Complex keys

JOINING DATA WITH DATA.TABLE IN R

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Misspecified joins

What happens when you don't use the correct columns for join keys?

- An error is thrown
- The result is a malformed `data.table`

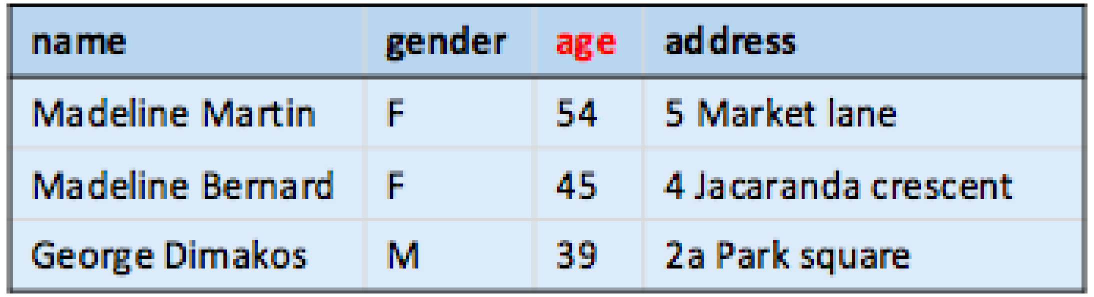
Column type mismatch

Using join key columns with different types will error

```
customers[web_visits, on = .(age = name)]
```

```
Error in bmerge(i, x, leftcols, rightcols, io, xo, roll, rollends,
nomatch,  :
  typeof x.age (double) != typeof i.name (character)
```

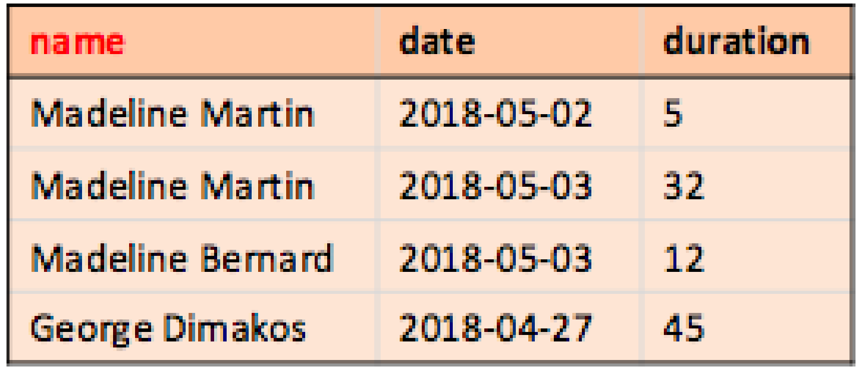
customers:



name	gender	age	address
Madeline Martin	F	54	5 Market lane
Madeline Bernard	F	45	4 Jacaranda crescent
George Dimakos	M	39	2a Park square

+

web_visits:



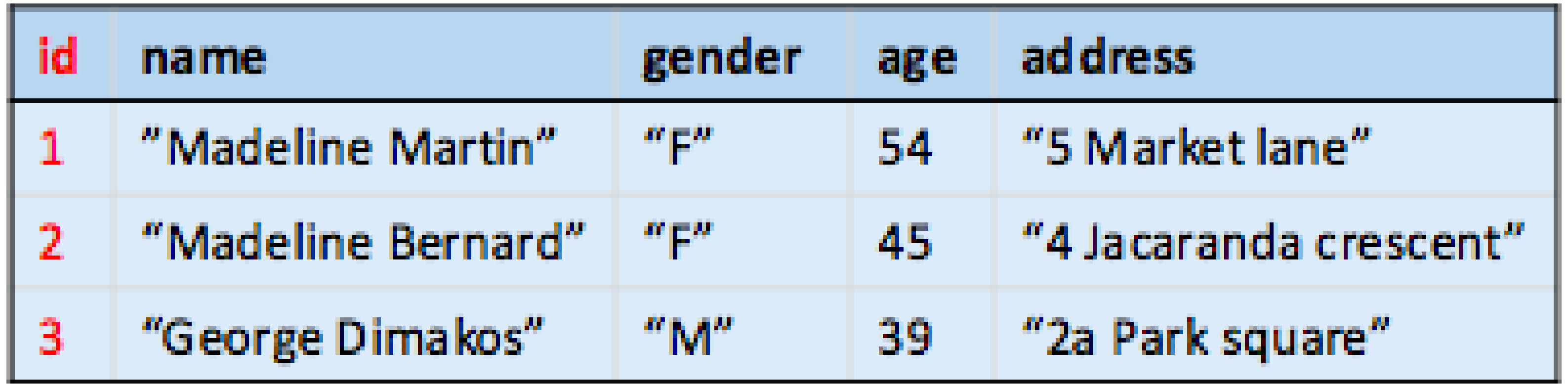
name	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

Column type mismatch

```
customers[web_visits, on = .(id)]
```

```
Error in bmerge(i, x, leftcols, rightcols, io, xo, roll, rollends,
nomatch,  :
  typeof x.id (integer) != typeof i.id(character)
```

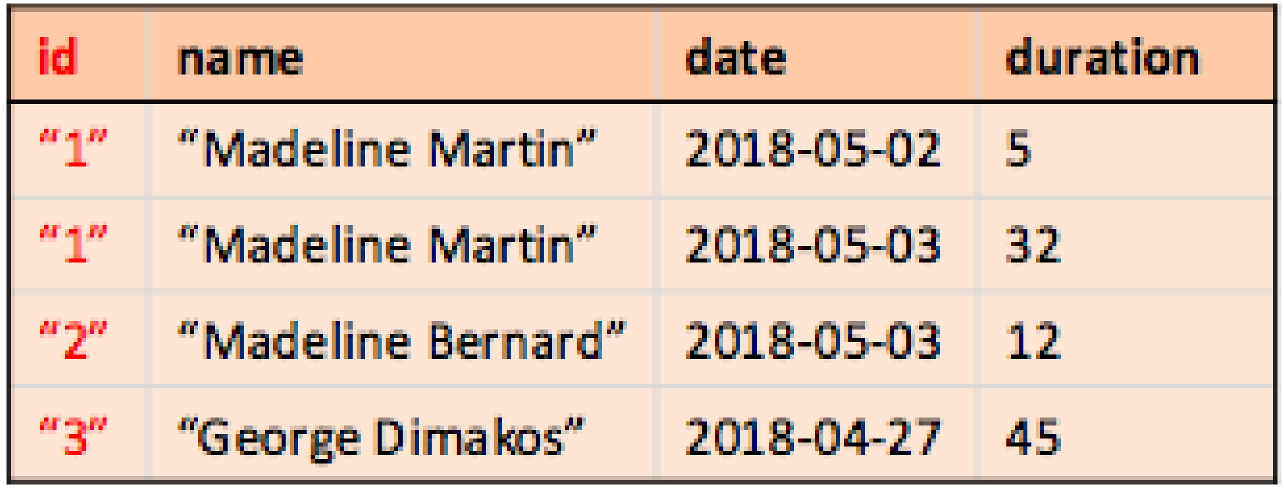
customers:



id	name	gender	age	address
1	"Madeline Martin"	"F"	54	"5 Market lane"
2	"Madeline Bernard"	"F"	45	"4 Jacaranda crescent"
3	"George Dimakos"	"M"	39	"2a Park square"

+

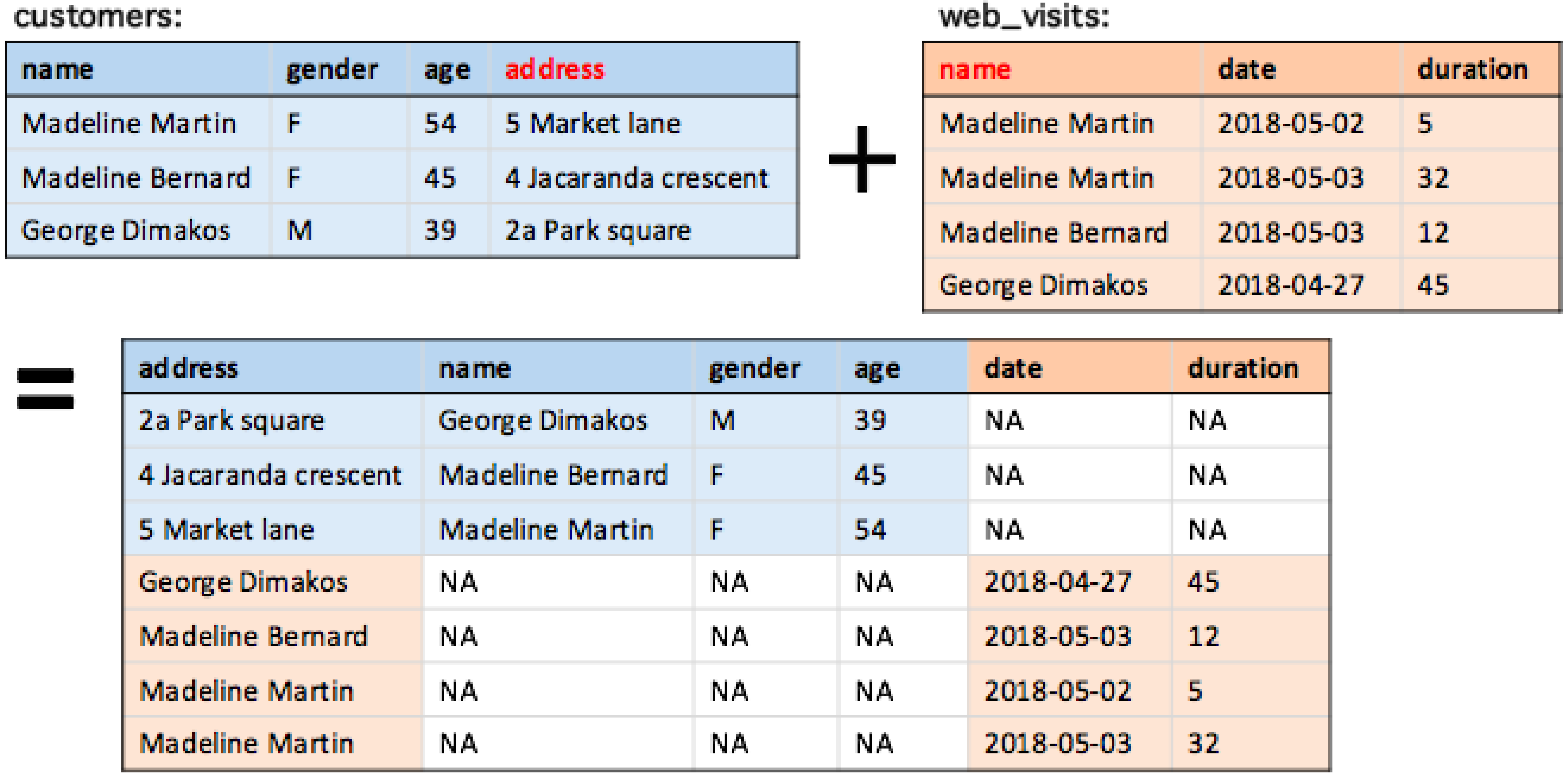
web_visits:



id	name	date	duration
"1"	"Madeline Martin"	2018-05-02	5
"1"	"Madeline Martin"	2018-05-03	32
"2"	"Madeline Bernard"	2018-05-03	12
"3"	"George Dimakos"	2018-04-27	45

Malformed full joins - no common key values

```
merge(customers, web_visits, by.x = "address", by.y = "name", all = TRUE)
```



customers:

name	gender	age	address
Madeline Martin	F	54	5 Market lane
Madeline Bernard	F	45	4 Jacaranda crescent
George Dimakos	M	39	2a Park square

+

web_visits:

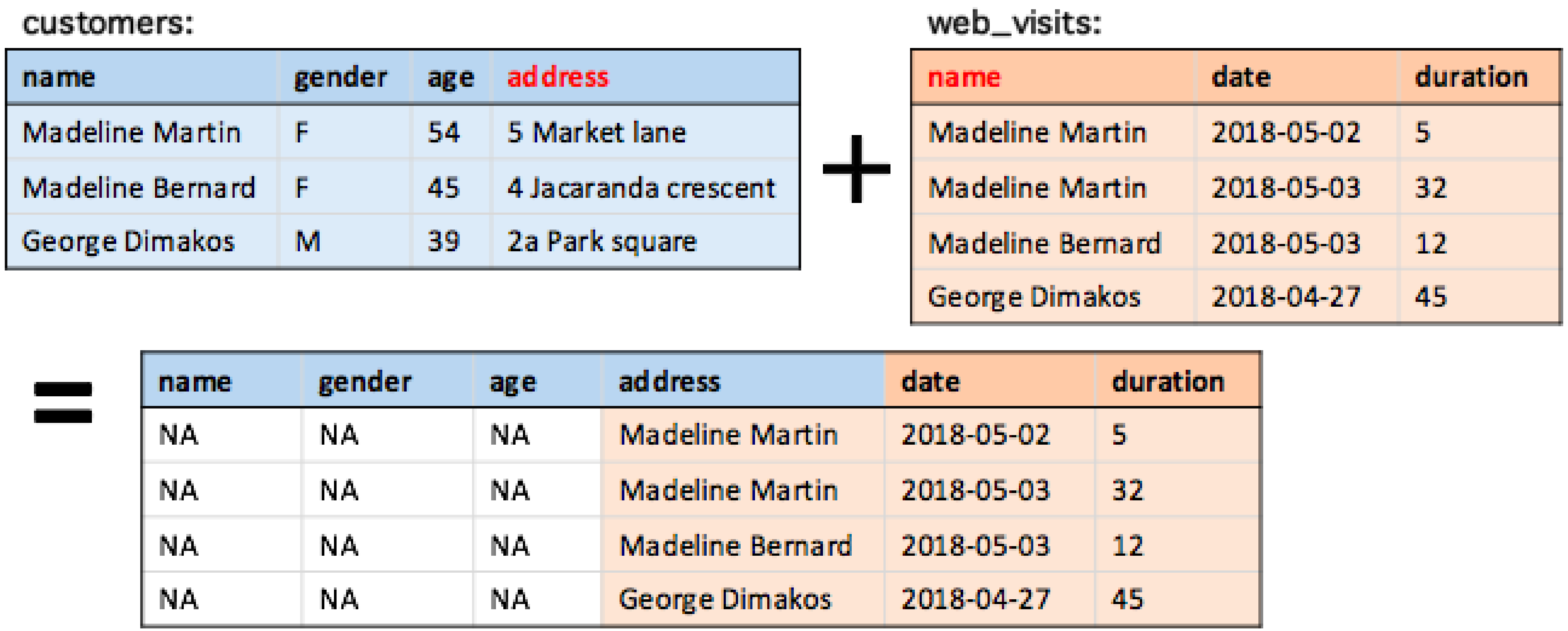
name	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

=

address	name	gender	age	date	duration
2a Park square	George Dimakos	M	39	NA	NA
4 Jacaranda crescent	Madeline Bernard	F	45	NA	NA
5 Market lane	Madeline Martin	F	54	NA	NA
George Dimakos	NA	NA	NA	2018-04-27	45
Madeline Bernard	NA	NA	NA	2018-05-03	12
Madeline Martin	NA	NA	NA	2018-05-02	5
Madeline Martin	NA	NA	NA	2018-05-03	32

Malformed right and left joins - no common key values

```
customers[web_visits, on = .(address = name)]
```



customers:

name	gender	age	address
Madeline Martin	F	54	5 Market lane
Madeline Bernard	F	45	4 Jacaranda crescent
George Dimakos	M	39	2a Park square

+

web_visits:

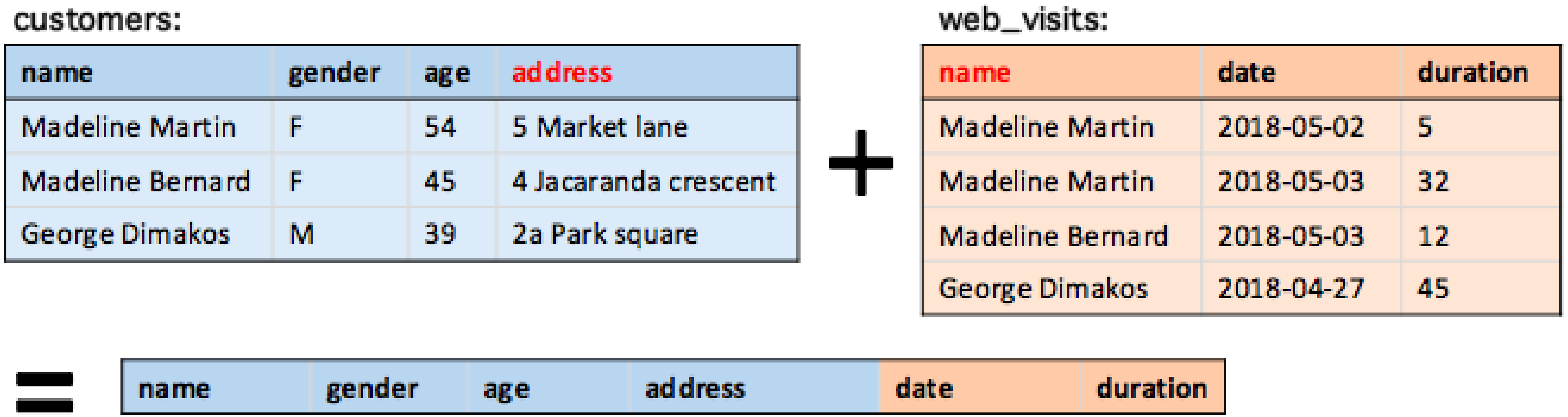
name	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

=

name	gender	age	address	date	duration
NA	NA	NA	Madeline Martin	2018-05-02	5
NA	NA	NA	Madeline Martin	2018-05-03	32
NA	NA	NA	Madeline Bernard	2018-05-03	12
NA	NA	NA	George Dimakos	2018-04-27	45

Malformed inner joins - no common key values

```
customers[web_visits, on = .(address = name), nomatch = 0]
```



customers:

name	gender	age	address
Madeline Martin	F	54	5 Market lane
Madeline Bernard	F	45	4 Jacaranda crescent
George Dimakos	M	39	2a Park square

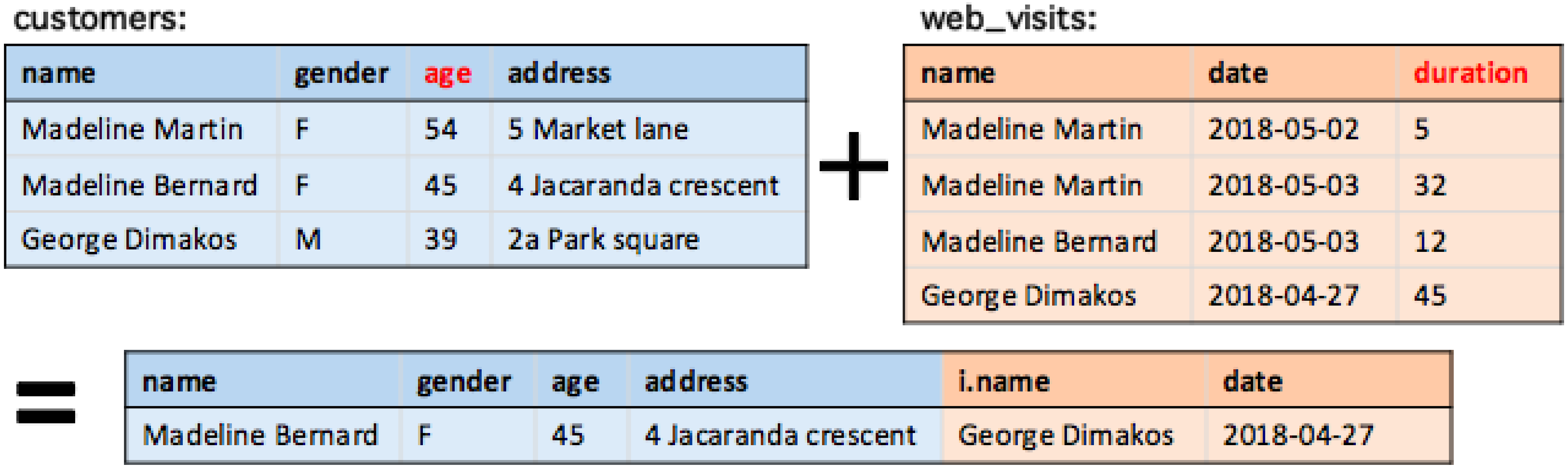
web_visits:

name	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

name	gender	age	address	date	duration

Malformed joins - coincidental common key values

```
customers[web_visits, on = .(age = duration), nomatch = 0]
```



customers:

name	gender	age	address
Madeline Martin	F	54	5 Market lane
Madeline Bernard	F	45	4 Jacaranda crescent
George Dimakos	M	39	2a Park square

+

web_visits:

name	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

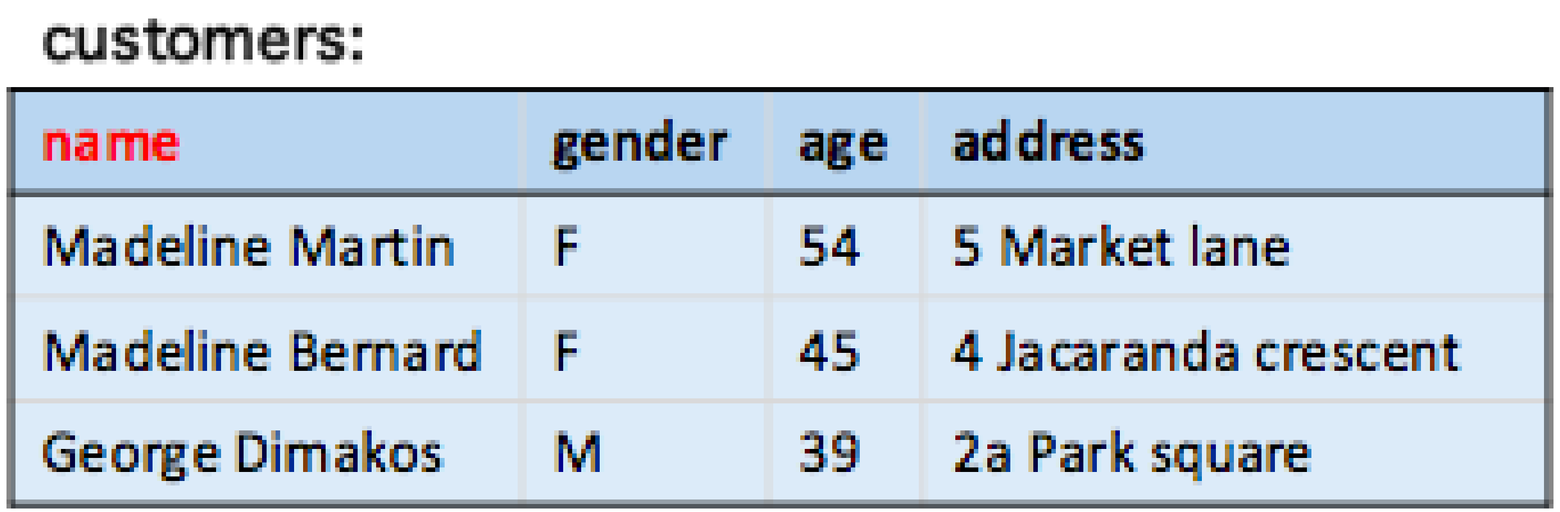
=

name	gender	age	address	i.name	date
Madeline Bernard	F	45	4 Jacaranda crescent	George Dimakos	2018-04-27

Avoiding misspecified joins

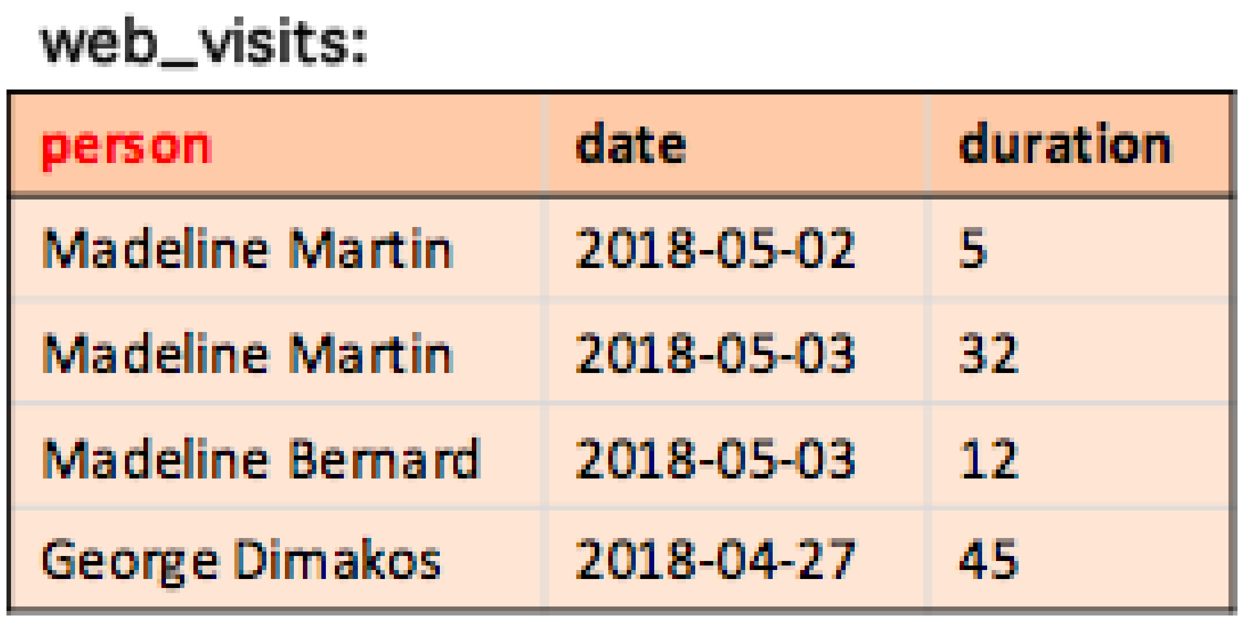
> Learning what each column represents before joins will help you avoid errors

Keys with different column names



customers:

name	gender	age	address
Madeline Martin	F	54	5 Market lane
Madeline Bernard	F	45	4 Jacaranda crescent
George Dimakos	M	39	2a Park square



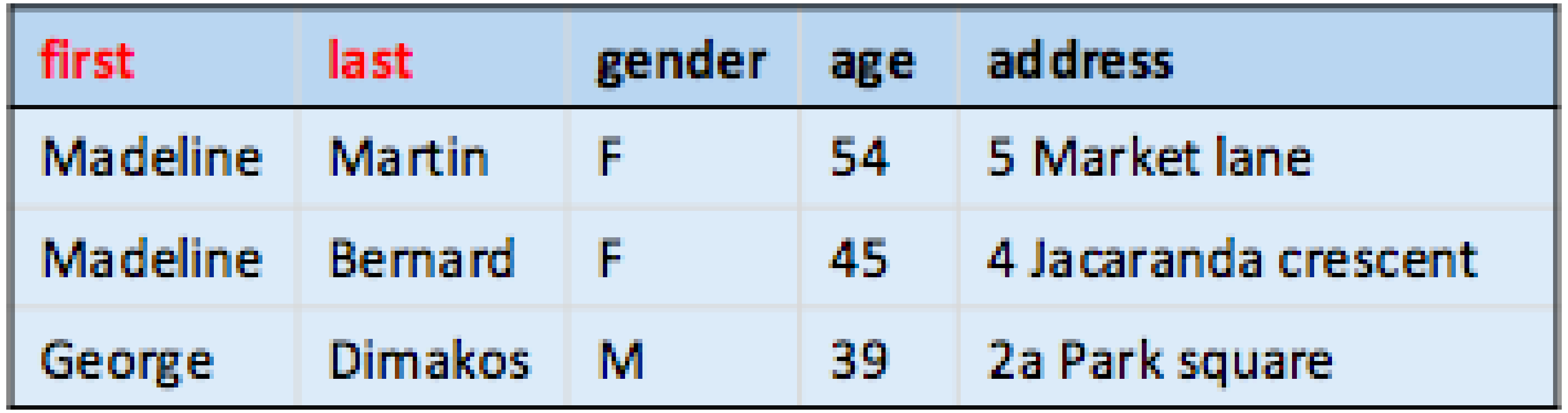
web_visits:

person	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

```
merge(customers, web_visits, by.x = "name", by.y = "person")
customers[web_visits, on = .(name = person)]
customers[web_visits, on = c("name" = "person")]
key <- c("name" = "person")
customers[web_visits, on = key]
```

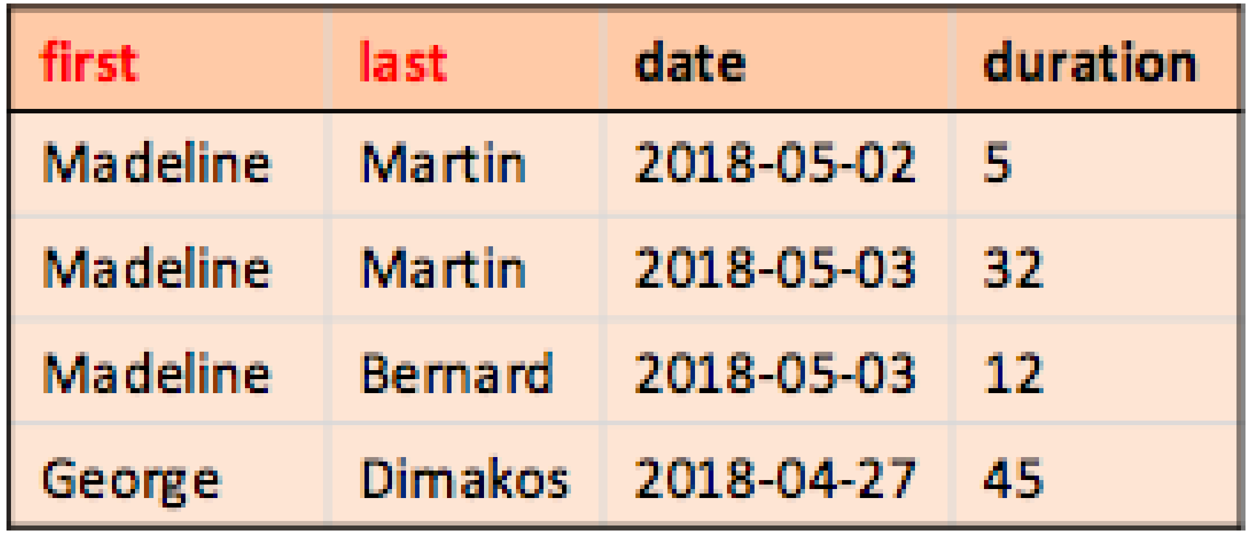
Multi-column keys

customers:



first	last	gender	age	address
Madeline	Martin	F	54	5 Market lane
Madeline	Bernard	F	45	4 Jacaranda crescent
George	Dimakos	M	39	2a Park square

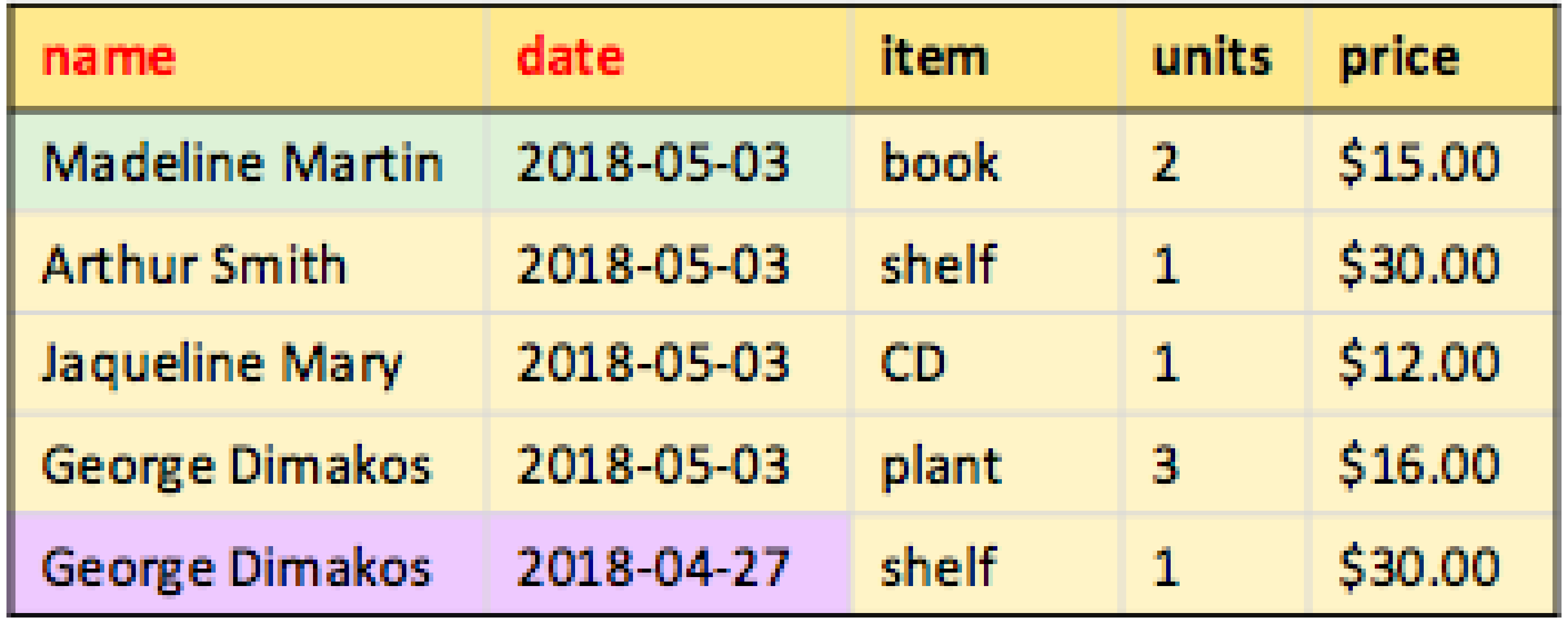
web_visits:



first	last	date	duration
Madeline	Martin	2018-05-02	5
Madeline	Martin	2018-05-03	32
Madeline	Bernard	2018-05-03	12
George	Dimakos	2018-04-27	45

Multi-column keys

purchases:



name	date	item	units	price
Madeline Martin	2018-05-03	book	2	$15.00
Arthur Smith	2018-05-03	shelf	1	$30.00
Jaqueline Mary	2018-05-03	CD	1	$12.00
George Dimakos	2018-05-03	plant	3	$16.00
George Dimakos	2018-04-27	shelf	1	$30.00

web_visits:

name	date	duration
Madeline Martin	2018-05-02	5
Madeline Martin	2018-05-03	32
Madeline Bernard	2018-05-03	12
George Dimakos	2018-04-27	45

Specifying multiple keys with merge()

```
merge(purchases, web_visits, by = c("name", "date"))
```

```
merge(purchases, web_visits,
      by.x = c("name", "date"),
      by.y = c("person", "date"))
```

Specifying multiple keys with the data.table syntax

```
purchases[web_visits, on = .(name, date)]
purchases[web_visits, on = c("name", "date")]
```

```
purchases[web_visits, on = .(name = person, date)]
purchases[web_visits, on = c("name" = "person", "date")]
```

Final Slide

JOINING DATA WITH DATA.TABLE IN R

Problem columns

JOINING DATA WITH DATA.TABLE IN R

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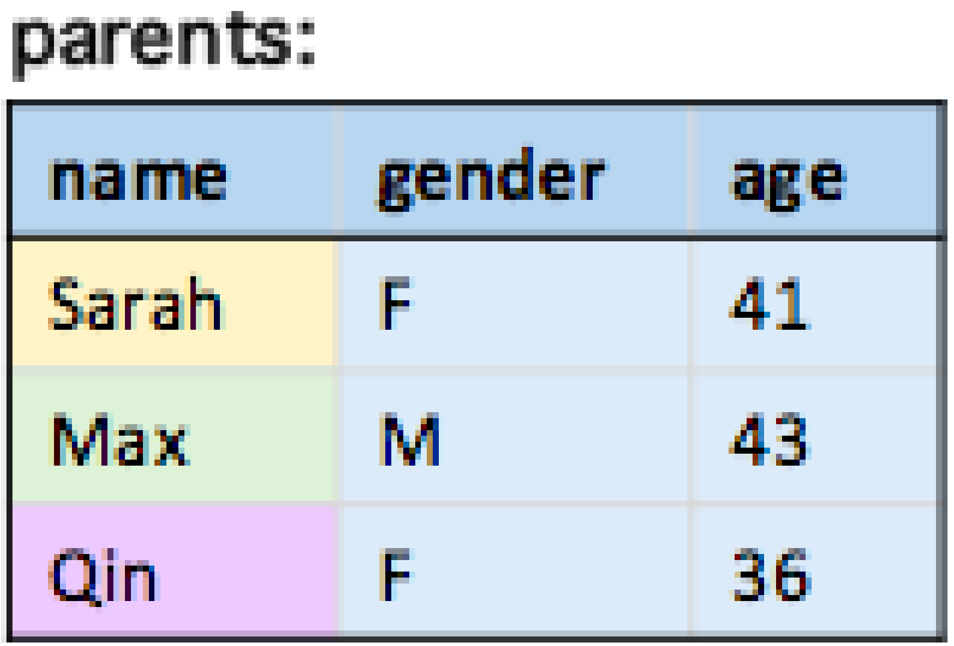
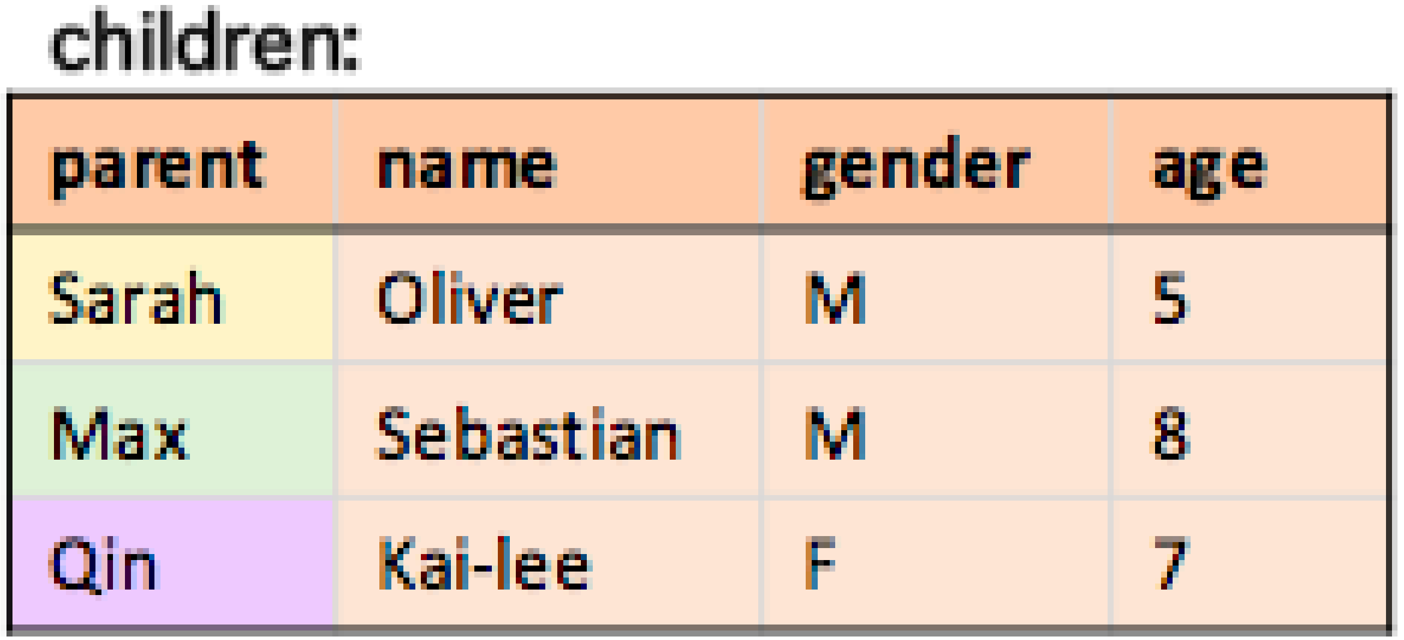
Common column names



parents:

name	gender	age
Sarah	F	41
Max	M	43
Qin	F	36



children:

parent	name	gender	age
Sarah	Oliver	M	5
Max	Sebastian	M	8
Qin	Kai-lee	F	7

Common column names

Using the `data.table` syntax

```
parents[children, on = .(name = parent)]
```

```
    name gender age    i.name i.gender i.age
1: Sarah      F  41    Oliver        M     5
2:    Max      M  43 Sebastian        M     8
3:    Qin      F  36   Kai-lee        F     7
```

Common column names with merge()

Using the `merge()` function

```
merge(x = children, y = parents, by.x = "parent", by.y = "name")
```

```
   parent      name gender.x age.x gender.y age.y
1:    Max Sebastian        M     8        M    43
2:    Qin   Kai-lee        F     7        F    36
3:  Sarah    Oliver        M     5        F    41
```

Adding context with your own suffixes

The `suffixes` argument can add useful context:

```r
merge(children, parents, by.x = "parent", by.y = "name",
      suffixes = c(".child", ".parent"))
```

```
   parent       name gender.child age.child gender.parent age.parent
1:    Max  Sebastian            M         8             M         43
2:    Qin    Kai-lee            F         7             F         36
3:  Sarah     Oliver            M         5             F         41
```

Renaming columns

Rename all columns using `setnames()`

```
setnames(parents, c("parent", "parent.gender", "parent.age"))
setnames(parents, old = c("gender", "age"),
         new = c("parent.gender", "parent.age"))
parents
```

```
   parent parent.gender parent.age
1:  Sarah             F         41
2:    Max             M         43
3:    Qin             F         36
```

Joining with `data.frames`

Join keys for `data.frames` may be in the rownames

```
parents
```

```
      gender age
Sarah      F  41
Max        M  43
Qin        F  36
```

```
parents <- as.data.table(parents, keep.rownames = "parent")
parents
```

```
   parent gender age
1:  Sarah      F  41
2:    Max      M  43
3:    Qin      F  36
```

Let's practice!

Duplicate matches

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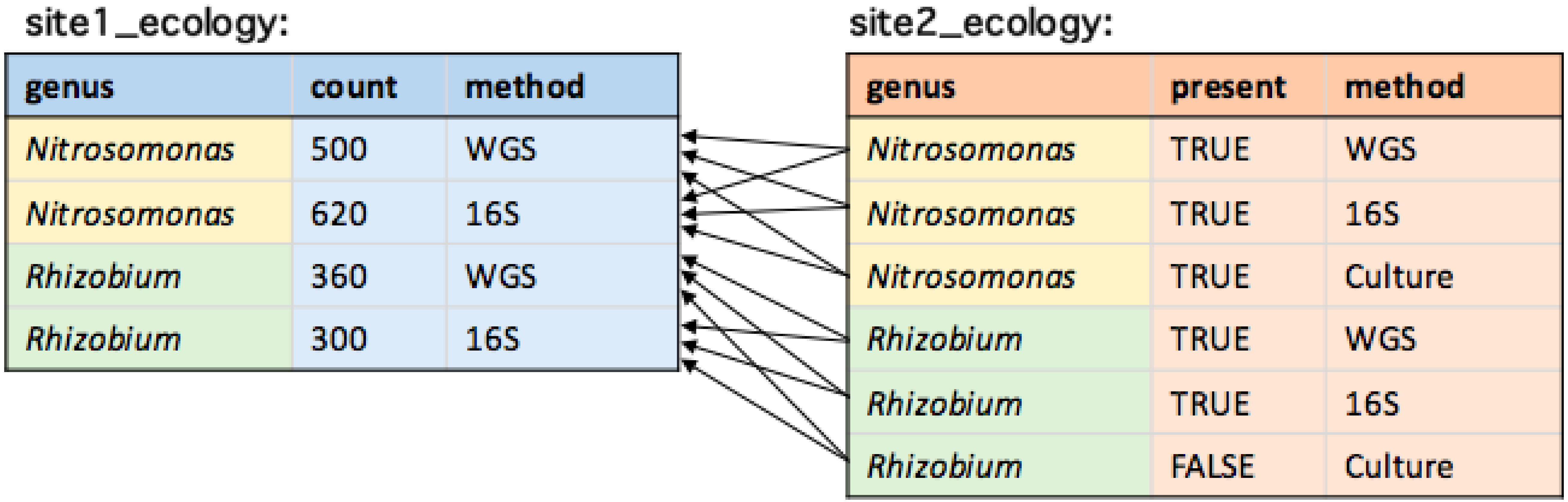
Join key duplicates

```r
# Which bacteria could be found at both sites using any method?
site1_ecology[site2_ecology, on = .(genus)]
```



site1_ecology:

genus	count	method
Nitrosomonas	500	WGS
Nitrosomonas	620	16S
Rhizobium	360	WGS
Rhizobium	300	16S

site2_ecology:

genus	present	method
Nitrosomonas	TRUE	WGS
Nitrosomonas	TRUE	16S
Nitrosomonas	TRUE	Culture
Rhizobium	TRUE	WGS
Rhizobium	TRUE	16S
Rhizobium	FALSE	Culture

Error from multiplicative matches

```
site1_ecology[site2_ecology, on = .(genus)]
```

```
Error in vecseq(f__, len__, if (allow.cartesian || notjoin ||
!anyDuplicated(f__,  :
  Join results in 12 rows; more than 10 = nrow(x)+nrow(i). Check for
  duplicate key values in i each of which join to the same group in x over
  and over again. If that's ok, try by=.EACHI to run j for each group to
  avoid the large allocation. If you are sure you wish to proceed, rerun
  with allow.cartesian=TRUE. Otherwise, please search for this error message
  in the FAQ, Wiki, Stack Overflow and data.table issue tracker for advice.
```

Allowing multiplicative matches

`allow.cartesian = TRUE` allows the join to proceed:

```
# data.table syntax
site1_ecology[site2_ecology, on = .(genus), allow.cartesian = TRUE]
```

```
# merge()
merge(site1_ecology, site2_ecology, by = "genus", allow.cartesian = TRUE)
```

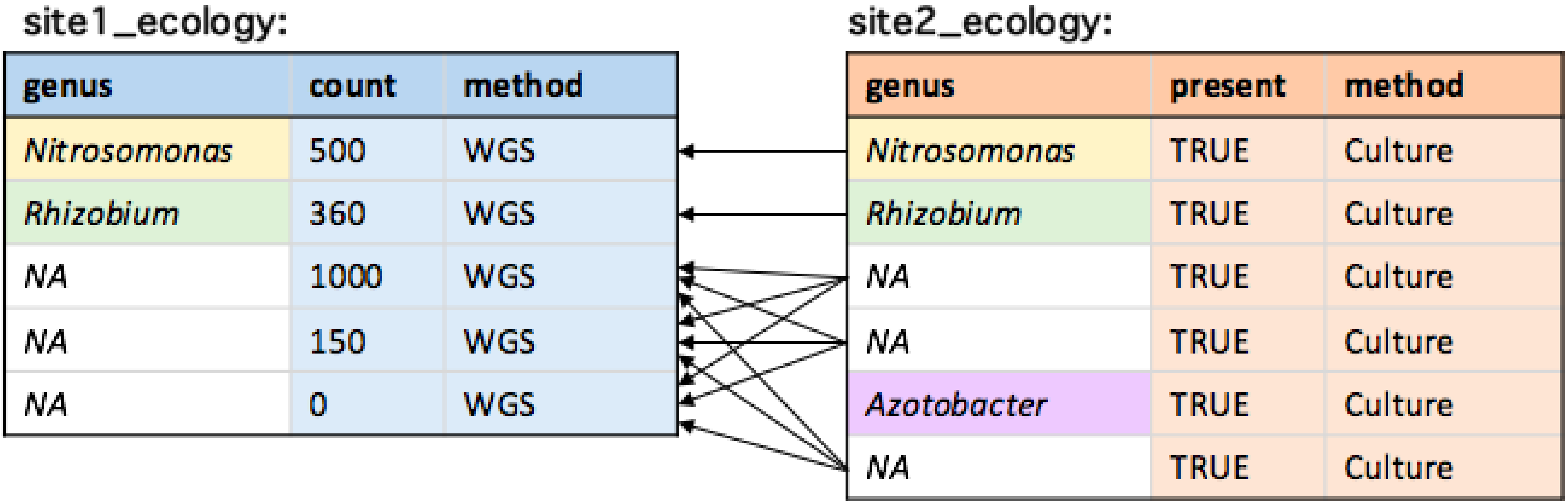
Allowing multiplicative matches

```
site1_ecology[site2_ecology, on = .(genus), allow.cartesian = TRUE]
```

```
           genus count method present i.method
 1: Nitrosomonas   500    WGS    TRUE      WGS
 2: Nitrosomonas   620    16S    TRUE      WGS
 3: Nitrosomonas   500    WGS    TRUE      16S
 4: Nitrosomonas   620    16S    TRUE      16S
 5: Nitrosomonas   500    WGS    TRUE  Culture
 6: Nitrosomonas   620    16S    TRUE  Culture
 7:    Rhizobium   360    WGS    TRUE      WGS
 8:    Rhizobium   300    16S    TRUE      WGS
 9:    Rhizobium   360    WGS    TRUE      16S
10:    Rhizobium   300    16S    TRUE      16S
11:    Rhizobium   360    WGS   FALSE  Culture
12:    Rhizobium   300    16S   FALSE  Culture
```

Missing values

Missing values (`NA`) will match all other missing values:



site1_ecology:

genus	count	method
Nitrosomonas	500	WGS
Rhizobium	360	WGS
NA	1000	WGS
NA	150	WGS
NA	0	WGS

site2_ecology:

genus	present	method
Nitrosomonas	TRUE	Culture
Rhizobium	TRUE	Culture
NA	TRUE	Culture
NA	TRUE	Culture
Azotobacter	TRUE	Culture
NA	TRUE	Culture

Filtering missing values

`!is.na()` can be used to filter rows with missing values

```
site1_ecology <- site1_ecology[!is.na(genus)]
site1_ecology
```

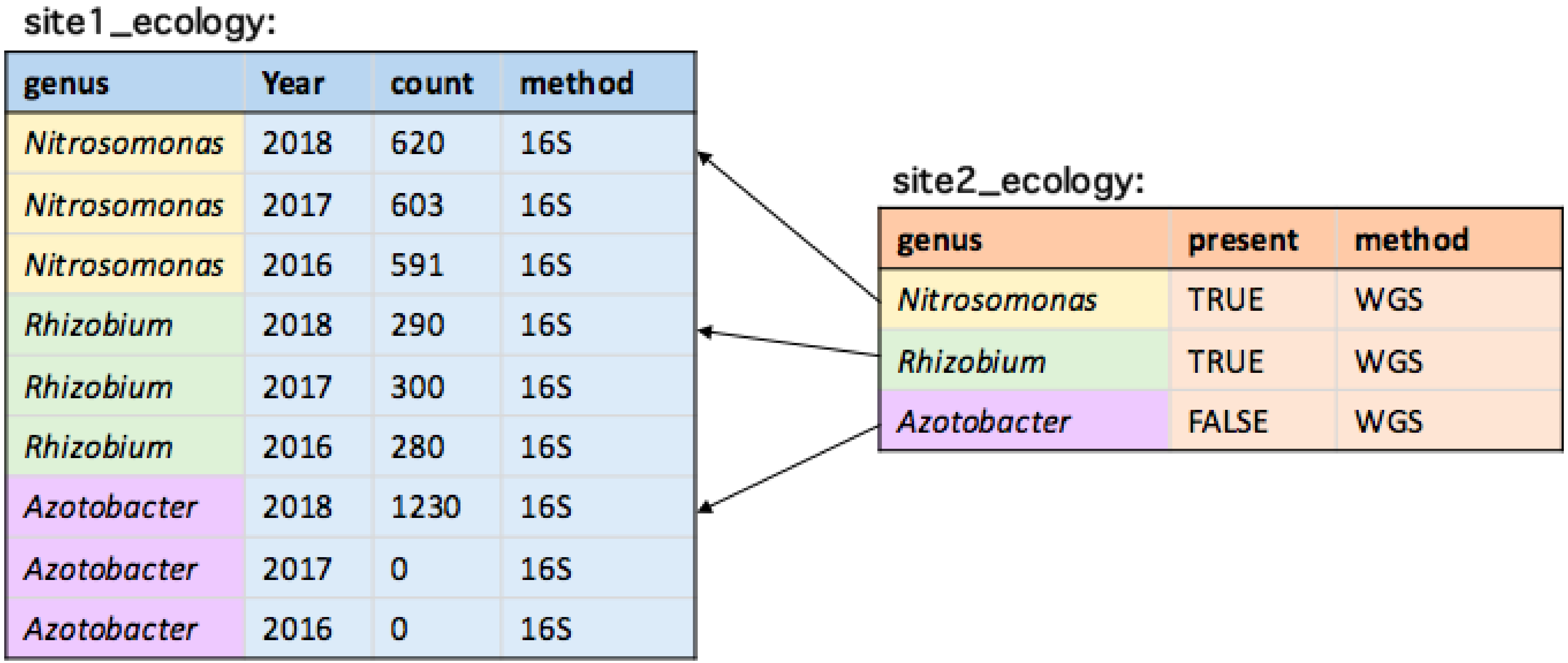
```
          genus count method
1: Nitrosomonas   500    WGS
2:    Rhizobium   360    WGS
```

```
site2_ecology <- site2_ecology[!is.na(genus)]
site2_ecology
```

```
          genus present  method
1: Nitrosomonas    TRUE Culture
2:    Rhizobium    TRUE Culture
3:  Azotobacter    TRUE Culture
```

Keeping only the first match

```
site1_ecology[site2_ecology, on = .(genus), mult = "first"]
```



site1_ecology:

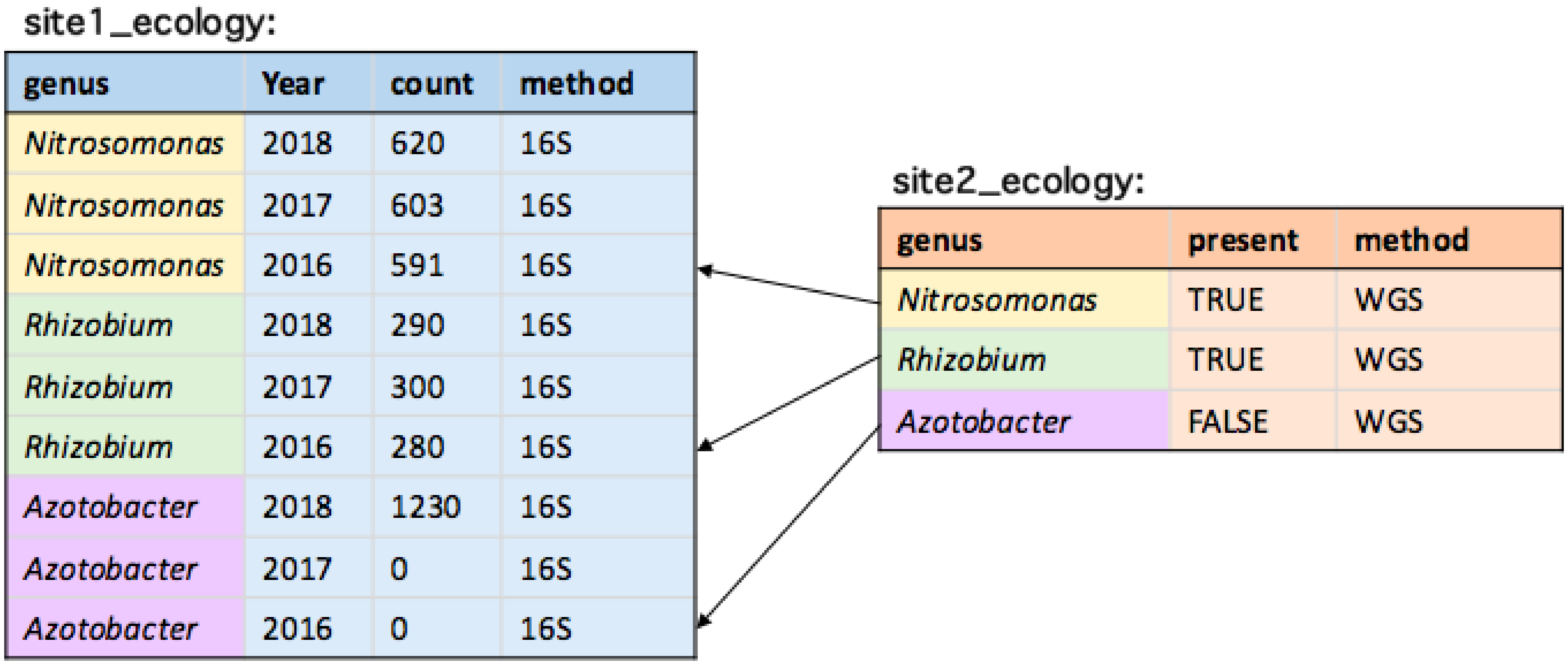
genus	Year	count	method
Nitrosomonas	2018	620	16S
Nitrosomonas	2017	603	16S
Nitrosomonas	2016	591	16S
Rhizobium	2018	290	16S
Rhizobium	2017	300	16S
Rhizobium	2016	280	16S
Azotobacter	2018	1230	16S
Azotobacter	2017	0	16S
Azotobacter	2016	0	16S

site2_ecology:

genus	present	method
Nitrosomonas	TRUE	WGS
Rhizobium	TRUE	WGS
Azotobacter	FALSE	WGS

Keeping only the last match

```
children[parents, on = .(parent = name), mult = "last"]
```



site1_ecology:

genus	Year	count	method
Nitrosomonas	2018	620	16S
Nitrosomonas	2017	603	16S
Nitrosomonas	2016	591	16S
Rhizobium	2018	290	16S
Rhizobium	2017	300	16S
Rhizobium	2016	280	16S
Azotobacter	2018	1230	16S
Azotobacter	2017	0	16S
Azotobacter	2016	0	16S

site2_ecology:

genus	present	method
Nitrosomonas	TRUE	WGS
Rhizobium	TRUE	WGS
Azotobacter	FALSE	WGS

Identifying and removing duplicates

`duplicated()` : what rows are duplicates?

`unique()` : filter a `data.table` to just unique rows

The duplicated() function

Using values in all columns:

```
duplicated(site1_ecology)
```

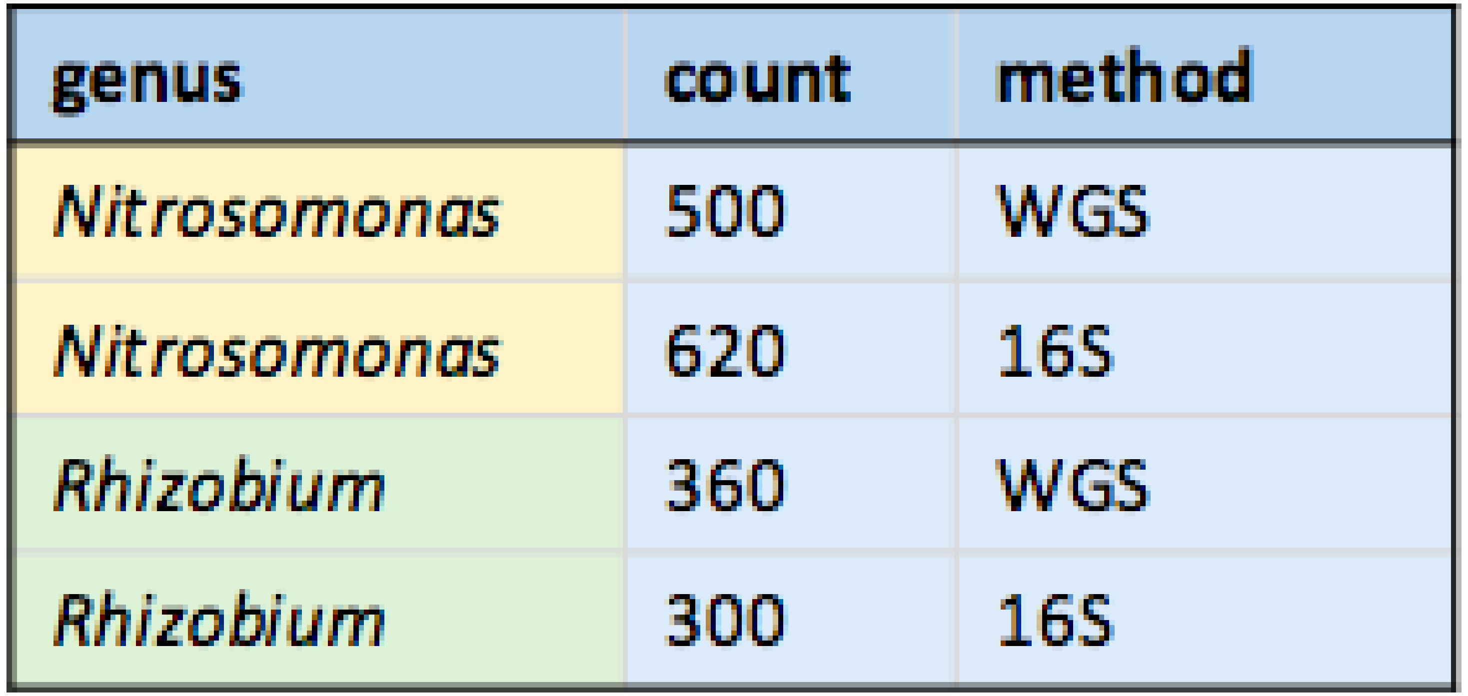
```
FALSE FALSE FALSE FALSE
```

Using values in a subset of columns:

```
duplicated(site1_ecology,
           by = "genus")
```

```
FALSE TRUE FALSE TRUE
```

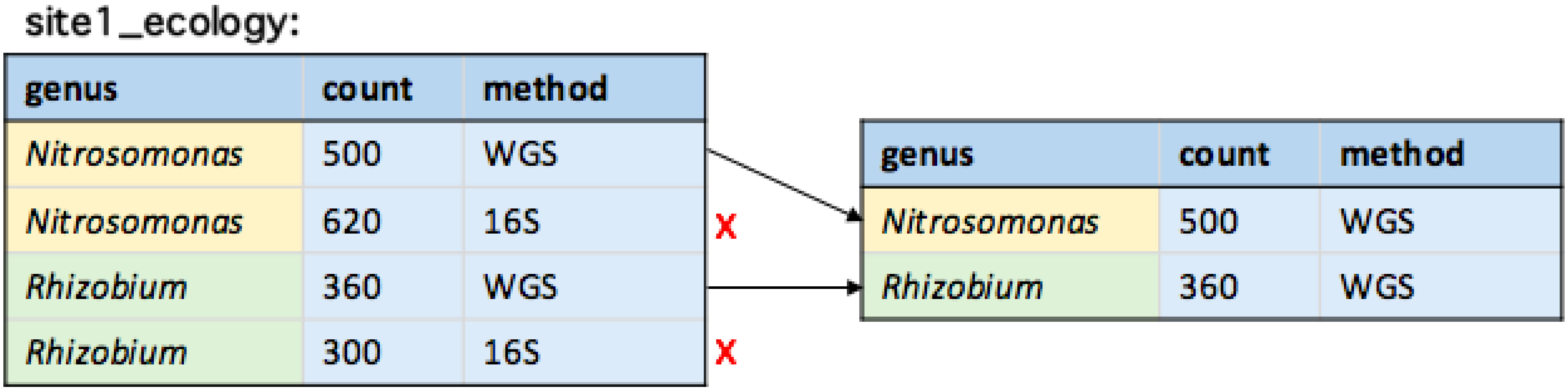
site1_ecology:



genus	count	method
Nitrosomonas	500	WGS
Nitrosomonas	620	16S
Rhizobium	360	WGS
Rhizobium	300	16S

The unique() function

```r
unique(site1_ecology, by = "genus")
```



site1_ecology:

genus	count	method
Nitrosomonas	500	WGS
Nitrosomonas	620	16S
Rhizobium	360	WGS
Rhizobium	300	16S

genus	count	method
Nitrosomonas	500	WGS
Rhizobium	360	WGS

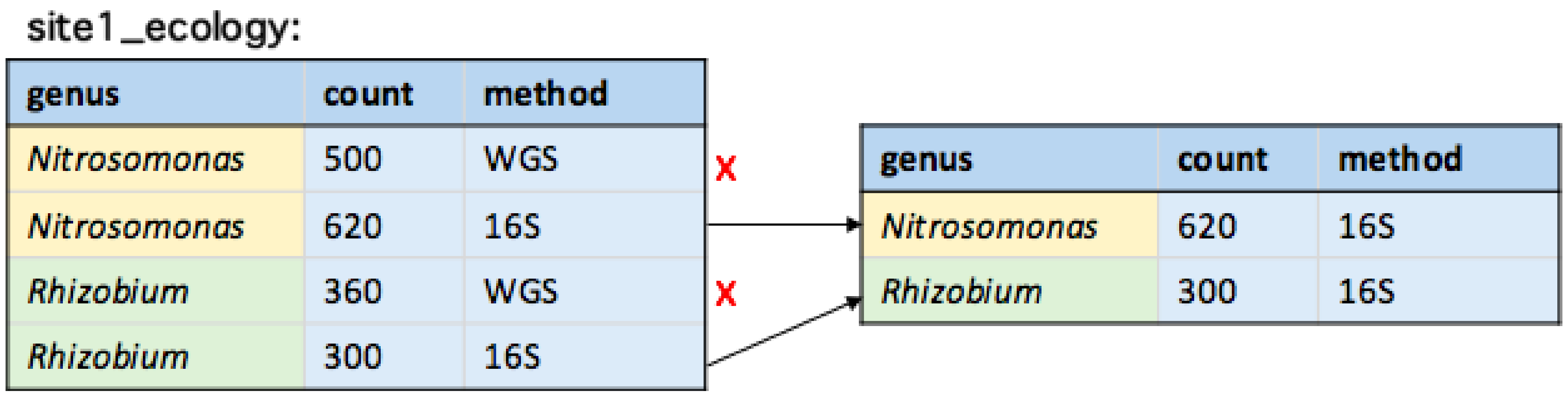
Changing the search order

`fromLast = TRUE` changes the direction of the search to start from the last row

```
duplicated(site1_ecology, by = "genus", fromLast = TRUE)
```

```
TRUE FALSE TRUE FALSE
```

```
unique(site1_ecology, by = "genus", fromLast = TRUE)
```



site1_ecology:

genus	count	method
Nitrosomonas	500	WGS
Nitrosomonas	620	16S
Rhizobium	360	WGS
Rhizobium	300	16S

genus	count	method
Nitrosomonas	620	16S
Rhizobium	300	16S

Let's practice!