ds4biomed

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Pre-Workshop Exercise

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Exercise 3

Using the same <code>ebola</code> dataset example from the previous exercise:

date <chr></chr>	da Cas	es_G	Guine - dbl		Case	_	oeria <dbl></dbl>
1/5/2015	289		277	6			NA
1/4/2015	288		277	5			NA
1/3/2015	287		276	9			8166
1/2/2015	286		N	4		ľ	8157
12/31/2014	284		273	0			8115
12/28/2014	281		270	6			8018
12/27/2014	280		269	5			NA
12/24/2014	277		263	0			7977
12/21/2014	273		259	7			NA
12/20/2014	272		257	1			7862
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- Tidy the dataset such that it looks like the below example
- Remember to drop missing values as the last step

date <chr></chr>	day country <dbl×chr></dbl×chr>	Ca <dbl></dbl>	Deaths <dbl></dbl>
1/5/2015	289 Guinea	2776	1786
1/5/2015	289 SierraLeone	10030	2977
1/4/2015	288 Guinea	2775	1781
1/4/2015	288 SierraLeone	9780	2943
1/3/2015	287 Guinea	2769	1767
1/3/2015	287 Liberia	8166	3496
1/3/2015	287 SierraLeone	9722	2915
1/2/2015	286 Liberia	8157	3496
12/31/2014	284 Guinea	2730	1739

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ds4biomed	dateday countryCaDeaths <chr><dbl><chr><dbl><dbl></dbl></dbl></chr></dbl></chr>				
	12/31/2014 284 Liberia 8115 3471				
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Exercise 1	R Code				
Exercise 2	<pre>1 ebola %>% 2() %>% 3 separate(name, into = c("case_death", "country")</pre>				
Exercise 3	4(names_from = case_death, values_from = values_from				
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