

# data cleaning principles

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These are slides for a talk for the csv,conf,v6 (<https://csvconf.com/>) on May 4–5, 2021.

Data analysts spend a lot of time organizing and cleaning data, but few of us have been trained to do so. Why is that?

Some say that data cleaning is difficult to generalize. But I think there are some general principles. Moreover, I think we have an important shared experience in data cleaning that we can commiserate about, and through which we can learn from each other.

Tidy data are all alike,  
but every messy dataset  
is messy in its own way.

— Hadley Wickham

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Hadley's talking more about data organization than data cleanliness. And his point is that if you make data tidy, it simplifies all the downstream analyses.

But **is** every messy dataset **uniquely** messy?

For sure, many my collaborators have shown impressive creativity in their approach to organizing and managing data. But we do see many of the same sorts of problems over and over.

If I clean up [Medicare] data ...  
does any of the knowledge I gain ...  
apply to the processing of RNA-seq data?

– Roger Peng

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In his discussion of David Donoho's paper about data science, Roger Peng wrote about how data cleaning is frustratingly difficult to generalize.

But my answer to his question is **absolutely!**

A person with experience cleaning one dataset has important experience to draw upon when moving to another dataset, even if it's of a totally different nature.

# Data Mishaps Night

Join us for the first inaugural Data Mishaps Night!  
We will feature a lineup of data mistake stories with  
a focus on the human aspect of data work and  
lessons learned the hard way.



Caitlin Hudon & Laura Ellis  
[dataMishapsNight.com](http://dataMishapsNight.com)

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In February, 2021, Caitlin Hudon and Laura Ellis organized a Friday evening conference where 16 people gave short presentations on data mishaps.

Many of the stories concerned mistakes in data cleaning, and these seemed to bring out a strong sense of shared experience. We have suffered and struggled through very similar data problems.

## Data cleaning

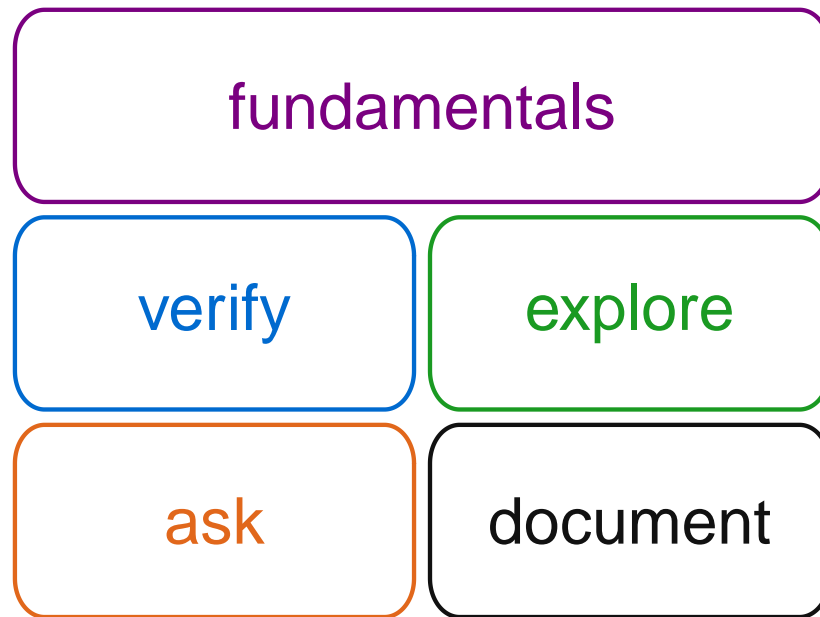
- ▶ tedious
- ▶ embarrassing
- ▶ needs context
- ▶ doesn't feel like progress
- ▶ requires creativity
- ▶ requires coding prowess
- ▶ source of most problems

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Really, I think we don't usually teach data cleaning because it's something we prefer to keep private.

We're shy about it.

And data cleaning code is our ugliest code.



I'm proposing a set of basic principles for data cleaning, and splitting them into five groups. There are some fundamental principles, followed by four basic ideas: verify things that you expect, explore to find further oddities, ask questions, and document what you've done.

## fundamentals

### 1. Don't clean data when you're tired or hungry.

(paraphrasing Ghazal Gulati)

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At her talk at the Data Mishaps night, Ghazal Gulati emphasized this point, of not cleaning data when you're tired or hungry.

Data cleaning requires considerable concentration, and you need to allow sufficient time to do the work. If you're in a hurry, you'll miss things.

## fundamentals

### 2. Don't trust anyone (even yourself)

“my motto is ‘trust no one’  
...except maybe @kwbroman?”

– Jenny Bryan

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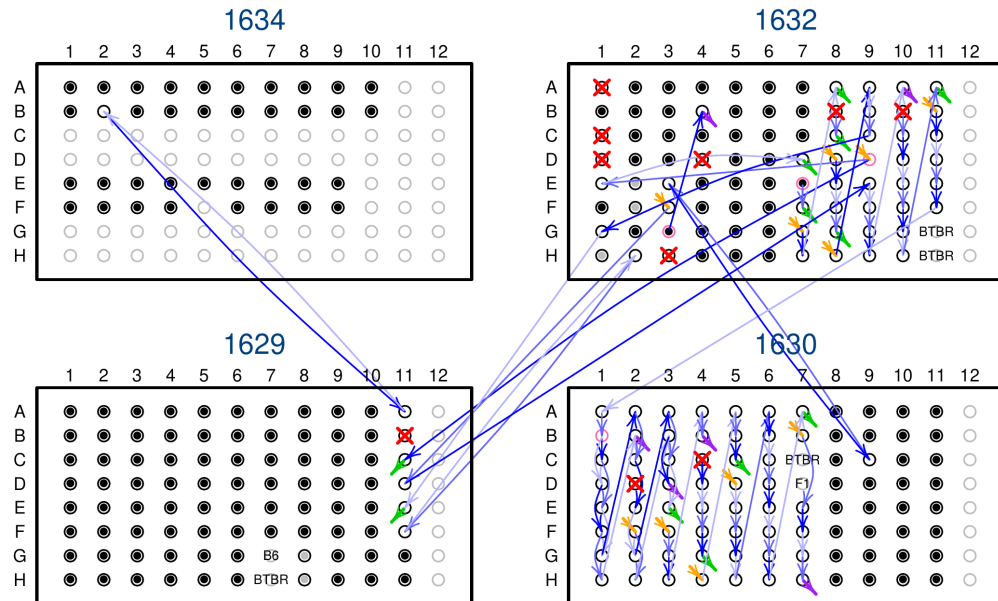
Next: don't trust anyone. Even if the initial data cleaning was done by someone you respect, you should double-check things that they may have missed. And data cleaning is an ongoing process.

Jenny Bryan's tweet is among the nicest things anyone has said about me.



## fundamentals

### 3. Think about what might have gone wrong and how it might be revealed



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Personally, I think this is the most important principle for data cleaning. It has been central in guiding my approach.

The figure here is an illustration of the most startlingly result I've had in data cleaning: a genetics project where 25% of the DNA samples had been mislabelled. The samples were arranged in wells in 8×12 plates; four of the six plates are shown here. The dots indicate the correct DNA was placed in the well, but the arrows point from where a sample should have been to where it actually was placed.

I ultimately came to this finding by thinking about what might have gone wrong in the project, checking for particularly problems, and then following the trail of evidence to this mess.

# fundamentals

## 4. Use care in merging

	A	B	C	D	E	F	G		
1	id	glucose.0	glucose.5	glucose.15	glucose.30	insulin.0	insulin.5		
2	DO-221	145.742786	206.452638	216.640608	299.55501	0.74455	2.0264		
3	DO-222								
4	DO-223								
5	DO-224								
6	DO-225								
7	DO-226								
8	DO-227								
9	DO-228								
10	DO-229								
11	DO-230								

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Many problems arise due to mistakes when merging data from multiple files. A common problem is a change in the data arrangement, such as in the order of columns.

Focus on the labels (which are more likely correct), rather than the position of variables in a file (which are more likely to change).

### 5. Dates & categories suck

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The fifth fundamental principle is that dates and categories suck. You'll expend an inordinate amount of time dealing with these: typos in category labels, different date formats, people who died a decade they were born or lived to be 150.

Just be glad if you're not dealing with time zones.

But you may be asking yourself, "How is this a principle."

Principle:

a fundamental truth that guides our thinking

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Yeah, are these principles? I was thinking the same thing. Was I drifting away from principles and more to just stuff to know or do?

This seems a pretty good definition, and is sufficiently broad to cover what I'm proposing, for the most part.

## fundamentals

### 5. Dates & categories suck

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So yeah, this counts as a principle.

Much of your pain will come from the dates and categorical data; you should be ready for that.

verify

## 6. Check that distinct things are distinct

	A	B	C	D	E	F	G
1	WiscID	ID	NEOID	Fem_CA	Fem_lmax	Fem_lmin	Fem_J
2	F2.C1W.F.1248	1248	NEO183	0.7524	0.1427	0.1006	0.2433
3	F2.C1W.M.1250	1250	NEO184	0.7669	0.1556	0.09652	0.2521
4	F2.C1W.F.1251	1251	NEO185	0.7613	0.1549	0.09659	0.2515
5	F2.C1W.F.1254	1254	NEO186	0.7475	0.1503	0.08603	0.2363
6	F2.C1W.M.1257	1257	NEO187	0.8197	0.1849	0.1056	0.2905
7	F2.__.F.715	715	NEO764	0.6017	0.09662	0.05969	0.1563
8	F2.__.F.751	751	NEO765	0.7273	0.1304	0.08735	0.2178
9	F2.__.F.1251	1251	NEO766	0.6675	0.1157	0.07814	0.1938
10	F2.__.M.1340	1340	NEO768	0.6656	0.1387	0.08122	0.2199
11	F2.C1W.M.739	739	NEO779	0.9336	0.2828	0.1628	0.4456

verify

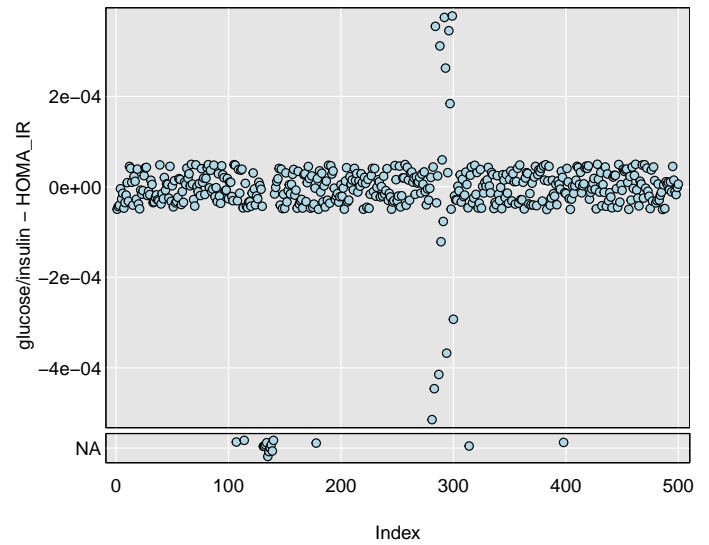
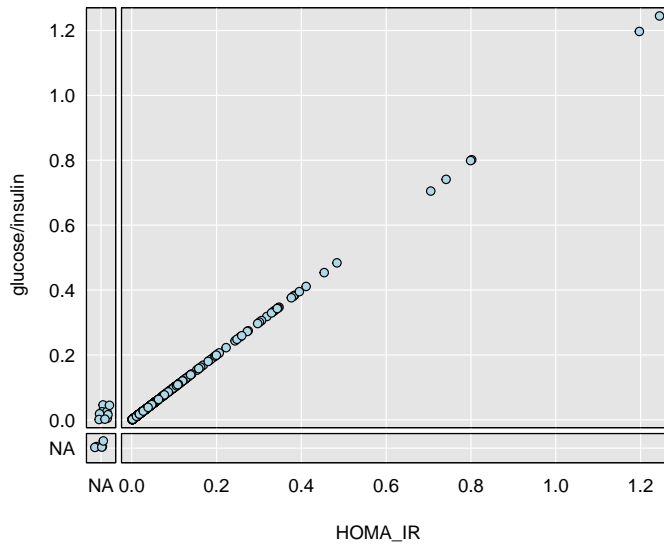
## 7. Check that matching things match

	A	B	C	D
1	id	sex	n_gen	age_days
2	F20.25	M	20	75
3	F21.30	M	21	75
4	F21.68	M	21	71
5	F22.52	M	22	73
6	F21.71	F	22	63
7	F22.116	F	22	57
8	F21.F20.9.M5	M	20	82
9	F21.F20.18.M5	M	20	77
10	F20.26	M	20	75
11	F21.62	M	21	72

	A	B	C	D
1	id	sex	age_at_dosing	n_gen
2	F22.69	F	67	22
3	F22.106	F	69	22
4	F22.70	F	67	22
5	F22.107	F	69	22
6	F21.71	F	65	21
7	F22.116	F	62	22
8	F22.73	F	65	22
9	F22.117	F	62	22
10	F21.108	F	62	21
11	F22.118	F	59	22

verify

## 8. Check calculations



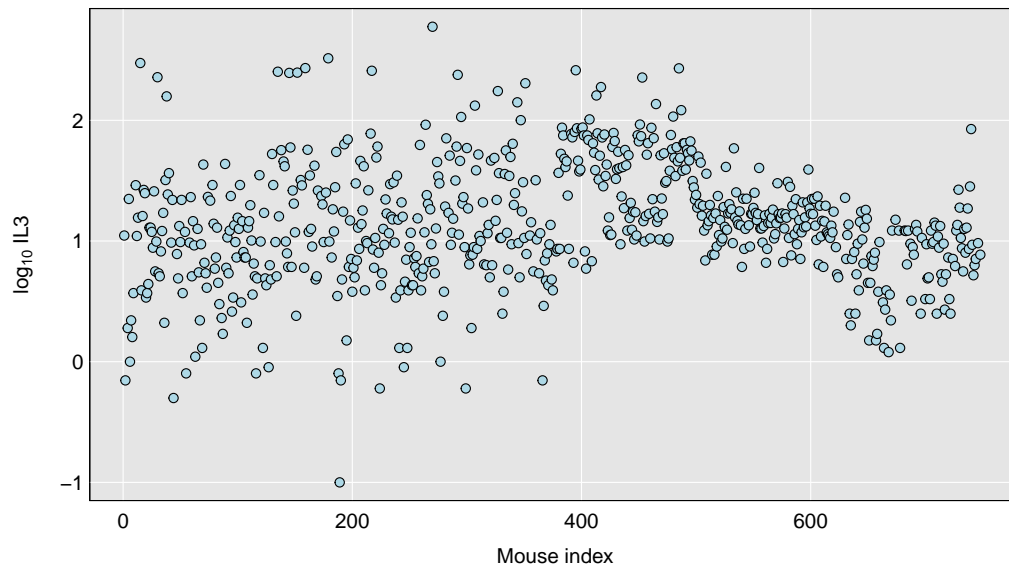


verify

9. Look for other instances of a problem

explore

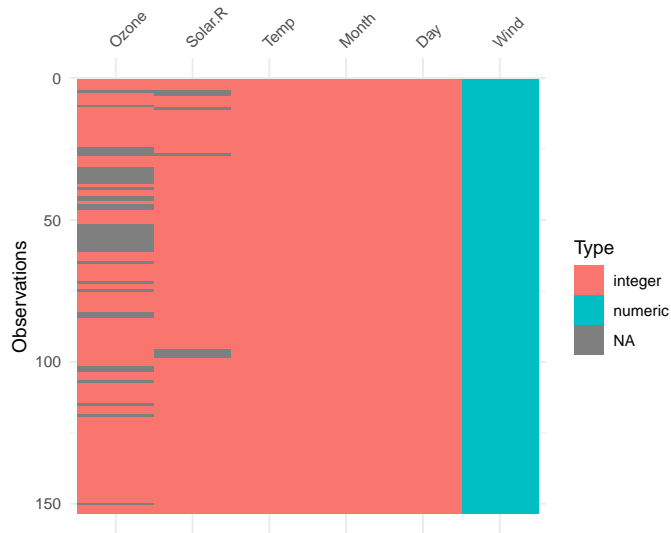
10. Make lots of plots



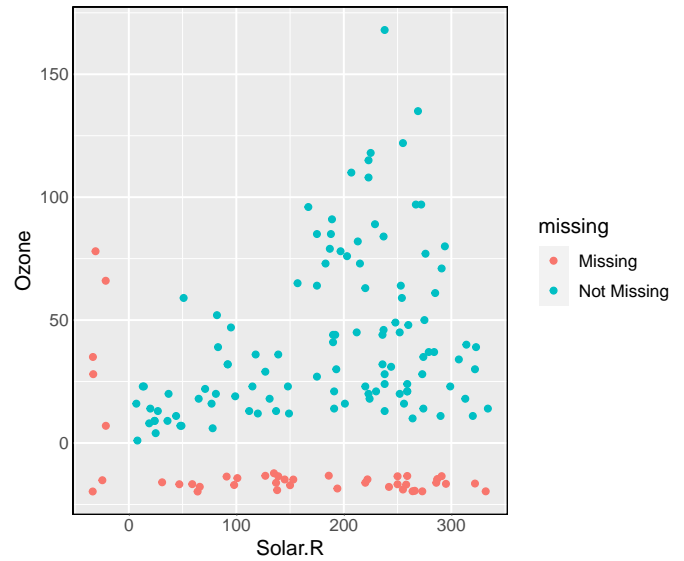
# explore

## 11. Look at missing value patterns

{visdat}



{naniar}



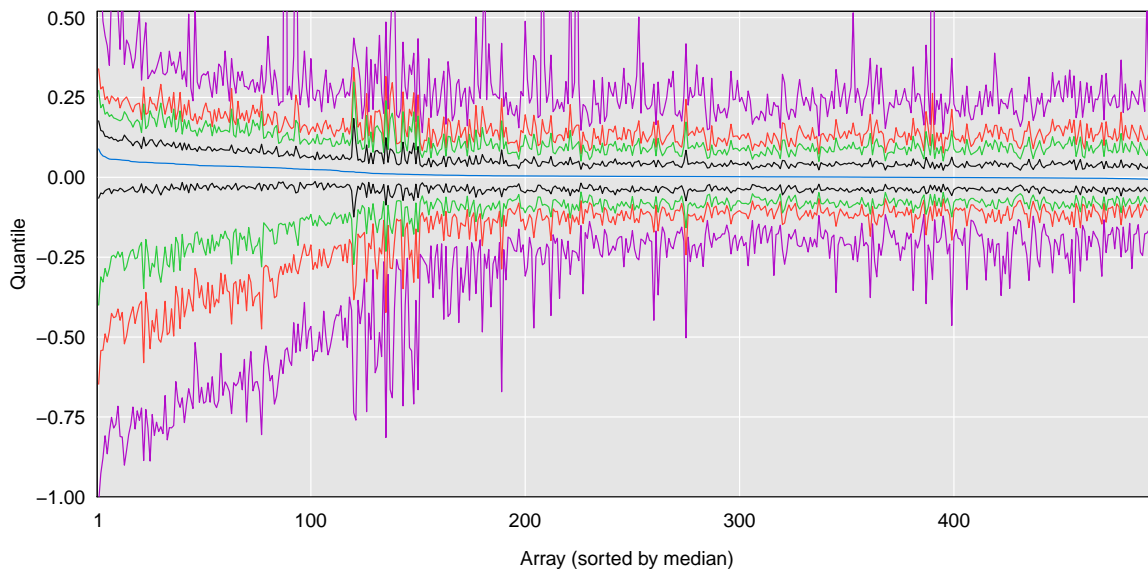
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visdat: <https://docs.ropensci.org/visdat/>

naniar: <http://naniar.njtierney.com/>

## explore

### 12. With massive data, make more plots not fewer



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With large-scale datasets, it can be hard to make the sort of exploratory plots that you'd typically make. With oodles of data, you'd think you'd be looking at oodles of plots, but there's a tendency to give up and not look at any.

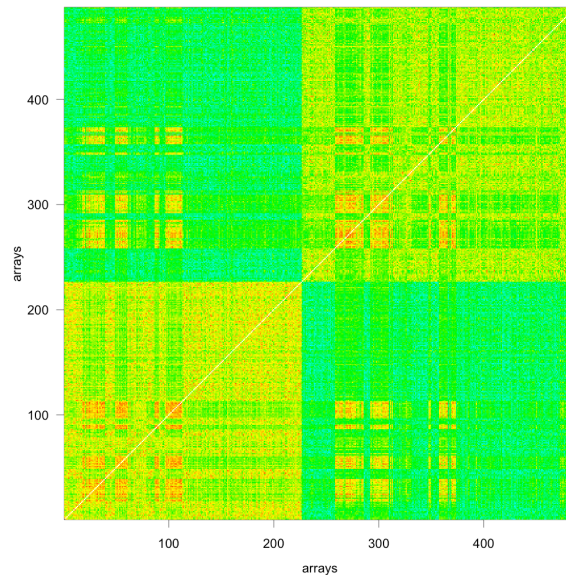
It's hard to look at 500 histograms, but it can be done. Superimpose a bunch of density estimates, maybe highlighting some portion of them. You can also pull out a couple of summary statistics, such as the median and inter-quartile range.

Or here I'm looking at the equivalent of 500 boxplots. I sorted a set of gene expression microarrays by their median, and then plotted the median in blue, the 25th and 75th percentile in black, the 10th and 90th in green, 5th and 95th in red, and 1st and 99th in purple.

With these data, it became apparent that there were 120 badly behaved arrays, with median shifted to the right and with a long left tail.

## explore

### 13. Follow up all artifacts



[kbroman.org/blog/2012/04/25/microarrays-suck](http://kbroman.org/blog/2012/04/25/microarrays-suck)

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Wow the clash of those colors is particularly bad.

This is a heat map of the correlation matrix for a set of gene expression microarrays. The plaid pattern was a shock to me, and was caused by a set of bad arrays that we hadn't noticed previously.

My point here is simply to follow up all artifacts.

If you see something weird, follow through and try to figure out the underlying cause. It could be an error, or a set of bad assays, or it could be the most interesting finding in the study.

ask

- 14. Ask questions
- 15. Ask for the primary data
- 16. Ask for metadata
- 17. Ask why data are missing

## document

- 18. Create checklists & pipelines
- 19. Document not just what but why
- 20. Expect to recheck

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3. Think about what might have gone wrong
4. Use care in merging
5. Dates & categories suck

## verify

6. Distinct things are distinct
7. Matching things match
8. Check calculations
9. Look for other instances

## explore

10. Make lots of plots
11. Look at missing value patterns
12. With big data make more plots
13. Follow up all artifacts

## ask

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In summary...



Slides: [kbroman.org/Talk\\_DataCleaning](http://kbroman.org/Talk_DataCleaning)



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