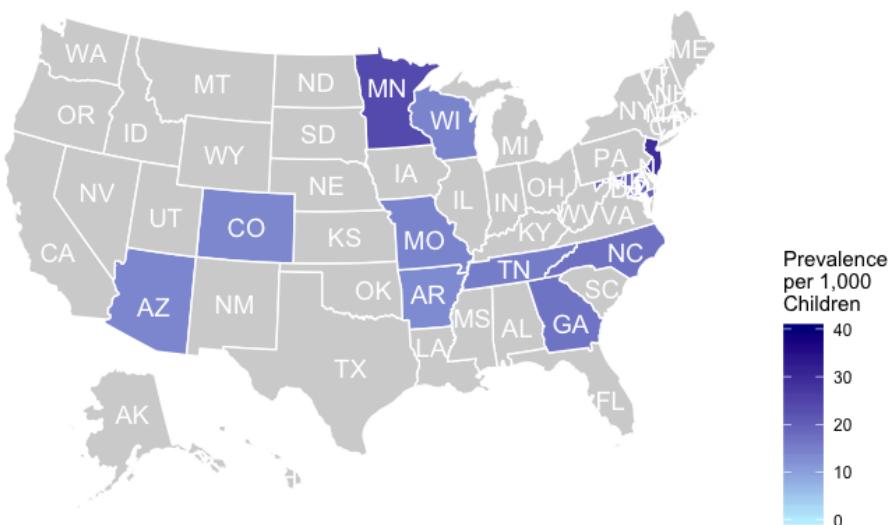
```
In [1179]: # The usmap package/function requires input data to have a column of 'state', or  
ASD_State_Subset$state = ASD_State_Subset$State  
# Glance  
head(ASD_State_Subset)
```

| State | Denominator | Prevalence | Lower.Cl | Upper.Cl | Year | Source | Source_Full1                                           | State_Full1 | State_Full2 | .. |
|-------|-------------|------------|----------|----------|------|--------|--------------------------------------------------------|-------------|-------------|----|
| AZ    | 24952       | 14.0       | 12.6     | 15.5     | 2014 | addm   | Autism & Developmental Disabilities Monitoring Network | Arizona     | AZ-Arizona  | .. |
| AR    | 39992       | 13.1       | 12.0     | 14.2     | 2014 | addm   | Autism & Developmental Disabilities Monitoring Network | Arkansas    | AR-Arkansas | .. |
| CO    | 41128       | 13.9       | 12.8     | 15.1     | 2014 | addm   | Autism & Developmental Disabilities Monitoring Network | Colorado    | CO-Colorado | .. |

Visualise: Prevalence Estimates by Geographic Area [ Source: ADDM ] [ Year: 2014 ]

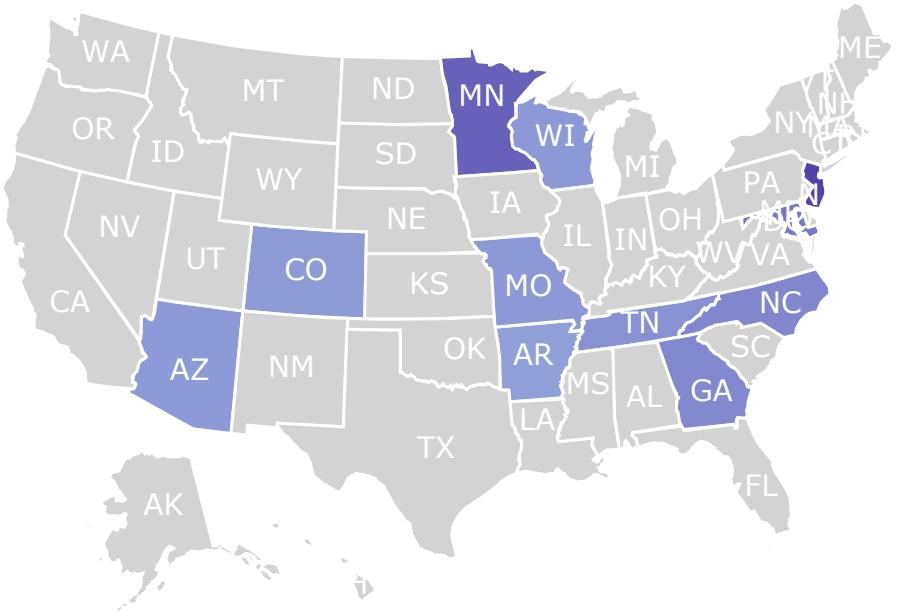
```
In [1180]: # Show data on map
p_map_addm_2014 <- plot_usmap(data = ASD_State_Subset, values = Map_Data_Value,
                                 color = "white", # map line colour
                                 labels = TRUE, # State name shown
                                 label_color = 'white' # State name colour
) +
  scale_fill_continuous(
    na.value = "lightgrey", # Set colour with no State data
    low="lightblue1", high = "darkblue",
    name = "Prevalence\nper 1,000\nChildren",
    limits=c(0, 40) #same colour levels/limits for plots
) +
  labs(title = paste("Prevalence Estimates by Geographic Area", '\n[ Measure :',
                     subtitle = 'https://www.cdc.gov/ncbddd/autism'
) +
  theme(panel.background = element_rect(color = "white", fill = "white"),
        legend.position = "right")
# Show map
p_map_addm_2014
```

Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : addm ] [ Year : 2014 ]  
<https://www.cdc.gov/ncbddd/autism>



```
In [1181]: # Dynamic map  
p_dynamic <- p_map_adm_2014  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```

Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : addm ] [ Year : 2014 ]



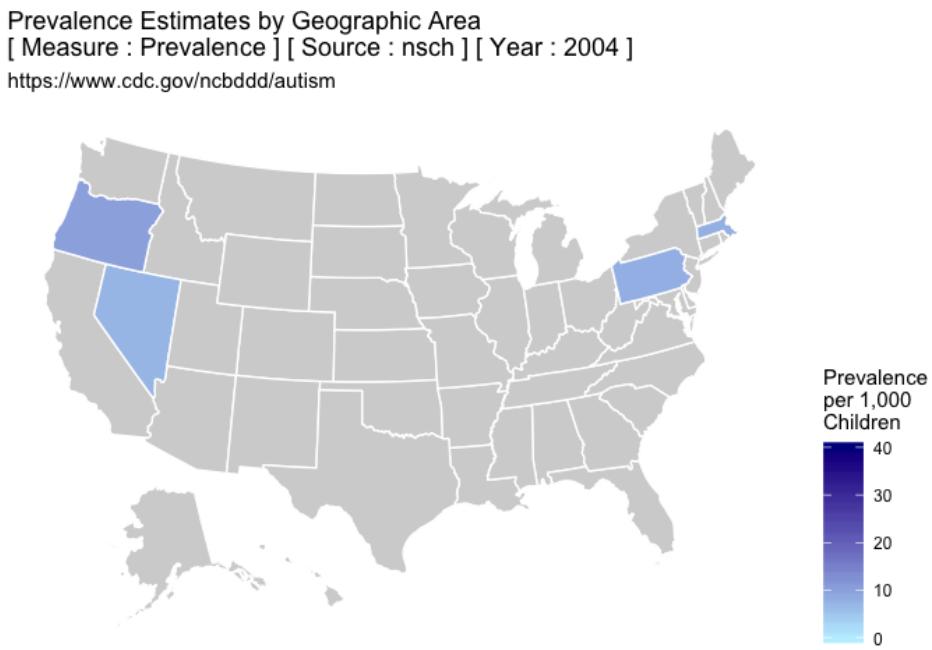
**Data Visualisation (Enhanced) - Plotting on Map [ R ] REPORTED PREVALENCE VARIES BY GEOGRAPHIC LOCATION [ Source: NSCH ] [ Year: 2004, 2008, 2012, 2016 ]**

**Prepare US State level data:** [ Source: NSCH ] [ Year: ALL ]

```
In [1182]: Map_Data_Source = 'nsch' # Available values lowercase: 'addm', 'medi', 'nsch', 's  
Map_Data_Value = 'Prevalence' # variable must be numeric, variable name in 'quota'
```

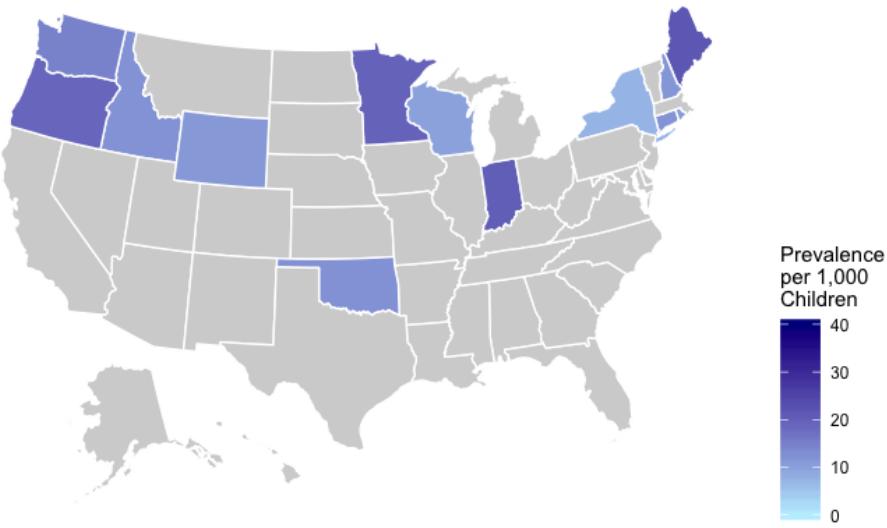
Visualise: **Prevalence Estimates by Geographic Area** [ Source: NSCH ] [ Year: 2004 ]

```
In [1183]: # Prepare data - nsch 2004
Map_Data_Year = 2004 # must be integer
ASD_State_Subset = subset(ASD_State, Source == Map_Data_Source & Year == Map_Data_Year)
ASD_State_Subset$state = ASD_State_Subset$State
# Plot on map
p_map_nsch_2004 <- plot_usmap(data = ASD_State_Subset, values = Map_Data_Value, color = Map_Data_Value)
p_map_nsch_2004
```



Visualise: Prevalence Estimates by Geographic Area [ Source: NSCH ] [ Year: 2008 ]

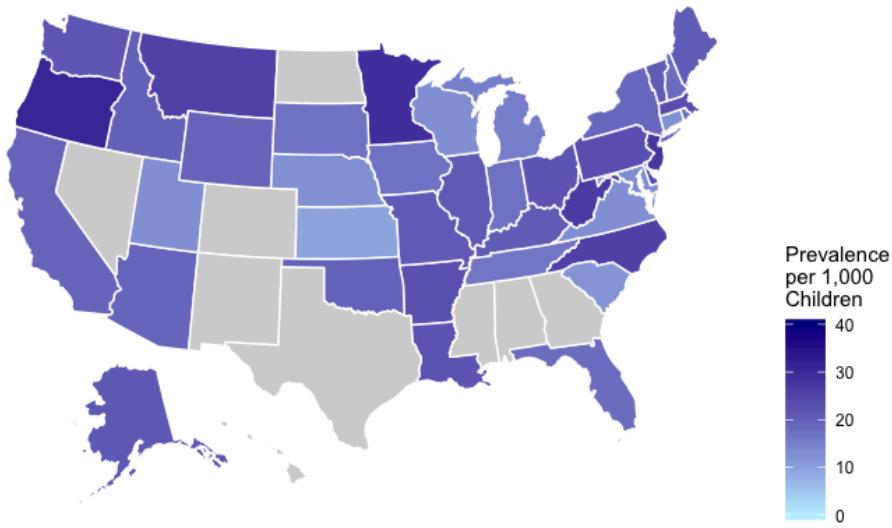
```
In [1184]: # Prepare data - nsch 2008
Map_Data_Year = 2008 # must be integer
ASD_State_Subset = subset(ASD_State, Source == Map_Data_Source & Year == Map_Data_Year)
ASD_State_Subset$state = ASD_State_Subset$State
p_map_nsch_2008 <- plot_usmap(data = ASD_State_Subset, values = Map_Data_Value, color = Map_Data_Value)
p_map_nsch_2008
```



Visualise: Prevalence Estimates by Geographic Area [ Source: NSCH ] [ Year: 2012 ]

```
In [1185]: # Prepare data - nsch 2012
Map_Data_Year = 2012 # must be integer
ASD_State_Subset = subset(ASD_State, Source == Map_Data_Source & Year == Map_Data_Year)
ASD_State_Subset$state = ASD_State_Subset$State
p_map_nsch_2012 <- plot_usmap(data = ASD_State_Subset, values = Map_Data_Value, c
p_map_nsch_2012
```

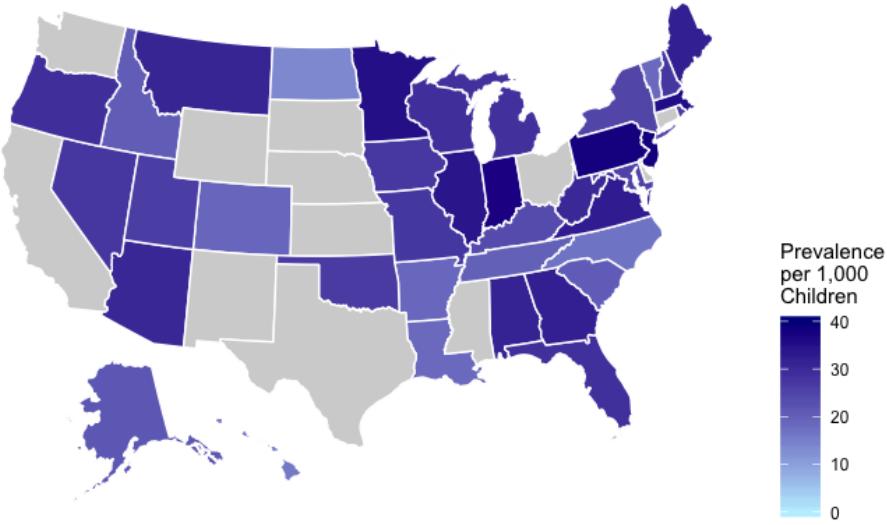
Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2012 ]  
<https://www.cdc.gov/ncbddd/autism>



Visualise: **Prevalence Estimates by Geographic Area** [ Source: NSCH ] [ Year: 2016 ]

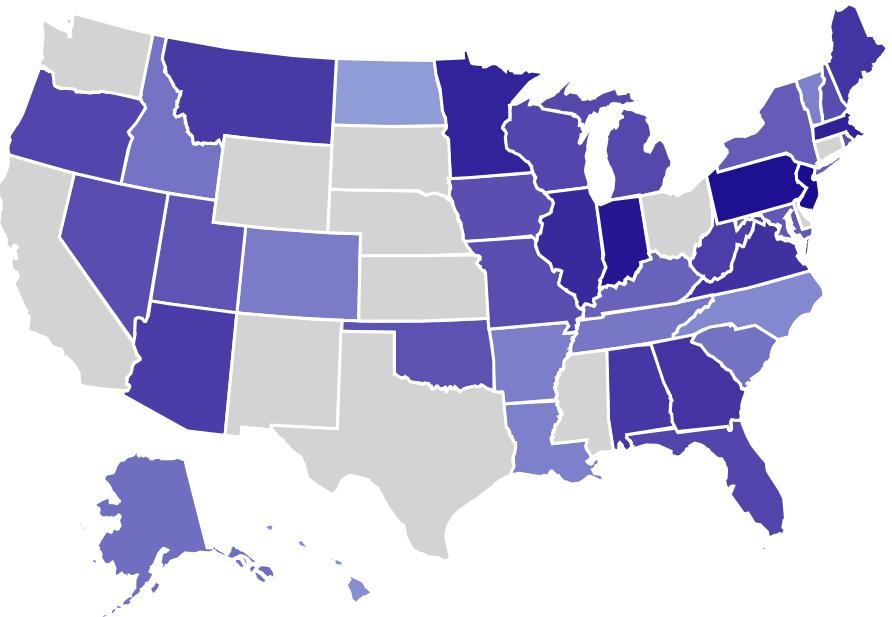
```
In [1186]: # Prepare data - nsch 2016
Map_Data_Year = 2016 # must be integer
ASD_State_Subset = subset(ASD_State, Source == Map_Data_Source & Year == Map_Data_Year)
ASD_State_Subset$state = ASD_State_Subset$State
p_map_nsch_2016 <- plot_usmap(data = ASD_State_Subset, values = Map_Data_Value, c
p_map_nsch_2016
```

Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2016 ]  
<https://www.cdc.gov/ncbddd/autism>



```
In [1187]: # Dynamic map  
p_dynamic <- p_map_nsch_2016 # [ Source: NSCH ] [ Year: 2016 ]  
p_dynamic <- ggplotly(p_dynamic)  
p_dynamic
```

Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2016 ]



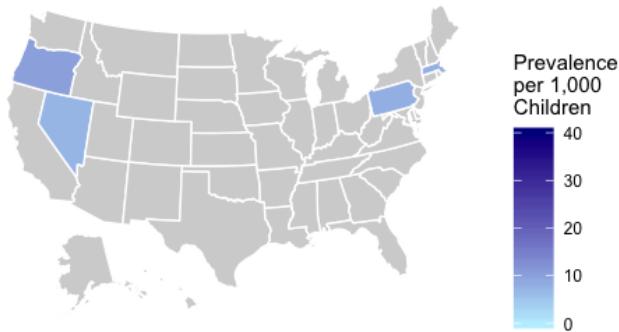
Combine multiple plots to show in one page/screen:

```
In [1188]: # Adjust in-line plot size to M x N  
options(repr.plot.width=8, repr.plot.height=6)
```

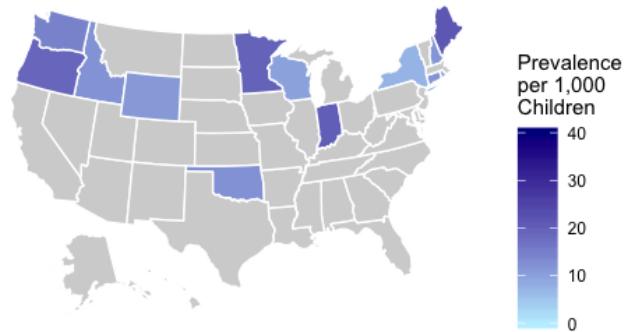
In [1189]: # -----

```
# Combine multiple plots
# -----
if(!require(cowplot)){install.packages("cowplot")}
library('cowplot')
cowplot::plot_grid(
  p_map_nsch_2004,
  p_map_nsch_2008,
  p_map_nsch_2012,
  p_map_nsch_2016,
  nrow = 2)
```

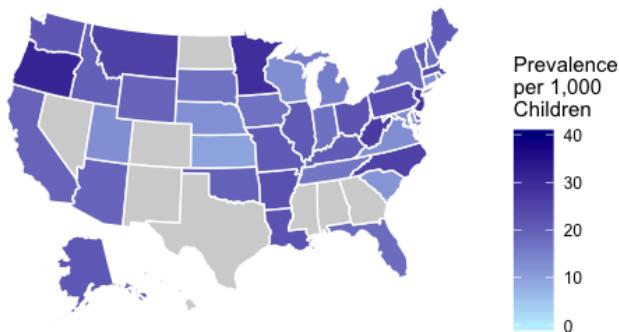
Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2004 ]  
<https://www.cdc.gov/ncbddd/autism>



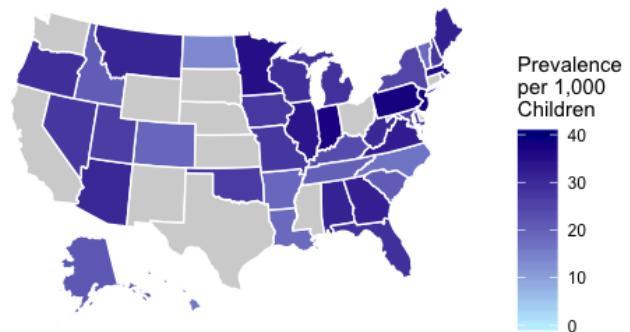
Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2008 ]  
<https://www.cdc.gov/ncbddd/autism>



Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2012 ]  
<https://www.cdc.gov/ncbddd/autism>



Prevalence Estimates by Geographic Area  
[ Measure : Prevalence ] [ Source : nsch ] [ Year : 2016 ]  
<https://www.cdc.gov/ncbddd/autism>



**Export current plot as image file:**

```
In [1190]: # -----
# Export current plot as image file
# -----
ggsave("plot Map Prevalence Estimates by Geographic Area [NSCH] [2004-2016].png",
       width = 60, height = 30, units = 'cm')
```

```
.0
```

## Sampling & Normality

### Sampling & Normality - Population & Sample

```
In [1191]: # Adjust in-line plot size to M x N
# options(repr.plot.width=8, repr.plot.height=4)
```

Create a **Population** of US. State level ASD Prevalence from Source SPED in Year 2016

```
In [1192]: # -----
# Create a *Population* of US. State level ASD Prevalence from Source SPED in Year 2016
# -----
ASD_State_SPED_2016 <- subset(ASD_State, Source == 'sped' & Year == 2016, select =
#
head(ASD_State_SPED_2016)
```

| State | Prevalence |
|-------|------------|
| AL    | 9.1        |
| AK    | 10.1       |
| AZ    | 10.4       |
| AR    | 9.5        |
| CA    | 13.9       |
| CO    | 7.3        |

```
In [1193]: dim(ASD_State_SPED_2016)
# *Population* mean Prevalence
mean(ASD_State_SPED_2016$Prevalence)
```

50 2

11.182

**Define a function to calculate population std-dev (Omega):**

```
In [1194]: # Use sd() to calculate *sample* std-dev (S)
# Use sd.p() to calculate *population* std-dev (Omega)

# Define a function sd.p() to calculate *population* std-dev (Omega)
# https://www.dummies.com/education/math/statistics/standard-deviation-r/

sd.p = function(x) {sd(x) * sqrt((length(x)-1)/length(x))}

# Treat as sample:
cat('sd() of ASD_State_SPED_2016$Prevalence : ', sd(ASD_State_SPED_2016$Prevalence))

# Treat as population:
cat('\nsd.p() of ASD_State_SPED_2016$Prevalence : ', sd.p(ASD_State_SPED_2016$Prevalence))

sd() of ASD_State_SPED_2016$Prevalence : 3.233226
sd.p() of ASD_State_SPED_2016$Prevalence : 3.200731
```

## Sampling & Normality - Central Limit Theorem (CLT)

**Create a Sample of US. State level ASD Prevalence from Source SPED in Year 2016**

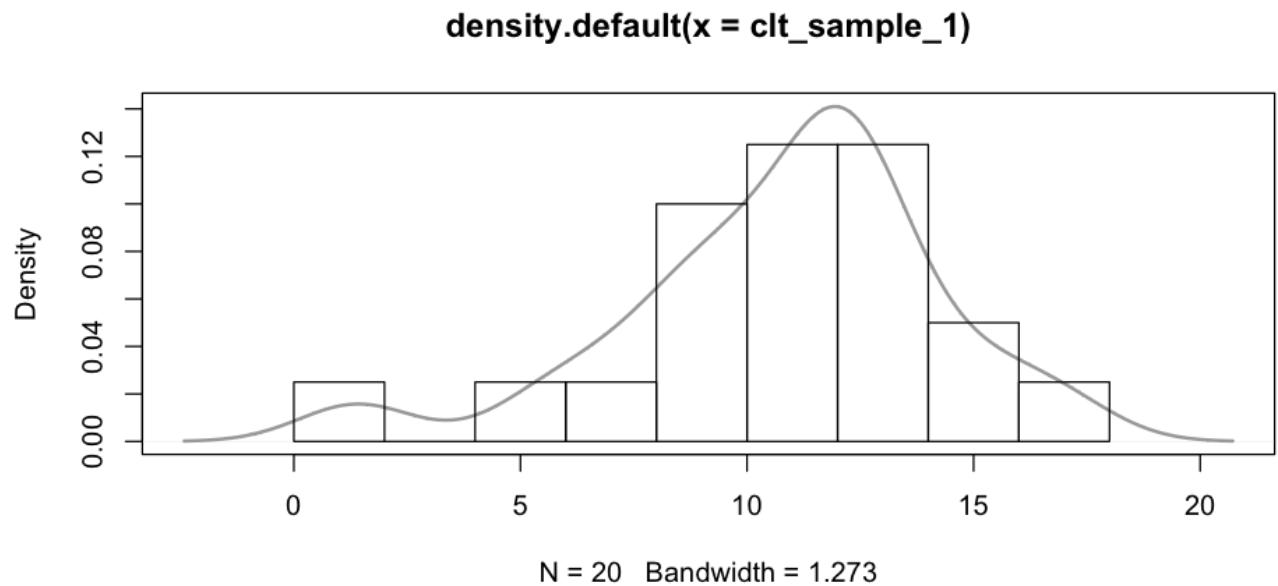
```
In [1195]: # Create a *Sample* from ASD_State_SPED_2016$Prevalence,
# with sample size n =
clt_n = 20
# clt_n = 40

set.seed(88)
clt_sample_1 = sample(x = ASD_State_SPED_2016$Prevalence, size = clt_n, replace = TRUE)

11.2 9.5 16.9 6.9 11.2 8.2 12.7 9.5 1.4 12.7 10.1 14.2 11.9 11.9 8.5 12.1 12.1
15.4 13 5.5
```

```
In [1196]: # Adjust in-line plot size to M x N
options(repr.plot.width=8, repr.plot.height=4)
```

```
In [1197]: plot(density(clt_sample_1), col="darkgrey", lwd=2)
hist(clt_sample_1, probability = T, add = T)
```



**Draw a large k number of samples, with sample size = n:**

```
In [1198]: # Repeatedly sample for k times, create a matrix/array to store these samples  
clt_k = 10000 # or called 'N', but this can be confusing due to N can also be pop  
  
set.seed(88) # Repeatable sampling using pseudo random method  
clt_sample_k <- (replicate(clt_k, sample(x = ASD_State_SPED_2016$Prevalence, size  
  
# first few samples  
clt_sample_k[, 1:6]
```

```
11.2 9.5 11.2 8.3 8.3 6.9  
9.5 11.9 10.4 11.9 11.9 15.2  
16.9 6.9 9.3 1.4 15.4 19.4  
6.9 13.0 19.4 12.7 8.5 15.1  
11.2 8.3 12.1 9.1 11.2 12.1  
8.2 12.1 10.1 14.2 10.2 1.4  
12.7 10.8 12.1 8.6 9.5 15.1  
9.5 15.2 14.1 14.1 10.8 6.9  
1.4 8.7 12.5 16.7 9.8 9.5  
12.7 9.0 5.5 13.9 19.4 14.2  
10.1 9.3 9.5 9.5 14.2 19.4  
14.2 12.1 16.7 12.5 14.1 16.9  
11.9 1.4 9.6 10.8 11.9 9.6
```

```
In [1199]: # last sample  
clt_sample_k[, clt_k]
```

```
8.6 14.1 12.1 19.4 12.7 10.3 10.3 11.2 10.4 9 10.4 13.9 9.3 14.2 11 12.1 9.5  
10.1 13 15.2
```

```
In [1200]: # mean values of first few samples  
mean(clt_sample_k[, 1])  
mean(clt_sample_k[, 2])  
mean(clt_sample_k[, 3])  
mean(clt_sample_k[, 4])  
mean(clt_sample_k[, 5])  
mean(clt_sample_k[, 6])  
  
# or use apply() function to loop  
apply(clt_sample_k[, 1:6], 2, mean)
```

```
10.745  
9.94  
12.705  
10.67  
12.045  
12.795  
10.745 9.94 12.705 10.67 12.045 12.795
```

```
In [1201]: # std-dev values of first few samples
sd(clt_sample_k[, 1])
sd(clt_sample_k[, 2])
sd(clt_sample_k[, 3])
sd(clt_sample_k[, 4])
sd(clt_sample_k[, 5])
sd(clt_sample_k[, 6])

# or use apply() function to loop
apply(clt_sample_k[, 1:6], 2, sd)
```

3.52158382430107

3.7529497170822

3.57115269611191

4.01026314926038

3.17895630009202

5.01140541270873

3.52158382430107 3.7529497170822 3.57115269611191 4.01026314926038 3.17895630009202  
5.01140541270873

## k sample's distributions (k many)

```
In [1202]: # -----
# k sample's distributions (k many)
# -----
# Show the first few sample's histogram
par(mfrow=c(2, 3))
apply(clt_sample_k[, 1:6], 2, FUN=hist)
# Reset
par(mfrow=c(1, 1))

[[1]]
$breaks
[1] 0 2 4 6 8 10 12 14 16 18

$counts
[1] 1 0 1 1 4 5 5 2 1

$density
[1] 0.025 0.000 0.025 0.025 0.100 0.125 0.125 0.050 0.025

$mid
[1] 1 3 5 7 9 11 13 15 17

$xname
[1] "newX[, i]"

$equidist
[1] TRUE
```

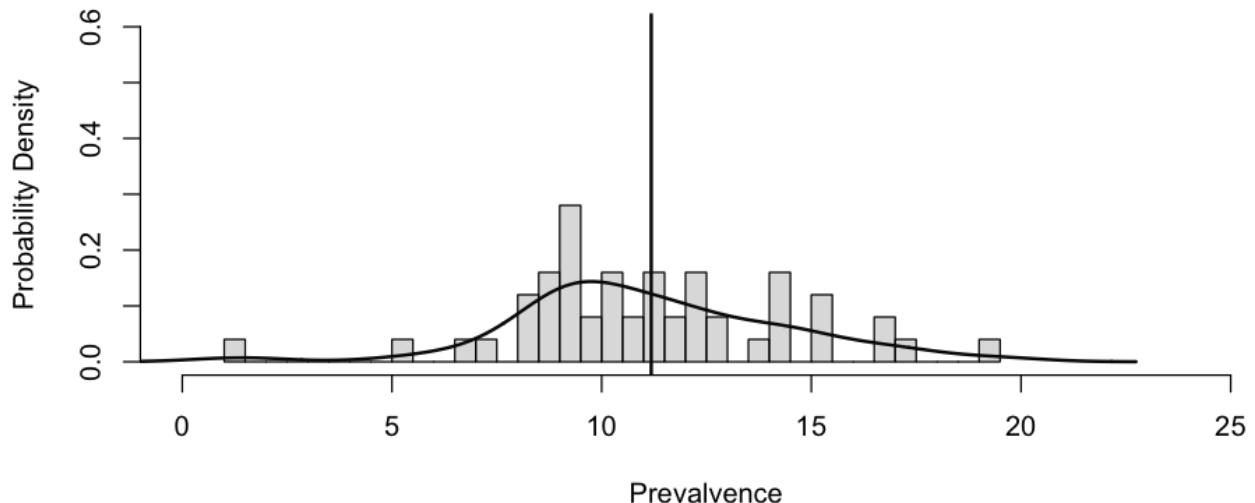
Show the first few sample's density, together with Population

```
In [1203]: # Show the first few sample's density, together with Population
# Population (Prevalence) histogram in probability
hist(ASD_State_SPED_2016$Prevalence, probability = T,
      col=rgb(0.75,0.75,0.75,0.5), breaks = 50,
      xlab = 'Prevalvence', xlim = (c(0, 25)),
      ylab = 'Probability Density',
      ylim = (c(0, 0.6)),
      main = 'Visualize Population & Samples')

# Overlay curve:
# Population (Prevalence) density
lines(density(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)

# Overlay line:
# mean = mean of Population (Prevalence)
abline(v=mean(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)
```

**Visualize Population & Samples**



```
In [1204]: # Show the first few sample's density, together with Population
# Population (Prevalence) histogram in probability
hist(ASD_State_SPED_2016$Prevalence, probability = T,
      col=rgb(0.75,0.75,0.75,0.5), breaks = 50,
      xlab = 'Prevalvence', xlim = (c(0, 25)),
      ylab = 'Probability Density',
      ylim = (c(0, 0.6)),
      main = 'Visualize Population & Samples')

# Overlay curve:
# Population (Prevalence) density
lines(density(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)

# Overlay line:
# mean = mean of Population (Prevalence)
abline(v=mean(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)

# Overlay:
# First few sample's density & mean
lines(density(clt_sample_k[, 1]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, 1]), col="blue", lwd=1)

lines(density(clt_sample_k[, 2]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, 2]), col="blue", lwd=1)

lines(density(clt_sample_k[, 3]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, 3]), col="blue", lwd=1)

lines(density(clt_sample_k[, 4]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, 4]), col="blue", lwd=1)

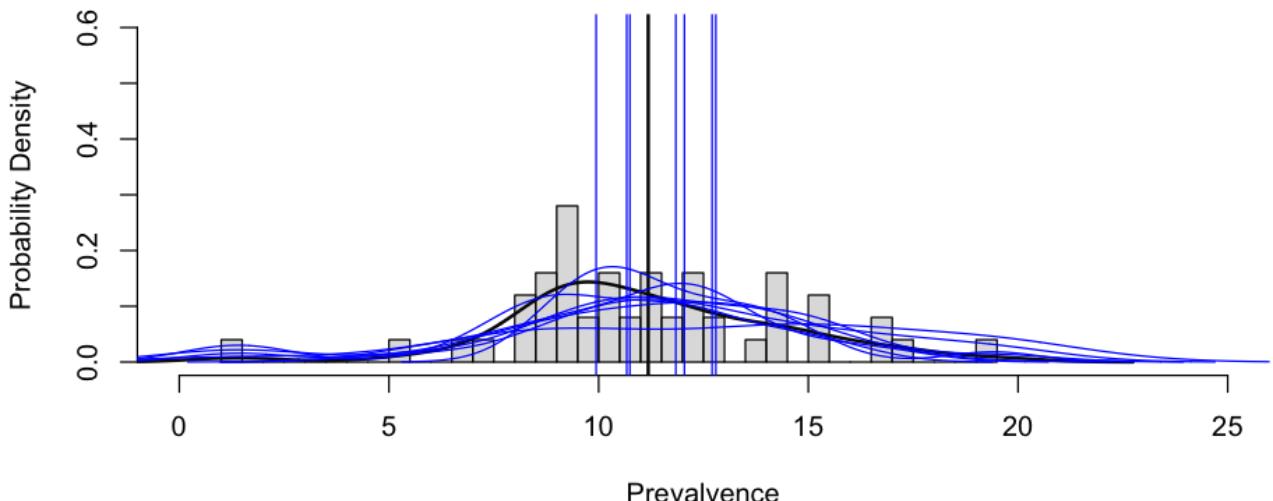
lines(density(clt_sample_k[, 5]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, 5]), col="blue", lwd=1)

lines(density(clt_sample_k[, 6]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, 6]), col="blue", lwd=1)

lines(density(clt_sample_k[, clt_k]), col="blue", lwd=1)
abline(v=mean(clt_sample_k[, clt_k]), col="blue", lwd=1)

# We can see that sample's distributions are all different.
```

## Visualize Population & Samples



[ Tips ] We notice that sample's distributions are all different.

Create Sampling Distribution (only one):

In [1205]: # -----

```
# Sampling distribution (only one)
# -----
# Calculate sample mean value for k samples
clt_sample_k_mean <- apply(clt_sample_k, 2, mean)
# Show first few sample means
clt_sample_k_mean[1:6]
```

10.745 9.94 12.705 10.67 12.045 12.795

In [1206]: # Calculate sample std-dev value for each individual sample (totally k std-dev)

```
clt_sample_k_sd <- apply(clt_sample_k, 2, sd)
# Show first few samples' std-dev
clt_sample_k_sd[1:6]
```

3.52158382430107 3.7529497170822 3.57115269611191 4.01026314926038 3.17895630009202  
5.01140541270873

In [1207]: # Calculate std-dev value for Sampling DIstdtribution (only one std-dev)

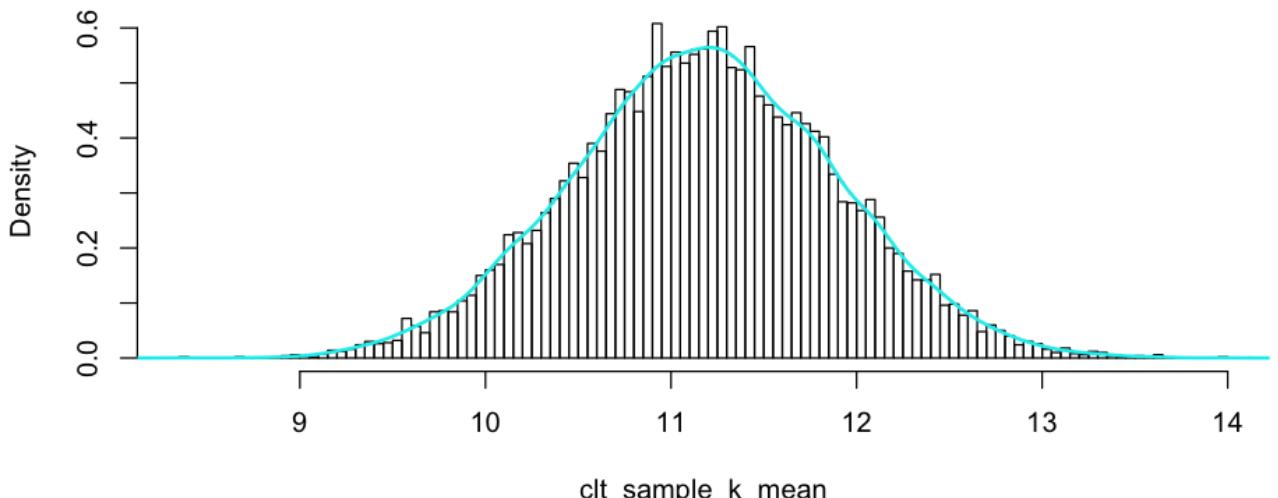
```
sd(clt_sample_k_mean)
```

0.713336703117785

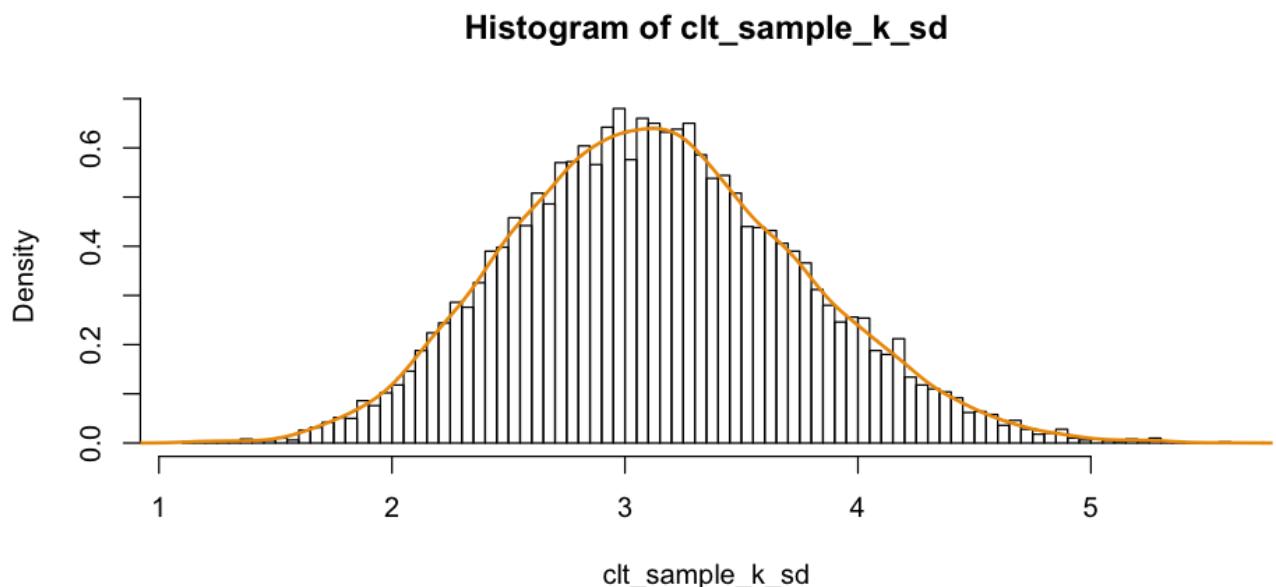
In [1208]: # histogram of sample means (Sampling distribution of the mean)

```
hist(clt_sample_k_mean, probability = T, breaks = 100)
lines(density(clt_sample_k_mean), col="cyan2", lwd=2)
```

Histogram of clt\_sample\_k\_mean



```
In [1209]: # histogram of sample std-dev  
hist(clt_sample_k_sd, probability = T, breaks = 100)  
lines(density(clt_sample_k_sd), col="orange2", lwd=2)
```



```
In [1210]: # k *Sample* (sample size = n) mean Prevalence  
mean(clt_sample_k_mean)
```

11.1788145

```
In [1211]: # *Population* mean Prevalence  
mean(ASD_State_SPED_2016$Prevalence)
```

11.182

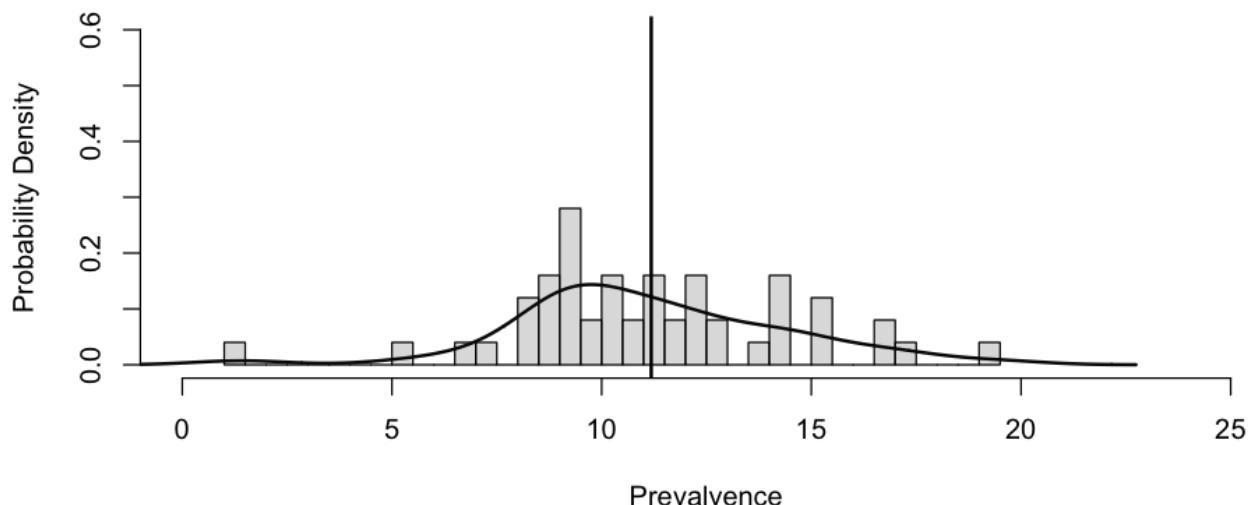
**[ Tips ]** We notice that the above two means are close.

**Visualise: Central Limit Theorem (CLT)**

In [1212]:

```
# -----  
# Sampling distribution vs. Population distribution vs. Z-Norm  
# -----  
# Create:  
# Population (Prevalence) histogram in probability  
hist(ASD_State_SPED_2016$Prevalence, probability = T,  
    col=rgb(0.75,0.75,0.75,0.5), breaks = 50,  
    xlab = 'Prevalvence', xlim = (c(0, 25)),  
    ylab = 'Probability Density', ylim = (c(0, 0.6)),  
    main = 'Visualize Central Limit Theorem (CLT)')  
  
# Overlay curve:  
# Population (Prevalence) density  
lines(density(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)  
  
# Overlay line:  
# mean = mean of Population (Prevalence)  
abline(v=mean(ASD_State_SPED_2016$Prevalence), col="black", lwd=2)
```

Visualize Central Limit Theorem (CLT)

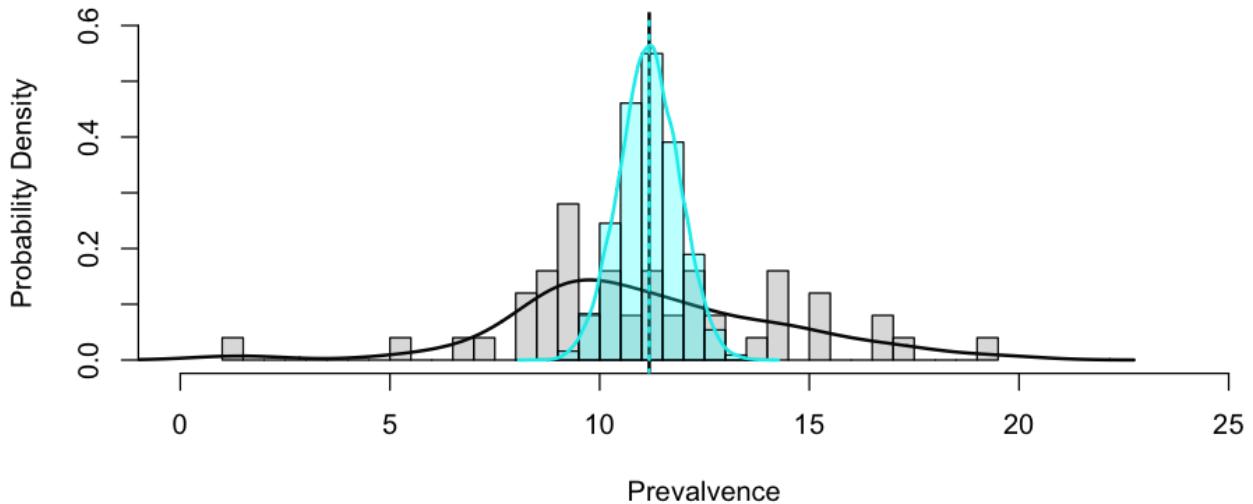


Overlay: Sample means histogram in probability (Sampling disribution)

In [1213]:

```
# -----  
# Sampling distribution vs. Population distribution vs. Z-Norm  
# -----  
# Create:  
# Population (Prevalence) histogram in probability  
hist(ASD_State_SPED_2016$Prevalence, probability = T,  
    col=rgb(0.75,0.75,0.75,0.5), breaks = 50,  
    xlab = 'Prevalvence', xlim = (c(0, 25)),  
    ylab = 'Probability Density', ylim = (c(0, 0.6)),  
    main = 'Visualize Central Limit Theorem (CLT)')  
  
# Overlay curve:  
# Population (Prevalence) density  
lines(density(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)  
  
# Overlay line:  
# mean = mean of Population (Prevalence)  
abline(v=mean(ASD_State_SPED_2016$Prevalence), col="black", lwd=2)  
  
# Overlay line:  
# Sample means histogram in probability (Sampling disribution)  
hist(clt_sample_k_mean, probability = T,  
    col=rgb(0,1,1,0.3), # https://www.dataanalytics.org.uk/make-transparent-colo  
    add=T)  
  
# Overlay curve:  
# Sample (Prevalence) density (Sampling disribution)  
lines(density(clt_sample_k_mean), col="cyan2", lwd=2)  
# Overlay line:  
# mean of Sampling distribution (of Prevelance, sample size n)  
abline(v=mean(clt_sample_k_mean), col="cyan2", lwd=2, lty=3)
```

## Visualize Central Limit Theorem (CLT)



< How to make transparent colors in R >

<https://www.dataanalytics.org.uk/make-transparent-colors-in-r/> (<https://www.dataanalytics.org.uk/make-transparent-colors-in-r/>)

```
col2rgb(c("cyan", "grey", "red")) / 255
```

```
In [1214]: col2rgb(c("cyan", "grey", "purple", "orange")) / 255
```

|       |   |          |           |           |
|-------|---|----------|-----------|-----------|
| red   | 0 | 0.745098 | 0.6274510 | 1.0000000 |
| green | 1 | 0.745098 | 0.1254902 | 0.6470588 |
| blue  | 1 | 0.745098 | 0.9411765 | 0.0000000 |

```
In [1215]: # Recall:
```

```
# k *Sample* (sample size = n) mean Prevalence  
mean(clt_sample_k_mean)  
# *Population* mean Prevalence  
mean(ASD_State_SPED_2016$Prevalence)  
# We see that the above two means are close. Good estimation!
```

```
11.1788145
```

```
11.182
```

[ Tips ] We notice that the above two means are close. **Good estimation!**

**Standard Error (SE) (of mean prevalence), can be estimated as: std-dev of the Sampling distribution (of mean prevalence):**

```
In [1216]: # -----  
# Standard Error (SE) (of mean prevalence), can be estimated as:  
# std-dev of the Sampling distribution (of mean prevalence)  
# -----  
# https://en.wikipedia.org/wiki/Sampling_distribution  
  
# [1] Actual SE: When Population std-dev is known, SE using Population standard d  
sd.p(ASD_State_SPED_2016$Prevalence) / sqrt(clt_n)  
  
# [2] Estimated SE with k samples: When Population std-dev is NOT known, but many  
sd(clt_sample_k_mean)  
  
# [3] Estimated SE with only one sample: When Population std-dev is NOT known, an  
clt_sample_k_sd[1] / sqrt(clt_n)
```

```
0.715705106870141
```

```
0.713336703117785
```

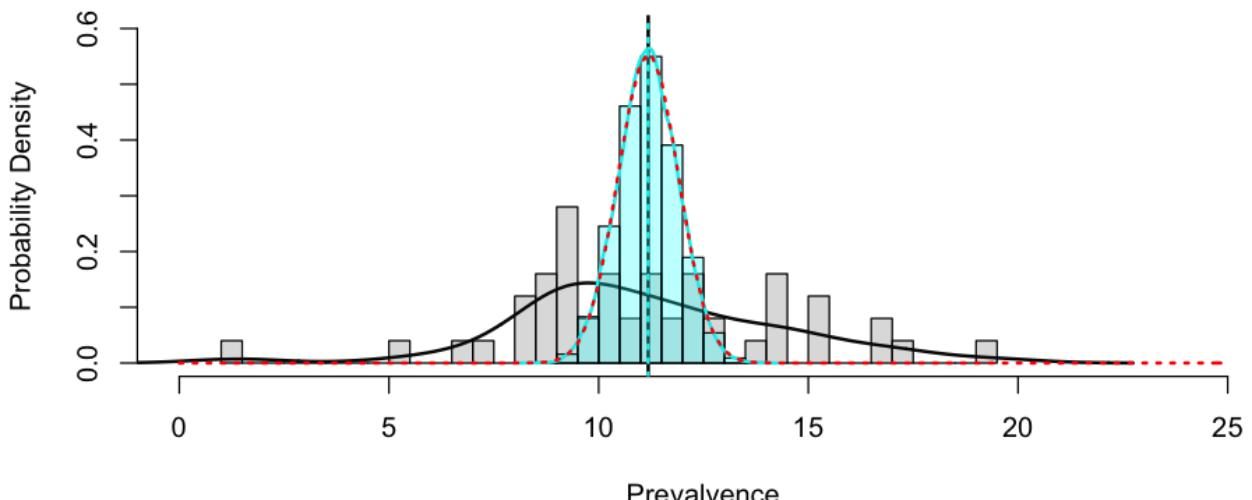
```
0.787450081960087
```

**Overlay: Theoretic Sampling Distribution with population mean & std-dev = Actual SE:**

In [1217]:

```
# -----  
# Sampling distribution vs. Population distribution vs. Z-Norm  
# -----  
# Create:  
# Population (Prevalence) histogram in probability  
hist(ASD_State_SPED_2016$Prevalence, probability = T,  
    col=rgb(0.75,0.75,0.75,0.5), breaks = 50,  
    xlab = 'Prevalvence', xlim = (c(0, 25)),  
    ylab = 'Probability Density', ylim = (c(0, 0.6)),  
    main = 'Visualize Central Limit Theorem (CLT)')  
  
# Overlay curve:  
# Population (Prevalence) density  
lines(density(ASD_State_SPED_2016$Prevalence), col="grey4", lwd=2)  
  
# Overlay line:  
# mean = mean of Population (Prevalence)  
abline(v=mean(ASD_State_SPED_2016$Prevalence), col="black", lwd=2)  
  
# Overlay line:  
# Sample means histogram in probability (Sampling disribution)  
hist(clt_sample_k_mean, probability = T,  
    col=rgb(0,1,1,0.3), # https://www.dataanalytics.org.uk/make-transparent-colo  
    add=T)  
  
# Overlay curve:  
# Sample (Prevalence) density (Sampling disribution)  
lines(density(clt_sample_k_mean), col="cyan2", lwd=2)  
# Overlay line:  
# mean of Sampling distribution (of Prevelance, sample size n)  
abline(v=mean(clt_sample_k_mean), col="cyan2", lwd=2, lty=3)  
  
# Overlay curve:  
# *Theoretic Sampling Distribution* with population mean & std-dev = Actual SE  
# mean = mean of Population (Prevalence) & std-dev = std-dev of Population (Preva  
curve(dnorm(x,  
    mean(ASD_State_SPED_2016$Prevalence), # Actual Population mean  
    sd.p(ASD_State_SPED_2016$Prevalence) / sqrt(clt_n)), # Actual SE (for  
    add=TRUE, col="red", lwd=2, lty=3)
```

## Visualize Central Limit Theorem (CLT)



## Sampling & Normality - Evaluate Normality

### Use QQ Plot

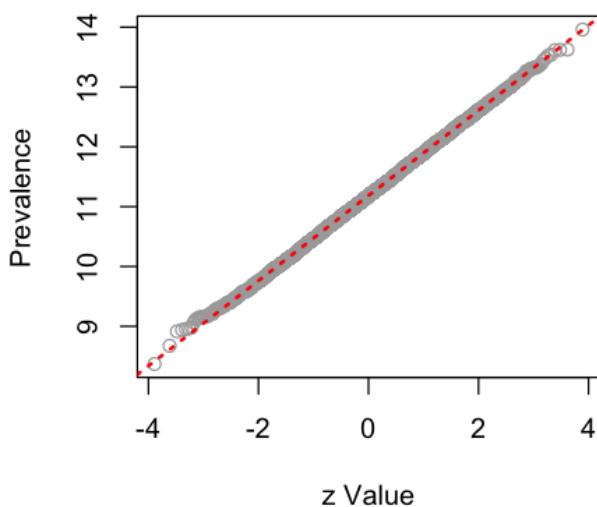
< Construct a Quantile-Quantile Plot (QQ plot) > <https://youtu.be/okjYjCISjOg> (<https://youtu.be/okjYjCISjOg>)

In [1218]:

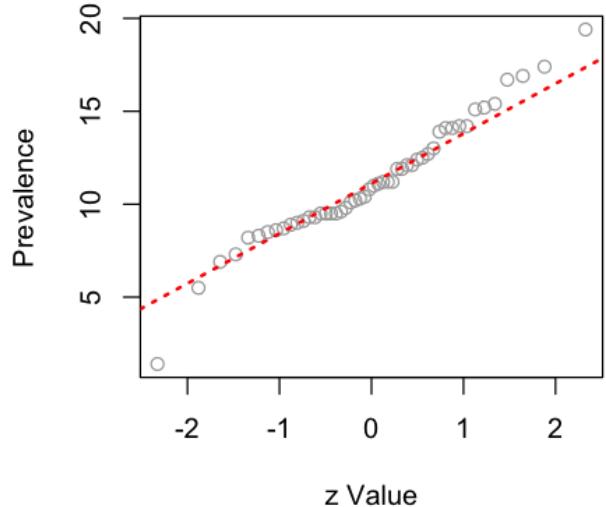
```
# -----
# Evaluate normality
# -----
# Construct a Quantile-Quantile Plot (QQ plot)
# https://youtu.be/okjYjCISjOg

par(mfrow=c(1, 2))
# Sample means
qqnorm(clt_sample_k_mean, col="darkgrey",
       xlab="z Value", ylab="Prevalence")
qqline(clt_sample_k_mean, col="red", lwd=2, lty=3)
# Population
qqnorm(ASD_State_SPED_2016$Prevalence, col="darkgrey",
       xlab="z Value", ylab="Prevalence")
qqline(ASD_State_SPED_2016$Prevalence, col="red", lwd=2, lty=3)
# Reset
par(mfrow=c(1, 1))
```

Normal Q-Q Plot



Normal Q-Q Plot



**[ Tips ]** If most/all data points are aligned with the red straight line, then the underlying data points are normally distributed.

```
In [1219]: # Alternatively, use shapiro.test() to test Normality
set.seed(88)

# Test data of k sample's means (Sampling Distribution data):
shapiro.test(sample(x = clt_sample_k_mean, size = 1000))

# Test data of population's Prevalence values (Population Distribution data):
shapiro.test(ASD_State_SPED_2016$Prevalence)
```

Shapiro-Wilk normality test

```
data: sample(x = clt_sample_k_mean, size = 1000)
W = 0.99904, p-value = 0.8907
```

Shapiro-Wilk normality test

```
data: ASD_State_SPED_2016$Prevalence
W = 0.96985, p-value = 0.2282
```

[ Tips ] General speaking, if p-value is greater than 0.05 (meaning more than 5% chance of being normally distributed), then the underlying data points are normally distributed.

## Confidence Interval (CI)

### Confidence Interval (CI) - Mean Estimation & Its CI

Use a Sample statistic (e.g. mean) to estimate a population statistic (e.g. mean). And quantitatively calculate the confidence of the estimation.

```
In [1220]: # -----
# Use a sample of a few US. State's ASD prevalence (mean) to estimate:
# Average prevalence of ALL US. States (the *Population*) [Source SPED, Year 2016]
# -----
dim(ASD_State_SPED_2016)
#
ASD_State_SPED_2016 # This is considered as a population now.
```

50 2

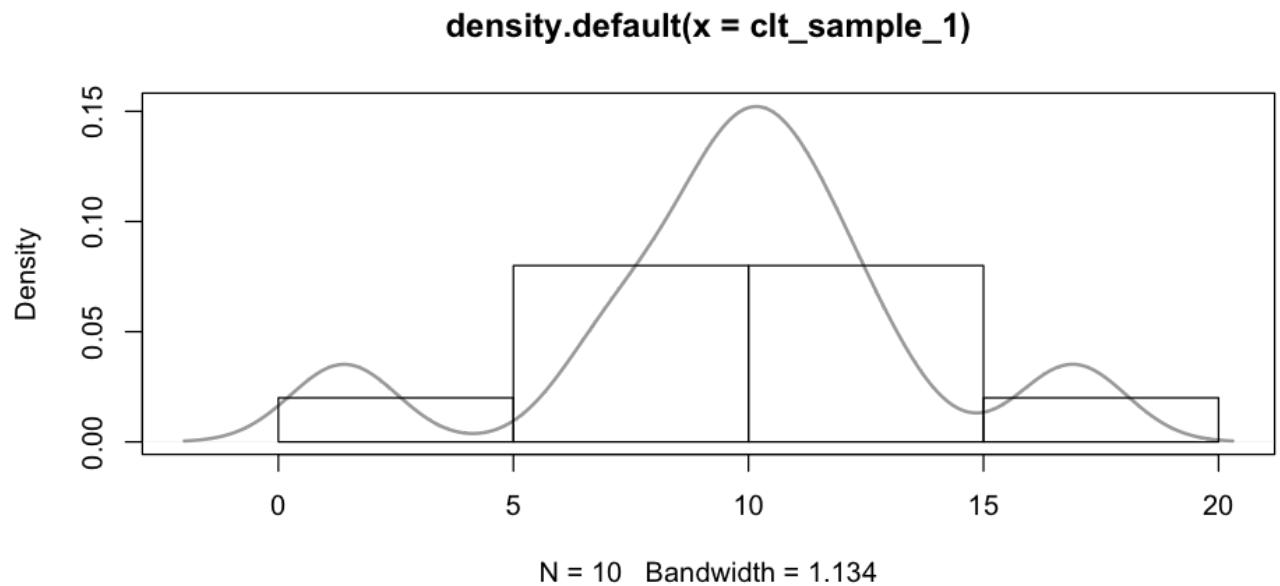
### Draw a Sample from ASD\_State\_SPED\_2016\$Prevalence

```
In [1221]: # Create a *Sample* from ASD_State_SPED_2016$Prevalence,
# with sample size n =
clt_n = 10
# Try 20 or 40, larger sample size, narrower the CI (more confident at xx% level)
# clt_n = 20

set.seed(88)
clt_sample_1 = sample(x = ASD_State_SPED_2016$Prevalence, size = clt_n, replace =
clt_sample_1
```

11.2 9.5 16.9 6.9 11.2 8.2 12.7 9.5 1.4 10.2

```
In [1222]: plot(density(clt_sample_1), col="darkgrey", lwd=2)
hist(clt_sample_1, probability = T, add = T)
```



```
In [1223]: # Sample mean Prevalence
mean(clt_sample_1)

# *Population* mean Prevalence
mean(ASD_State_SPED_2016$Prevalence)
```

9.77

11.182

1. Calculate Confidence Interval of mean estimation: **CI using Z (Standard Normal) distribution**

```
In [1224]: # -----  
# CI using Z (Standard Normal) distribution  
# -----  
# sample mean  
sample_mean = mean(clt_sample_1)  
sample_mean
```

9.77

```
In [1225]: # sample size n  
sample_size_n = length(clt_sample_1)  
sample_size_n
```

10

```
In [1226]: # sample standard deviation  
sample_sd = sd(clt_sample_1)  
sample_sd
```

4.00833853083516

```
In [1227]: # sample standard error  
sample_se = sample_sd / sqrt(sample_size_n)  
sample_se
```

1.26754793904522

```
In [1228]: # 95% quantile (z score)  
z_score = qnorm(p = 0.975)  
z_score
```

1.95996398454005

```
In [1229]: # ?qnorm
```

```
In [1230]: # CI using Z distribution  
sample_ci = z_score * sample_se  
sample_ci
```

2.4843483092066

```
In [1231]: # Lower CI: mean + CI  
sample_mean - sample_ci  
  
# Upper CI: mean + CI  
sample_mean + sample_ci  
  
# Display  
cat('\t< Confidence Interval (Prevalence) >\n', '\tLower CI : ', sample_mean -
```

7.2856516907934

12.2543483092066

```
< Confidence Interval (Prevalence) >  
Lower CI : 7.285652      Mean : 9.77      Upper CI : 12.25435
```

[?] Is the population mean in this CI range?

2. Calculate Confidence Interval of mean estimation: CI using T distribution

```
In [1232]: # -----
# CI using T distribution
# -----
# sample mean
sample_mean = mean(clt_sample_1)
sample_mean
# sample size n
sample_size_n = length(clt_sample_1)
sample_size_n
# sample standard deviation
sample_sd = sd(clt_sample_1)
sample_sd
# sample standard error
sample_se = sample_sd / sqrt(sample_size_n)
sample_se
```

9.77

10

4.00833853083516

1.26754793904522

```
In [1233]: # 95% quantile (t score)
t_score = qt(p = 0.975, df = sample_size_n - 1)
t_score
```

2.2621571627982

```
In [1234]: # ?qt
```

```
In [1235]: # CI using T distribution
sample_ci = t_score * sample_se
sample_ci

# Lower CI: mean + CI
sample_mean - sample_ci

# Upper CI: mean + CI
sample_mean + sample_ci

# Display
cat('\t< Confidence Interval (Prevalence) >\n', '\tLower CI : ', sample_mean -
```

2.86739264950124

6.90260735049876

12.6373926495012

< Confidence Interval (Prevalence) >

|            |        |            |
|------------|--------|------------|
| Lower CI : | Mean : | Upper CI : |
| 6.902607   | 9.77   | 12.63739   |

[?] Is the population mean in this CI range?

[?] Compare CIs of Z and T distribution, which CI has wider range? Is it reasonable?

```
In [1236]: # Alternatively, calculate CI using t.test() function  
t.test(clt_sample_1, conf.level = 0.95)
```

One Sample t-test

```
data: clt_sample_1  
t = 7.7078, df = 9, p-value = 2.976e-05  
alternative hypothesis: true mean is not equal to 0  
95 percent confidence interval:  
 6.902607 12.637393  
sample estimates:  
mean of x  
 9.77
```

```
In [1237]: # Two group hypothesis test : sample mean vs. population mean  
t.test(clt_sample_1, conf.level = 0.95, mu = mean(ASD_State_SPED_2016$Prevalence))
```

One Sample t-test

```
data: clt_sample_1  
t = -1.114, df = 9, p-value = 0.2942  
alternative hypothesis: true mean is not equal to 11.182  
95 percent confidence interval:  
 6.902607 12.637393  
sample estimates:  
mean of x  
 9.77
```

### Quiz:

Obtain CI using smaller/larger sample size (clt\_n) at 99% confidence. Compare CI width.

Observe: larger sample size, narrower the CI (more confident at xx% level)

```
In [1238]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

## Confidence Interval (CI) - Proportion Estimation & Its CI

Use a **Sample statistic (e.g. proportion)** to estimate a **population statistic (e.g. proportion)**. And quantitatively calculate the confidence of the estimation.

```
In [1239]: # -----
# Use a sample of one US. State's ASD prevalence (proportion) to estimate:
# Prevalence of THAT US. State's ALL Children (the *Population*) [Source SPED, Ye
# -----

# No. Children with ASD
ASD <- ASD_State_SPED$Numerator_ASD[ASD_State_SPED$Year == 2016]
#
str(ASD)

int [1:50] 6140 1204 10746 4181 79041 5902 7391 1383 782 30920 ...
```

```
In [1240]: # No. Children with ASD of first US. State (AL-Alabama)
ASD[1]

6140
```

```
In [1241]: # No. Children surveyed
Children <- ASD_State_SPED$Denominator[ASD_State_SPED$Year == 2016]
#
str(Children)

int [1:50] 674701 119217 1033241 440130 5686400 808556 479961 124609 65732 255
5399 ...
```

```
In [1242]: # No. Children surveyed of first US. State (AL-Alabama)
Children[1]

674701
```

**1. Calculate Confidence Interval of proportion estimation: CI using Z score interval (standard normal distribution)**

```
In [1243]: # -----
# CI using Z score interval (standard normal distribution)
# https://en.wikipedia.org/wiki/Binomial\_proportion\_confidence\_interval
# -----

# sample proportion of first US. State (AL-Alabama) in year 2016 of source SPED
sample_proportion = ASD[1] / Children[1]
sample_proportion
```

0.00910032740428723

```
In [1244]: # sample size n
sample_size_n = Children[1]
sample_size_n
```

674701

```
In [1245]: # 95% quantile (z score)
z_score = qnorm(p = 0.975)
z_score
```

1.95996398454005

```
In [1246]: sample_ci = z_score * sqrt(sample_proportion * (1 - sample_proportion) / sample_size)
```

```
0.000226587404757579
```

```
In [1247]: # Lower CI: mean + CI  
sample_proportion - sample_ci
```

```
# Upper CI: mean + CI  
sample_proportion + sample_ci
```

```
# Display
```

```
cat('\t< Confidence Interval >\n', '\tLower CI : ', sample_proportion - sample_ci)
```

```
0.00887373999952965
```

```
0.00932691480904481
```

```
< Confidence Interval >
```

```
Lower CI : 0.00887374 Mean : 0.009100327 Upper CI : 0.009326915
```

```
In [1248]: # Display * 1000 -> Prevalence
```

```
cat('\t< Confidence Interval (Prevalence) >\n', '\tLower CI : ', 1000*(sample_p
```

```
< Confidence Interval (Prevalence) >
```

```
Lower CI : 8.87374 Mean : 9.100327 Upper CI : 9.326915
```

**[ Tips ]** Based above calculation upon [ Source: SPED ] [ Year: 2016 ] data, we have 95% confidence that: The actual AL-Alabama state level ASD prevalence (if ALL childrens in Alabama state were surveyed) would be in the above calculated CI range 95% times.

Or, asumming there are 100 independently different Alabama states exist in 100 parallel universe, we obtained 100 actual prevelance proportions. 95 of them will likely fall into the CI value range.

## 2. Calculate Confidence Interval of proportion estimation: CI using Wilson score interval

```
In [1249]: # -----
# CI using Wilson score interval
# https://en.wikipedia.org/wiki/Binomial_proportion_confidence_interval
# -----

sample_proportion # = ASD[1] / Children[1]

# Yates' chi-squared test = Wilson score interval with continuity correction - pr
prop.test(ASD[1], Children[1], conf.level = 0.95)

# Pearson's chi-squared test = Wilson score interval - wilson
prop.test(ASD[1], Children[1], conf.level = 0.95, correct = FALSE)
```

0.00910032740428723

```
1-sample proportions test with continuity correction

data: ASD[1] out of Children[1], null probability 0.5
X-squared = 650363, df = 1, p-value < 2.2e-16
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.008875786 0.009330477
sample estimates:
      p
0.009100327
```

```
1-sample proportions test without continuity correction

data: ASD[1] out of Children[1], null probability 0.5
X-squared = 650365, df = 1, p-value < 2.2e-16
alternative hypothesis: true p is not equal to 0.5
95 percent confidence interval:
 0.008876518 0.009329726
sample estimates:
      p
0.009100327
```

### Quiz:

Obtain CI of Male.Prevalence propotion [ Source: ADDM] [ Year: 2014 ] at 99% confidence.

```
In [1250]: # Write your code below and press Shift+Enter to execute
```

Double-click **here** for the solution.

### Quiz:

Obtain CI of Female.Prevalence propotion [ Source: ADDM] [ Year: 2014 ] at 99% confidence.

Then Compare CI range with Male children's CI range. Which gender has statistically higer ASD prevalence/proportion?

In [1251]: # Write your code below and press Shift+Enter to execute

Double-click **here** for the solution.

0.

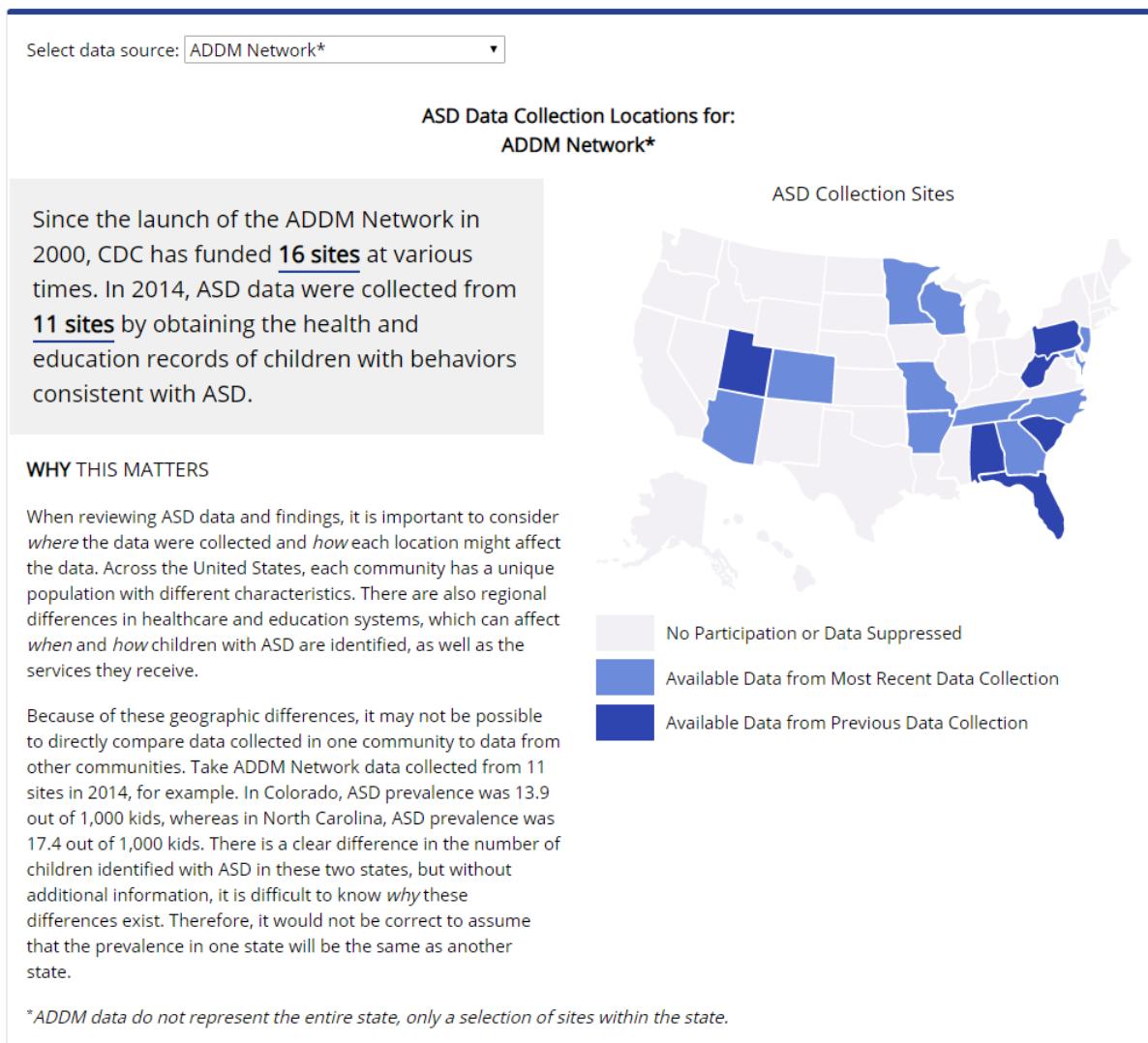
## Workshop Submission

### What to submit?

Choose one of below visualisations/charts, use R to construct the chart nicely.

Optionally, enhance it with additional data dimensions to be better than original chart.

<https://www.cdc.gov/ncbdd/autism/data/index.html>  
(<https://www.cdc.gov/ncbdd/autism/data/index.html>)



## 2014 ADDM NETWORK DATA

In this section, explore the most recent ADDM data, both overall and among certain demographic groups by study area.

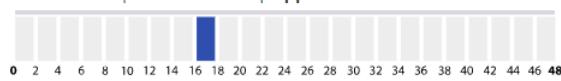
Select a location:  ▾

MOST RECENT STUDY YEAR: 2014

### ASD PREVALENCE PER 1,000 8-YEAR-OLD CHILDREN

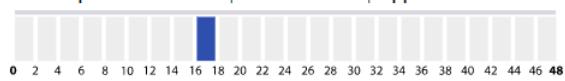
#### Prevalence Overall

Overall: 16.8 | Lower CI: 16.4 | Upper CI: 17.3



#### Prevalence By Race/Ethnicity

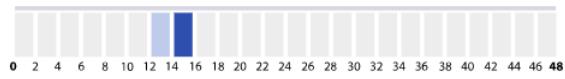
Non-Hispanic White: 17.2 | Lower CI: 16.5 | Upper CI: 17.8



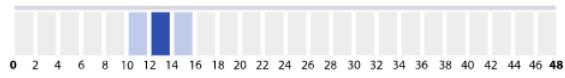
Non-Hispanic Black: 16 | Lower CI: 15.1 | Upper CI: 16.9



Hispanic: 14 | Lower CI: 13.1 | Upper CI: 14.9

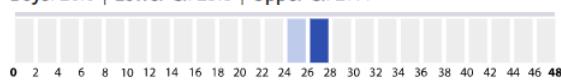


Asian/Pacific Islander: 13.5 | Lower CI: 11.8 | Upper CI: 15.4

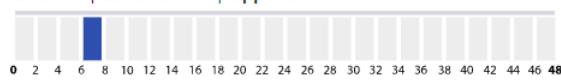


#### Prevalence By Sex

Boys: 26.6 | Lower CI: 25.8 | Upper CI: 27.4



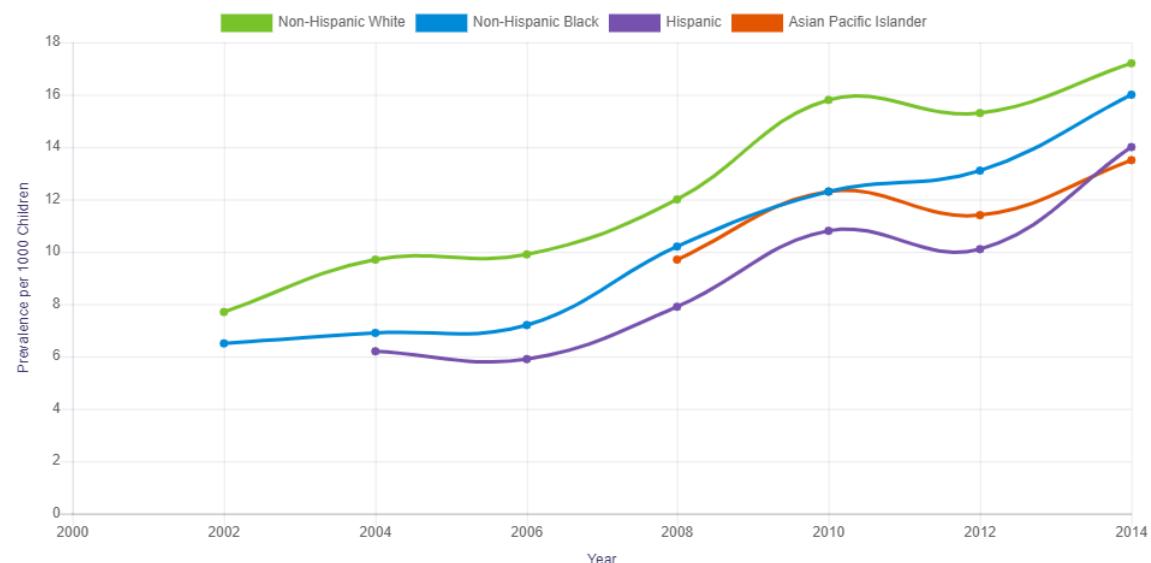
Girls: 6.6 | Lower CI: 6.2 | Upper CI: 7



<sup>†</sup>ADDM estimate = the total for all sites combined.

### Prevalence Estimates by Race/Ethnicity

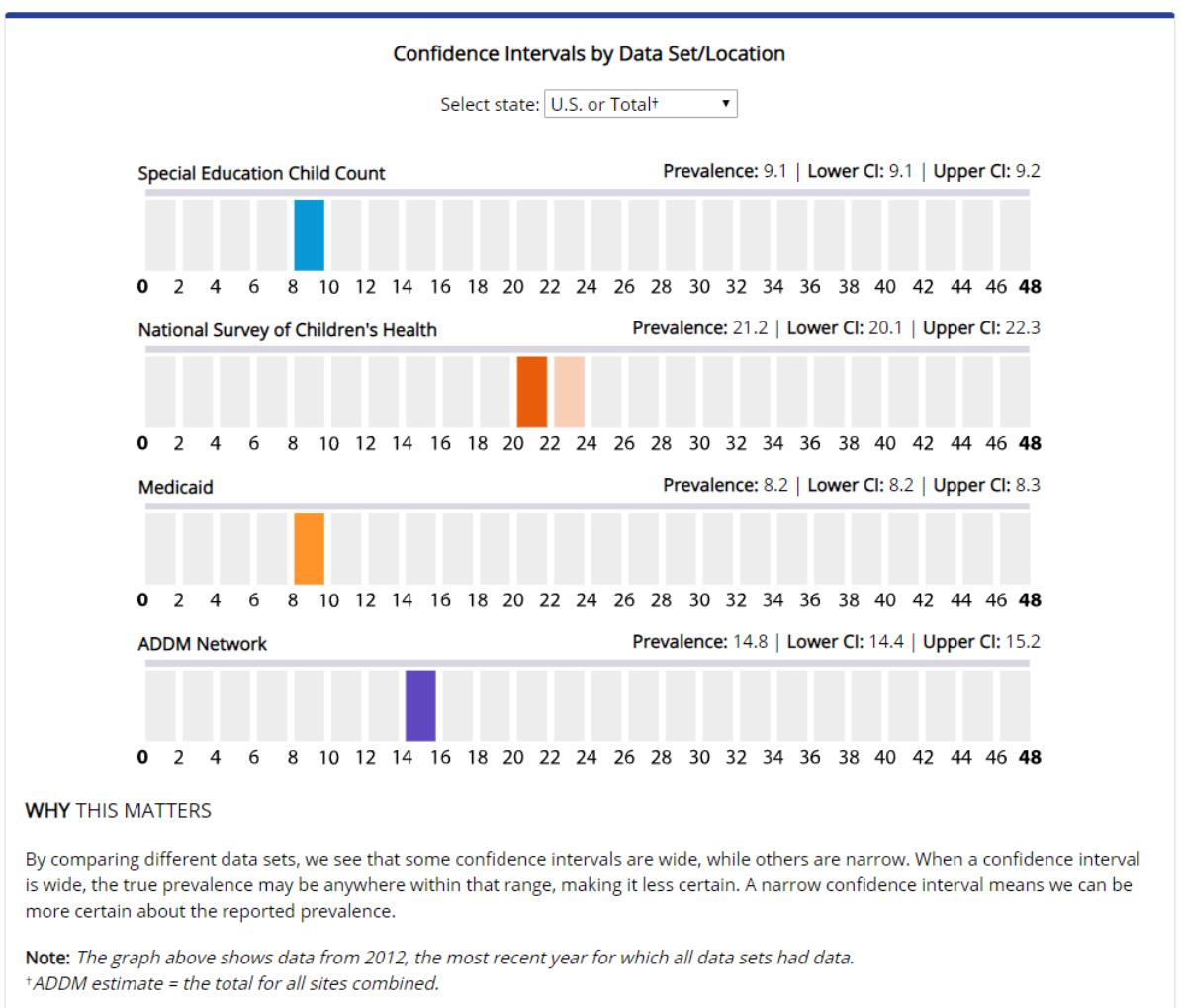
Show ADDM prevalence estimates\* by race/ethnicity for:  ▾



Note: Click the icons and racial/ethnic groups above the chart to hide or unhide data. Hover your mouse over data points to show prevalence by year.

\*ADDM data do not represent the entire state, only a selection of sites within the state.

<sup>†</sup>ADDM estimate = the total for all sites combined.



In [1252]: # Write your code below and press Shift+Enter to execute

**Excellent! You have completed the workshop notebook!**

**Connect with the author:**

This notebook was written by [GU Zhan \(Sam\)](https://sg.linkedin.com/in/zhan-gu-27a82823).

[Sam](https://www.iss.nus.edu.sg/about-us/staff/detail/201/GU%20Zhan) is currently a lecturer in [Institute of Systems Science](https://www.iss.nus.edu.sg/) in [National University of Singapore](https://www.nus.edu.sg/). He devotes himself into pedagogy & andragogy, and is very passionate in inspiring next generation of artificial intelligence lovers and leaders.

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## Appendices

### Interactive workshops: < Learning R inside R > using swirl() (in R/RStudio)

```
In [1253]: # -----
# Interactive workshops: < Learning R inside R > using swirl() (in R/RStudio)
# -----
if(!require(swirl)){install.packages("swirl")}
library("swirl")
install_course("R Programming")
install_course("Exploratory Data Analysis")
install_course("Regression Models")
install_course("Statistical Inference")
swirl()
```

| ====== | 100%

| Course installed successfully!

| ====== | 100%

| Course installed successfully!

| ====== | 100%

| Course installed successfully!

| ====== | 100%

## Neural Network 101 using nnet()

```
In [1254]: # -----
# Neural Network 101 using nnet()
# -----
if(!require(nnet)){install.packages("nnet")}
library("nnet")
# ?nnet

# < Case: predict three different iris flower types >

# https://en.wikipedia.org/wiki/Iris_flower_data_set
# https://archive.ics.uci.edu/ml/datasets/iris

# Data preparation: split iris data in two halves, for training & testing respect
ir <- rbind(iris3[,1],iris3[,2],iris3[,3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
# Model training (machine learning / data fitting)
irl1 <- nnet(ir[samp,], targets[samp,], size = 2, rang = 0.1,
              decay = 5e-4, maxit = 200)
# Model prediction
test.cl <- function(true, pred) {
  true <- max.col(true)
  cres <- max.col(pred)
  table(true, cres)
}

# Model evaluation
test.cl(targets[-samp,], predict(irl1, ir[-samp,]))
```

```
# weights:  19
initial  value 56.720484
iter    10 value 48.312067
iter    20 value 29.096504
iter    30 value 18.239805
iter    40 value 17.345523
iter    50 value 17.180673
iter    60 value 16.944589
iter    70 value 16.897683
iter    80 value 16.883344
iter    90 value 16.882703
final   value 16.882577
converged

      cres
true  1  2  3
  1 20  0  5
  2  0 25  0
  3  0  0 25
```

## Hypothesis Test - Mean - Z Test & t.test()

```
In [1255]: # -----  
# Hypothesis Test - Mean - Z Test & t.test()  
# -----  
  
# Create sample 1  
set.seed(88)  
sample_1 = rnorm(n = 10)  
# sample_1 = rnorm(n = 1000)  
  
# Create sample 2  
set.seed(88)  
sample_2 = rchisq(n = 10, df = 30) - 29  
# sample_2 = rchisq(n = 1000, df = 30) - 29  
  
mean(sample_1)  
mean(sample_2)  
  
par(mfrow=c(1, 2))  
hist(sample_1)  
hist(sample_2)  
par(mfrow=c(1, 1))  
  
t.test(sample_1, sample_2)
```

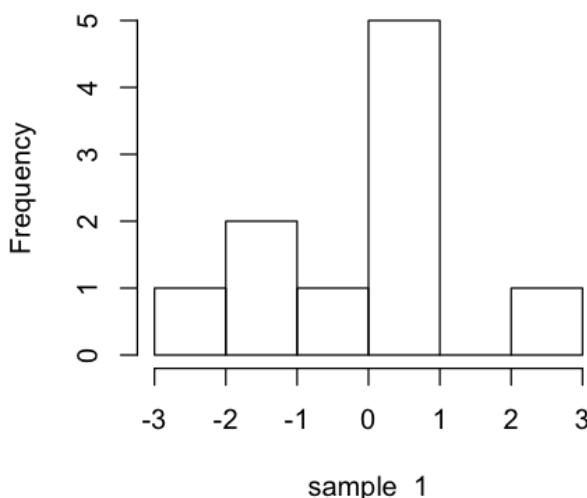
-0.10035252728447

1.47209538362297

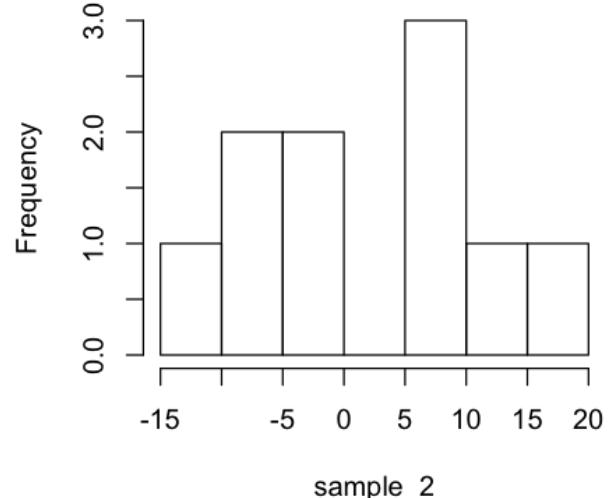
#### Welch Two Sample t-test

```
data: sample_1 and sample_2  
t = -0.53406, df = 9.3705, p-value = 0.6057  
alternative hypothesis: true difference in means is not equal to 0  
95 percent confidence interval:  
-8.193020 5.048124  
sample estimates:  
mean of x mean of y  
-0.1003525 1.4720954
```

**Histogram of sample\_1**



**Histogram of sample\_2**



## Hypothesis Test - Proportion - prop.test()

In [1256]:

```
# -----  
# Hypothesis Test - Proportion - prop.test()  
# -----  
if(!require(binom)){install.packages("binom")}  
library('binom')  
  
# Different flavours of proportion test:  
binom.confint (x=ASD[1], n=Children[1], conf.level =0.95, method="all")  
  
# Multiple group hypothesis test : proportions (Prevalence) among all US. States  
prop.test(ASD, Children)
```

Warning message in binom.bayes(x, n, conf.level = conf.level, ...):  
"1 confidence interval failed to converge (marked by '\*').  
Try changing 'tol' to a different value."

| method        | x    | n      | mean        | lower       | upper       |
|---------------|------|--------|-------------|-------------|-------------|
| agresti-coull | 6140 | 674701 | 0.009100327 | 0.008876501 | 0.009329744 |
| asymptotic    | 6140 | 674701 | 0.009100327 | 0.008873740 | 0.009326915 |
| bayes*        | 6140 | 674701 | 0.009101055 | 0.008874879 | 0.009328049 |
| cloglog       | 6140 | 674701 | 0.009100327 | 0.008875951 | 0.009329145 |
| exact         | 6140 | 674701 | 0.009100327 | 0.008875108 | 0.009329776 |
| logit         | 6140 | 674701 | 0.009100327 | 0.008876513 | 0.009329732 |
| probit        | 6140 | 674701 | 0.009100327 | 0.008876195 | 0.009329400 |
| profile       | 6140 | 674701 | 0.009100327 | 0.008875600 | 0.009328782 |
| lrt           | 6140 | 674701 | 0.009100327 | 0.008845578 | 0.009330138 |
| prop.test     | 6140 | 674701 | 0.009100327 | 0.008875786 | 0.009330477 |
| wilson        | 6140 | 674701 | 0.009100327 | 0.008876518 | 0.009329726 |

50-sample test for equality of proportions without continuity correction

```
data: ASD out of Children  
X-squared = 28593, df = 49, p-value < 2.2e-16  
alternative hypothesis: two.sided  
sample estimates:  
prop 1      prop 2      prop 3      prop 4      prop 5      prop 6  
0.009100327 0.010099231 0.010400284 0.009499466 0.013900007 0.007299433  
prop 7      prop 8      prop 9      prop 10     prop 11     prop 12  
0.015399168 0.011098717 0.011896793 0.012099872 0.010300278 0.008299863  
prop 13     prop 14     prop 15     prop 16     prop 17     prop 18  
0.009498530 0.011000237 0.014200361 0.001399357 0.008200786 0.009299486  
prop 19     prop 20     prop 21     prop 22     prop 23     prop 24  
0.006900015 0.016696937 0.011900547 0.017399589 0.011199751 0.019400428  
prop 25     prop 26     prop 27     prop 28     prop 29     prop 30  
0.009499812 0.012399961 0.005500221 0.010800730 0.012698882 0.014097784  
prop 31     prop 32     prop 33     prop 34     prop 35     prop 36  
0.014100222 0.008501570 0.012999924 0.011199812 0.009796534 0.012499686  
prop 37     prop 38     prop 39     prop 40     prop 41     prop 42  
0.008899480 0.015100037 0.016899883 0.015201438 0.009599935 0.008997355  
prop 43     prop 44     prop 45     prop 46     prop 47     prop 48  
0.009500416 0.010199940 0.008699269 0.012103956 0.014200156 0.011200227  
prop 49     prop 50  
0.008601179 0.009299132
```

