R₀ figure for SARS-CoV-2 Random Walk Epidemiological Model

Andrew Chu¹, Greg Huber¹, Aaron McGeever¹, Boris Veytsman², and David Yllanes¹

ABSTRACT

Here we generate figures for the random walkers paper.

Setting things up:

Reading the data:

```
data <- read_csv("../data/R0griddata.csv.gz")</pre>
## Parsed with column specification:
## cols(
## p = col_double(),
## tau = col_double(),
## r0 = col_double()
## )
data
## # A tibble: 340 x 3
## p tau r0
## <dbl> <dbl> <dbl>
     p tau r0
## 1 0.1 1 0.101
## 2 0.2
                1 0.199
## 2 0.2 1 0.199
## 3 0.3 1 0.3
## 4 0.4 1 0.399
## 5 0.5 1 0.501
## 6 0.6 1 0.601
```

 ¹Chan Zuckerberg Biohub, 499 Illinois Street, San Francisco, CA 94158, USA
 ²Chan Zuckerberg Initiative, 601 Marshall St, Redwood City, CA 94063, USA

```
## 7 0.7 1 0.701

## 8 0.8 1 0.8

## 9 0.9 1 0.898

## 10 1 1 0.999

## # ... with 330 more rows
```

First, naïve prediction

```
data <- data %>% mutate(naive=p*tau)
```

Now, the theoretical prediction. Let us use zero adjustable parameters, taking c_2 from the structure factor and assuming $q_0 = 1$:

```
ggplot(data) + geom_point(aes(prediction,
    r0, color=as.factor(p))) +
    xlim(0,100) + ylim(0,100) +
    coord_fixed(ratio=1) +
    facet_wrap(~type, nrow=1) +
    geom_abline(intercept=0, slope=1) +
    xlab("$R_0^{\\text{(predicted)}}$") +
    ylab("$R_0^{\\text{(simulated)}}$") +
    labs(color="$p$") + coord_fixed()
```

Coordinate system already present. Adding new coordinate system, which will replace the existing one.

