Отчет по лабораторной работе №4

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1 Цель работы

Целью лабораторной работы является изучение реализации эпидемиологической модели SIR в агентном подходе, исследование влияния параметров на динамику распространения инфекции, освоение литературного программирования с использованием пакета Literate.jl, а также выполнение дополнительных вычислительных экспериментов, связанных с порогом эпидемии, гетерогенностью, миграцией, карантинными мерами и оптимизацией параметров модели.

2 Постановка задачи

В ходе выполнения лабораторной работы требовалось:

1. реализовать базовую модель SIR в агентном подходе;
2. выполнить запуск скриптов в обычном формате;
3. оформить решения в literate-стиле;
4. сгенерировать notebook и документацию Quarto;
5. выполнить параметрические исследования;
6. проанализировать влияние миграции;
7. исследовать эффекты карантинных мер;
8. решить задачу оптимизации параметров;
9. оформить результаты в виде отчёта.

3 Теоретические сведения

3.1 Агентное моделирование

Агентное моделирование представляет систему как совокупность взаимодействующих агентов. Каждый агент описывается собственным состоянием и набором правил поведения. Глобальная динамика системы формируется как результат большого числа локальных взаимодействий.

3.2 Модель SIR

Модель SIR описывает распространение инфекционного заболевания через три состояния агента:

- S — восприимчивый;
- I — инфицированный;
- R — выздоровевший.

В агентной постановке каждый человек задаётся отдельным агентом. В рассматриваемой лабораторной работе учитываются заражение, выздоровление, повторное заражение, смертность и перемещение агентов между городами.

4 Выполнение работы

4.1 Инициализация проекта

На первом этапе была выполнена активация проекта, проверка установленных библиотек Julia и подготовка первого рабочего файла.

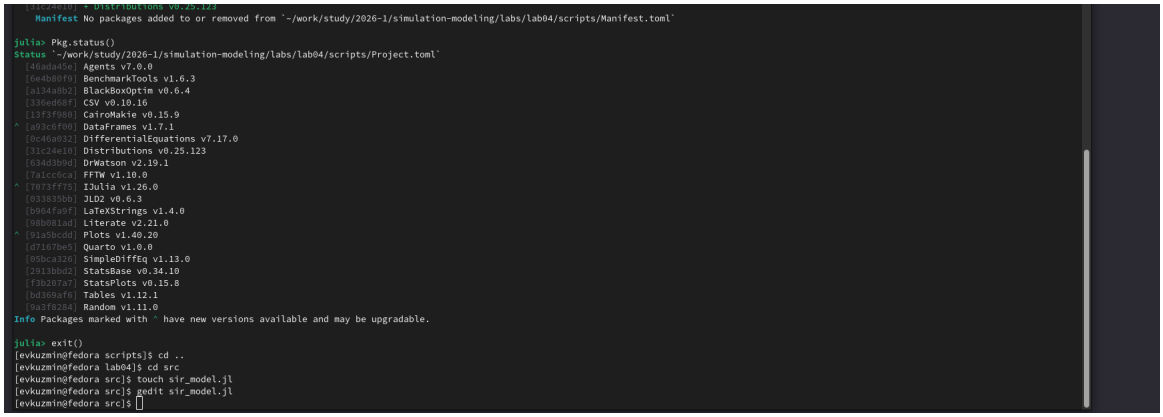

Рисунок 4.1: Проверка установленных пакетов Julia и создание первого файла

На рисунке показан этап инициализации проекта. Видно, что окружение Julia активировано корректно и доступны необходимые библиотеки для выполнения лабораторной работы.

4.2 Базовый скрипт модели SIR

4.2.1 Обычная версия

Для начала была подготовлена и выполнена обычная версия первого скрипта, реализующего базовую динамику модели SIR.

Листинг 4.1. Обычная версия базового скрипта sir_run_basic.jl

```
using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots
using JLD2

include(srcdir("sir_model.jl"))

# □□□□□□□□□ □□□□□□□□□□□□
params = Dict(
    :Ns => [1000, 1000, 1000],
    :□_und => [0.5, 0.5, 0.5],
    :□_det => [0.05, 0.05, 0.05],
    :infection_period => 14,
    :detection_time => 7,
    :death_rate => 0.02,
    :reinfection_probability => 0.1,
    :Is => [0, 0, 1],
    :seed => 42,
    :n_steps => 100,
)
```

```julia
# □□□□□□□□□□□□□ □□□□□□
model = initialize_sir(; params...)

# □□□□□□□□□□ □□□□□□□□ □□□ □□□□□□□□ □□□□□□
times = Int[]
S_vals = Int[]
I_vals = Int[]
R_vals = Int[]
total_vals = Int[]

# □□□□□□ □□□□□□□□□ □□□□□□□
for step = 1:params[:n_steps]
    Agents.step!(model, 1)
    push!(times, step)
    push!(S_vals, susceptible_count(model))
    push!(I_vals, infected_count(model))
    push!(R_vals, recovered_count(model))
    push!(total_vals, total_count(model))
end

# □□□□□□□ DataFrame □□□ □□□□□□□□ (□□□□□□□□□□□)
agent_df = DataFrame(
    time = times,
    susceptible = S_vals,
    infected = I_vals,
    recovered = R_vals,
)
```

```
model_df = DataFrame(
    time = times,
    total = total_vals,
)

# □□□□□□□□□□□□
plot(
    agent_df.time,
    agent_df.susceptible,
    label = "□□□□□□□□□□□□□",
    xlabel = "□□□",
    ylabel = "□□□□□□□□□□",
)
plot!(agent_df.time, agent_df.infected, label = "□□□□□□□□□□□□□□")
plot!(agent_df.time, agent_df.recovered, label = "□□□□□□□□□□□□□")
plot!(agent_df.time, model_df.total, label = "□□□□□ (□□□□□□□ □□□□□□□)",

savefig(plotsdir("sir_basic_dynamics.png"))

# □□□□□□□□□□ □□□□□□
@save datadir("sir_basic_agent.jld2") agent_df
@save datadir("sir_basic_model.jld2") model_df
```

4.2.2 Выполнение и генерация literate-версии

После запуска обычной версии была сформирована literate-версия и сгенерированы производные файлы: чистый код, notebook и Quarto-документация.

Рисунок 4.2: Выполнение первого скрипта, создание literate-версии и генерация необходимых файлов

На рисунке показан этап выполнения первого скрипта и генерации literate-артефактов. Также видна проверка того, что необходимые файлы были созданы.

4.2.3 Notebook literate-версии первого скрипта

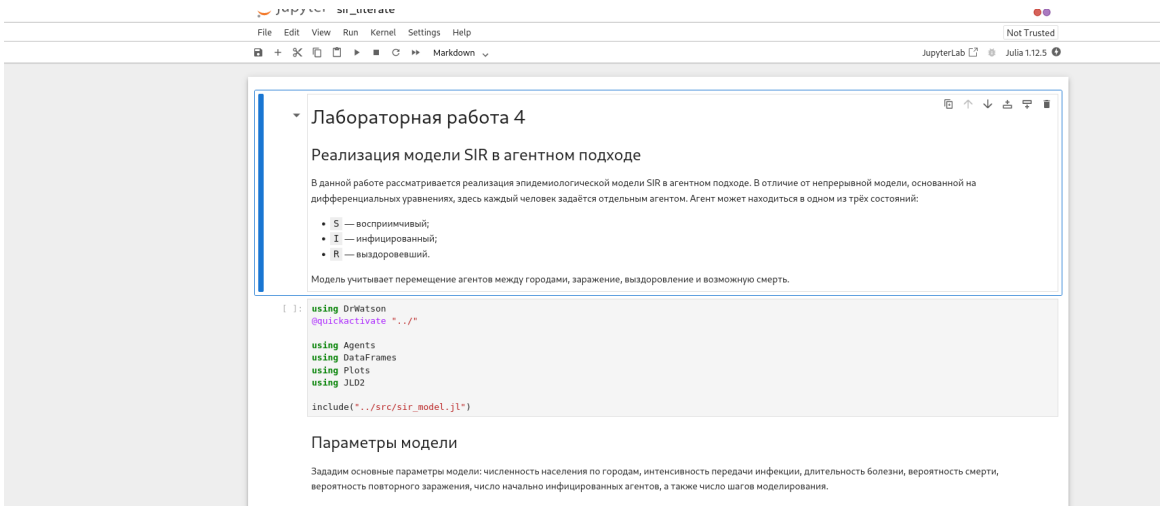

Рисунок 4.3: Notebook literate-версии первого скрипта

На рисунке представлен notebook, полученный из literate-версии первого скрипта. Это подтверждает корректность преобразования исходного файла в

формат документации.

4.2.4 Результат выполнения базовой модели

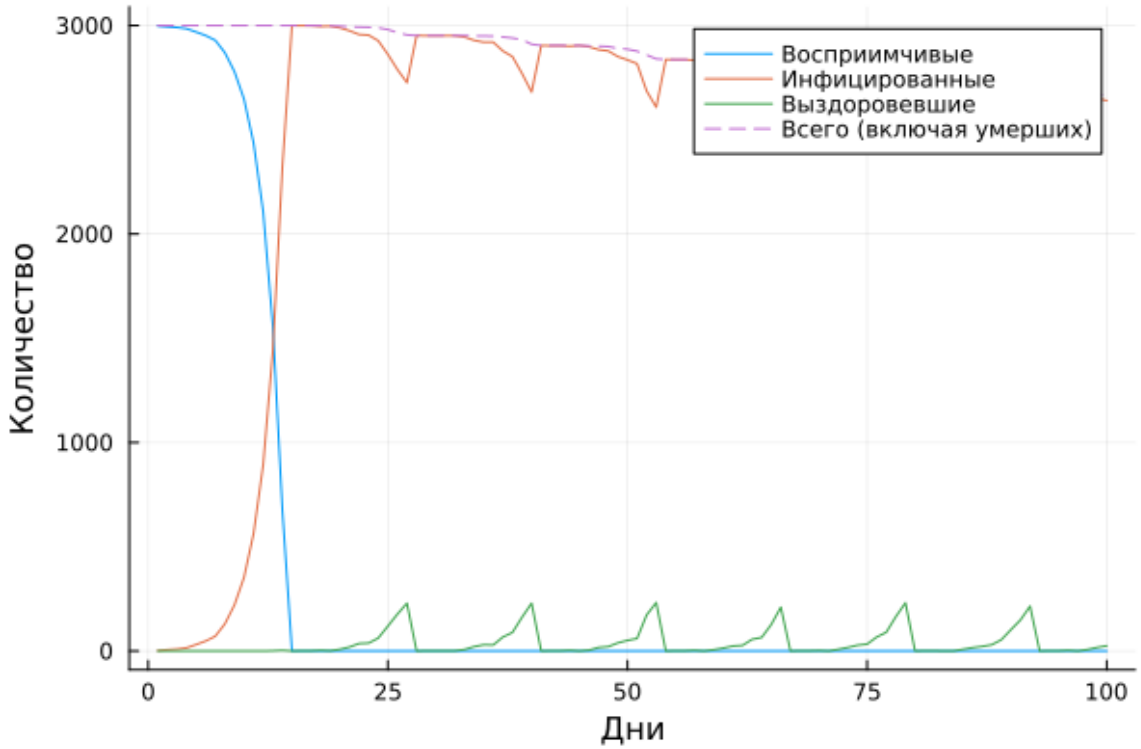

Рисунок 4.4: График динамики базовой модели SIR

На рисунке представлена динамика числа восприимчивых, инфицированных и выздоровевших агентов в базовой модели. В начале моделирования число инфицированных растёт, затем после достижения максимума начинает уменьшаться. Одновременно сокращается число восприимчивых агентов и увеличивается число выздоровевших, что соответствует классической интерпретации модели SIR.

4.2.5 Literate-версия базового скрипта

Листинг 4.2. Literate-версия базового скрипта sir_literate.jl

```
# # [illegible] 4
# ## [illegible] SIR [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] SIR
# [illegible] [illegible]. [illegible] [illegible] [illegible], [illegible] [illegible]
# [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]:
#
# - `S` — [illegible];
# - `I` — [illegible];
# - `R` — [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible], [illegible],
# [illegible] [illegible] [illegible].

using DrWatson
@quickactivate "../"

using Agents
using DataFrames
using Plots
using JLD2

include("../src/sir_model.jl")
```

```
# ## [redacted]
#
# [redacted]: [redacted] [redacted] [redacted],
# [redacted] [redacted], [redacted], [redacted], [redacted],
# [redacted] [redacted] [redacted], [redacted] [redacted] [redacted],
# [redacted] [redacted] [redacted] [redacted].

params = Dict(
    :Ns => [1000, 1000, 1000],
    :[redacted]_und => [0.5, 0.5, 0.5],
    :[redacted]_det => [0.05, 0.05, 0.05],
    :infection_period => 14,
    :detection_time => 7,
    :death_rate => 0.02,
    :reinfection_probability => 0.1,
    :Is => [0, 0, 1],
    :seed => 42,
    :n_steps => 100,
)

# ## [redacted]
#
# [redacted] [redacted] [redacted] [redacted] [redacted].

model = initialize_sir(; params...)

# ## [redacted] [redacted] [redacted] [redacted]
#
```

```
# □□ □□□□□□ □□□□ □□□□□□□□□□□□□ □□□□□ □□□□□□□□□:
#
# - □□□□□ □□□□;
# - □□□□□ □□□□□□□□□□□□□;
# - □□□□□ □□□□□□□□□□□□□□;
# - □□□□□ □□□□□□□□□□□□□;
# - □□□□□ □□□□□ □□□□□□□.

times = Int[]
S_vals = Int[]
I_vals = Int[]
R_vals = Int[]
total_vals = Int[]

# ## □□□□□□□□□□ □□□□□□□□□□□□□
#
# □□□□□□□□ □□□□□□ □□ □□□□□□□□ □□□□□ □□□□□ □ □□ □□□□□□ □□□□ □□□□□□□□ □□□□□□□
# □□□□□□□□ □□□□□□□□ □□□□□□□□□□□□□.

for step = 1:params[:n_steps]
    Agents.step!(model, 1)
    push!(times, step)
    push!(S_vals, susceptible_count(model))
    push!(I_vals, infected_count(model))
    push!(R_vals, recovered_count(model))
    push!(total_vals, total_count(model))
end
```

```
# ## □□□□□□□□□□□□ □□□□□□ □□□□□□□□□□□
#
# □□□ □□□□□□□□ □□□□□□□□□□□ □□□□□□□ □□□□□□□ □□□□□□□□□□□ □□□□□□ □ □□□□ □□□□□□.

agent_df = DataFrame(
    time = times,
    susceptible = S_vals,
    infected = I_vals,
    recovered = R_vals,
)

model_df = DataFrame(
    time = times,
    total = total_vals,
)

# ## □□□□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□ □□□□□□ □□□□□□□□□ □□□□□□□□□□□ □□□□□ □□ □□□□□□□.

plot(
    agent_df.time,
    agent_df.susceptible,
    label = "□□□□□□□□□□□□□□",
    xlabel = "□□□",
    ylabel = "□□□□□□□□□□",
)
plot!(agent_df.time, agent_df.infected, label = "□□□□□□□□□□□□□□□")
```

```
plot!(agent_df.time, agent_df.recovered, label = "[redacted]")
plot!(agent_df.time, model_df.total, label = "[redacted] ([redacted] [redacted])",

savefig(plotsdir("sir_basic_dynamics_literate.png"))

# ## [redacted] [redacted]
#
# [redacted] [redacted] [redacted] [redacted] [redacted] JLD2.

@save datadir("sir_basic_agent_literate.jld2") agent_df
@save datadir("sir_basic_model_literate.jld2") model_df

# ## [redacted]
#
# [redacted] [redacted] [redacted] [redacted] [redacted] [redacted] [redacted]
# [redacted], [redacted] [redacted] [redacted], [redacted] [redacted]
# [redacted] [redacted] [redacted] [redacted].
```

4.3 Параметризованная версия базового скрипта

Следующим этапом была подготовлена параметризованная literate-версия первого скрипта.

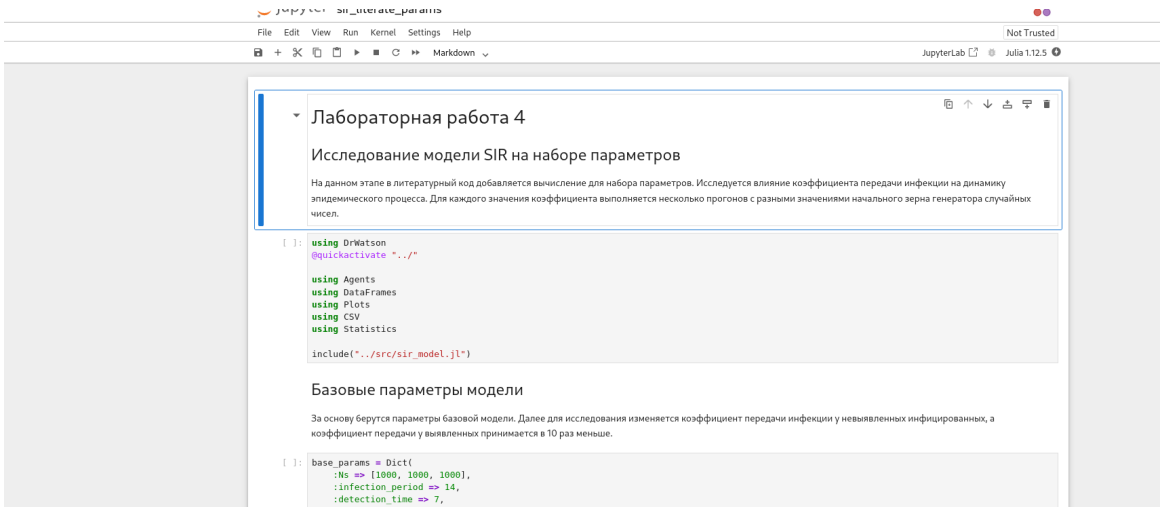

Рисунок 4.5: Notebook параметризованной literate-версии первого скрипта

На рисунке показан notebook параметризованной версии первого скрипта.

4.3.1 Результаты параметризованной версии

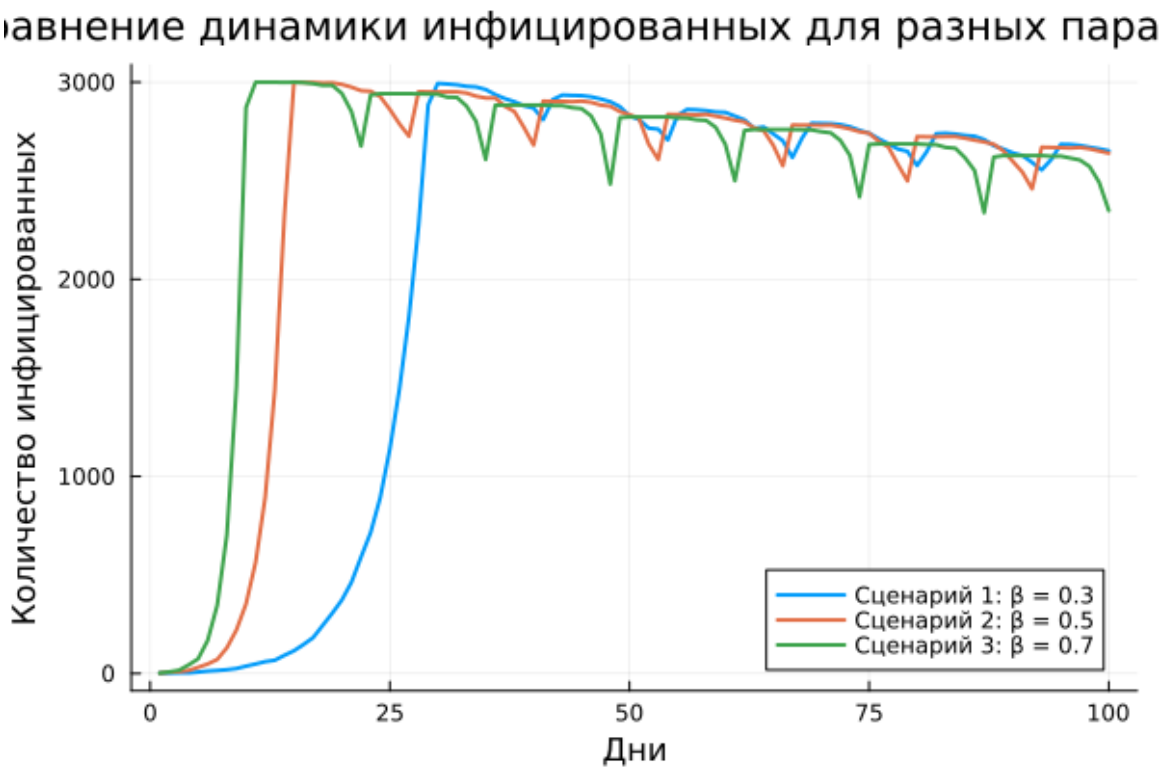

Рисунок 4.6: Сравнение сценариев по доле инфицированных

На рисунке сравниваются сценарии по доле инфицированных. Видно, что более высокий коэффициент заражения ускоряет развитие эпидемии и увеличивает максимум числа инфицированных.

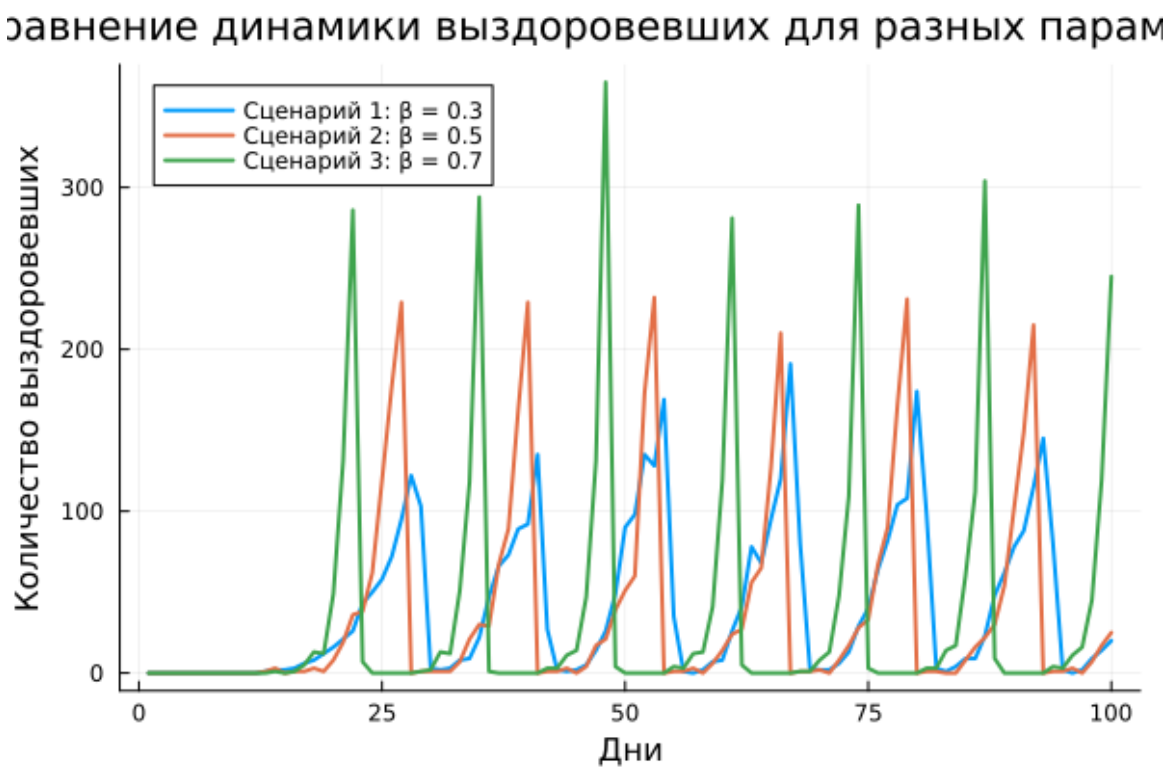

Рисунок 4.7: Сравнение сценариев по доле выздоровевших

На рисунке показана динамика выздоровевших для различных параметров. При более интенсивном распространении инфекции число выздоровевших также растёт быстрее.

Листинг 4.3. Параметризованная literate-версия базового скрипта sir_literate_params.jl

```
# # [illegible] 4
# ## [illegible] SIR [illegible] [illegible]
# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible], [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
```

```julia
# □□□ □□□□□□ □□□□□□□□ □□□□□□□□□□□□ □□□□□□□□ □□□□□□□□.

using DrWatson
@quickactivate "../"

using Agents
using DataFrames
using Plots
using JLD2

include("../src/sir_model.jl")

# ## □□□□□□□ □□□□□□□□□ □□□□□□
#
# □□□□□□□ □□□□□□□□□, □□□□□□□ □□□□□ □□□□□□□□□□□□ □□□ □□□□ □□□□□□□□□.

base_params = Dict(
    :Ns => [1000, 1000, 1000],
    :infection_period => 14,
    :detection_time => 7,
    :death_rate => 0.02,
    :reinfection_probability => 0.1,
    :Is => [0, 0, 1],
    :seed => 42,
    :n_steps => 100,
)

# ## □□□□□ □□□□□□□□□□
```

```
#
# □□□□□□□□□□ □□□□□□□□□ □□□□□□□□□ □ □□□□□□□ □□□□□□□□□□ □□□□□□□□□□□□
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# □□□□□□□□□□□□□□ □□□□□□□□□□□ □□□□□□□□ □□□□□□ □ 10 □□□ □□□□□□.

param_sets = [
    (name = "□□□□□□□□ 1: □ = 0.3", □_und = [0.3, 0.3, 0.3], □_det = [0
    (name = "□□□□□□□□ 2: □ = 0.5", □_und = [0.5, 0.5, 0.5], □_det = [0
    (name = "□□□□□□□□ 3: □ = 0.7", □_und = [0.7, 0.7, 0.7], □_det = [0
]

# ## □□□□□□□ □□□□□□□ □□□□□□ □□□□□□□□
#
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# □ □□□□□□□□□□□ □□□□□□□□□ □□□□ □□□□□□□□ □□□□□□□□□□□□□.

function run_scenario(base_params, □_und, □_det, scenario_name)
    params = Dict(
        :Ns => base_params[:Ns],
        :□_und => □_und,
        :□_det => □_det,
        :infection_period => base_params[:infection_period],
        :detection_time => base_params[:detection_time],
        :death_rate => base_params[:death_rate],
        :reinfection_probability => base_params[:reinfection_probab
        :Is => base_params[:Is],
        :seed => base_params[:seed],
        :n_steps => base_params[:n_steps],
```

```
    )

    model = initialize_sir(; params...)

    times = Int[]
    S_vals = Int[]
    I_vals = Int[]
    R_vals = Int[]
    total_vals = Int[]

    for step = 1:params[:n_steps]
        Agents.step!(model, 1)
        push!(times, step)
        push!(S_vals, susceptible_count(model))
        push!(I_vals, infected_count(model))
        push!(R_vals, recovered_count(model))
        push!(total_vals, total_count(model))
    end

    agent_df = DataFrame(
        time = times,
        susceptible = S_vals,
        infected = I_vals,
        recovered = R_vals,
        scenario = fill(scenario_name, length(times)),
    )

    model_df = DataFrame(
```

```
        time = times,
        total = total_vals,
        scenario = fill(scenario_name, length(times)),
    )

    return agent_df, model_df
end

# ## □□□□□□□□□□ □□□□□□□□□□□□□ □□□ □□□□ □□□□□□□ □□□□□□□□□□
#
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# □ □□□□□ □□□□□□□.

all_agent_df = DataFrame()
all_model_df = DataFrame()

for p in param_sets
    agent_df, model_df = run_scenario(base_params, p.□_und, p.□_det,
    append!(all_agent_df, agent_df)
    append!(all_model_df, model_df)
end

# ## □□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□ □□□□□□ □□□□□□ □□□□□□□□□□□□ □□□□□□□.

first(all_agent_df, 10)
```

```
# ## □□□□□□□□□□□□ □□□□□□□□□□□□
#
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plot(
    xlabel = "□□□□",
    ylabel = "□□□□□□□□□□□ □□□□□□□□□□□□□□□",
    title = "□□□□□□□□□□ □□□□□□□□□ □□□□□□□□□□□□□□□ □□□□ □□□□□□ □□□□□□□□□□□",
)

for p in param_sets
    subset_df = all_agent_df[all_agent_df.scenario .== p.name, :]
    plot!(
        subset_df.time,
        subset_df.infected,
        label = p.name,
        lw = 2,
    )
end

savefig(plotsdir("sir_literate_params_infected.png"))

# ## □□□□□□□□□□□□□□□ □□□□□□□
#
# □□□□□□□□□ □□□□□□ □□□□□□□□□□□□□□ □□□□□□□ □□□□□□ □□□□□□□□□□□□□□□.

plot(
    xlabel = "□□□□",
```

```
    ylabel = "□□□□□□□□□□ □□□□□□□□□□□□□",
    title = "□□□□□□□□□ □□□□□□□□ □□□□□□□□□□□□□ □□□ □□□□□□ □□□□□□□□□□",
)

for p in param_sets
    subset_df = all_agent_df[all_agent_df.scenario .== p.name, :]
    plot!(
        subset_df.time,
        subset_df.recovered,
        label = p.name,
        lw = 2,
    )
end

savefig(plotsdir("sir_literate_params_recovered.png"))

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□ □□□□□□□□□□□□ □□□□□□□□□□ □ □□□□□ □□□□□□□ JLD2.

@save datadir("sir_literate_params_agent.jld2") all_agent_df
@save datadir("sir_literate_params_model.jld2") all_model_df

# ## □□□□□
#
# □ □□□□□□□□□□ □□□□ □□□□□□□□□ □□□□□□□□□ □□□□□□□□ □□□□□□ SIR
# □□□ □□□□□□□□□ □□□□□□□□ □□□□□□□□□□□□ □□□□□□□□ □□□□□□□□.
# □□□ □□□□□□□□□ □□□□□□□□ □□□□□□□□ □□□□□ □□□□□□□□□□□□□□ □ □□□□□□□□□□□□□
```

```
# □□□□□□□ □□ □□□□□□□ □□□ □□□□□□ □□□□□□□□□ □□□□□□□□ □□□□□□□□.
```

4.4 Скрипт параметрического исследования коэффициента заражения

Во втором скрипте реализуется перебор значений коэффициента заражения β и вычисление ключевых характеристик эпидемического процесса.

4.4.1 Обычная версия

Листинг 4.4. Обычная версия скрипта параметрического исследования sir_scan_beta.jl

```
using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Random
using Statistics

include(srcdir("sir_model.jl"))

# □□□□□□□ □□□□□□□ □□□□□□ □□□□□□□□□□□□ □ □□□□□□□□ □□□□□□
function run_experiment(p)
# □□□□□□□ □_und □ □_det □□ □□□□□□ □□□□□□□□□□ beta
beta = p[:beta]
□_und = fill(beta, 3)
□_det = fill(beta / 10, 3)
```

```
# □□□□□□□□□□□□□ □□□□□□
model = initialize_sir(;
Ns = p[:Ns],
□_und = □_und,
□_det = □_det,
infection_period = p[:infection_period],
detection_time = p[:detection_time],
death_rate = p[:death_rate],
reinfection_probability = p[:reinfection_probability],
Is = p[:Is],
seed = p[:seed],
n_steps = p[:n_steps],
)

# □□□□ □□□□□□□□□□□□□ □ □□□□□□□ □□□□□□
infected_fraction(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

peak_infected = 0.0

# □□□□□□□□ □□□□ □□□□□□□□□□□□□
for step = 1:p[:n_steps]
# □□□□□□ □□□□□□□□□□ □□□ □□ □□□□□□□
agent_ids = collect(allids(model))
for id in agent_ids
agent = try
model[id]
catch
```

```
nothing
end

if agent !== nothing
sir_agent_step!(agent, model)
end
end

frac = infected_fraction(model)
if frac > peak_infected
peak_infected = frac
end
end

# ⌧⌧⌧⌧⌧⌧⌧⌧ ⌧⌧⌧⌧⌧⌧⌧
final_infected = infected_fraction(model)
final_recovered = count(a.status == :R for a in allagents(model)) /
total_deaths = sum(p[:Ns]) - nagents(model)

return (
peak = peak_infected,
final_inf = final_infected,
final_rec = final_recovered,
deaths = total_deaths,
)
end

# ⌧⌧⌧⌧⌧⌧⌧⌧ ⌧⌧⌧⌧⌧⌧⌧⌧ beta
```

```
beta_range = 0.1:0.1:1.0

# □□□□□ □□□□□□□□ seed □□□ □□□□□□□□□ □□□□□□□□
seeds = [42, 43, 44]

# □□□□□□□□□□□□ □□□□□□ □□□□□□□□□□□
params_list = []

for b in beta_range
for s in seeds
push!(
params_list,
Dict(
:beta => b,
:Ns => [1000, 1000, 1000],
:infection_period => 14,
:detection_time => 7,
:death_rate => 0.02,
:reinfection_probability => 0.1,
:Is => [0, 0, 1],
:seed => s,
:n_steps => 100,
),
)
end
end

# □□□□□□□ □□□□□ □□□□□□□□□□□□□□
```

```
results = []

for params in params_list
data = run_experiment(params)
push!(results, merge(params, Dict(pairs(data))))
println("□□□□□□□□ □□□□□□□□□□□ □ beta = $(params[:beta]), seed = $(params
end

# □□□□□□□□□ □□□□□□□□□□ □□□□ □□□□□□□□
df = DataFrame(results)
CSV.write(datadir("beta_scan_all.csv"), df)

# □□□□□□□□□□ □□□□□□□□□□ □□ □□□□□□□□□□ □□□□□□□□□ beta
grouped = combine(
groupby(df, [:beta]),
:peak => mean => :mean_peak,
:final_inf => mean => :mean_final_inf,
:deaths => mean => :mean_deaths,
)

# □□□□□□□□□□ □□□□□□□□□ □□□□□□□
plot(
grouped.beta,
grouped.mean_peak,
label = "□□□ □□□□□□□□",
xlabel = "□□□□□□□□□□□ □□□□□□□□□□ □",
ylabel = "□□□□ □□□□□□□□□□□□□□",
marker = :circle,
```

```
linewidth = 2,
)

plot!(
grouped.beta,
grouped.mean_final_inf,
label = "□□□□□□□□ □□□□ □□□□□□□□□□□□□□",
marker = :square,
)

plot!(
grouped.beta,
grouped.mean_deaths ./ 3000,
label = "□□□□ □□□□□□□",
marker = :diamond,
)

savefig(plotsdir("beta_scan.png"))

println("□□□□□□□□□□ □□□□□□□□□ □ data/beta_scan_all.csv □ plots/beta_scan
```

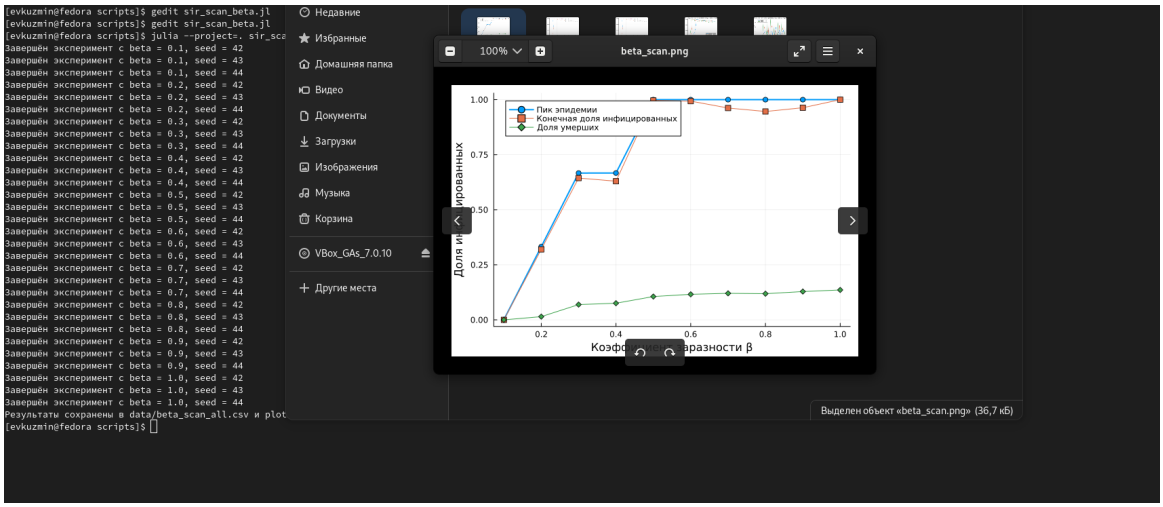


Рисунок 4.8: Выполнение второго скрипта в обычном формате

На рисунке показан запуск второго скрипта в обычной версии.

4.4.2 Notebook literate-версии

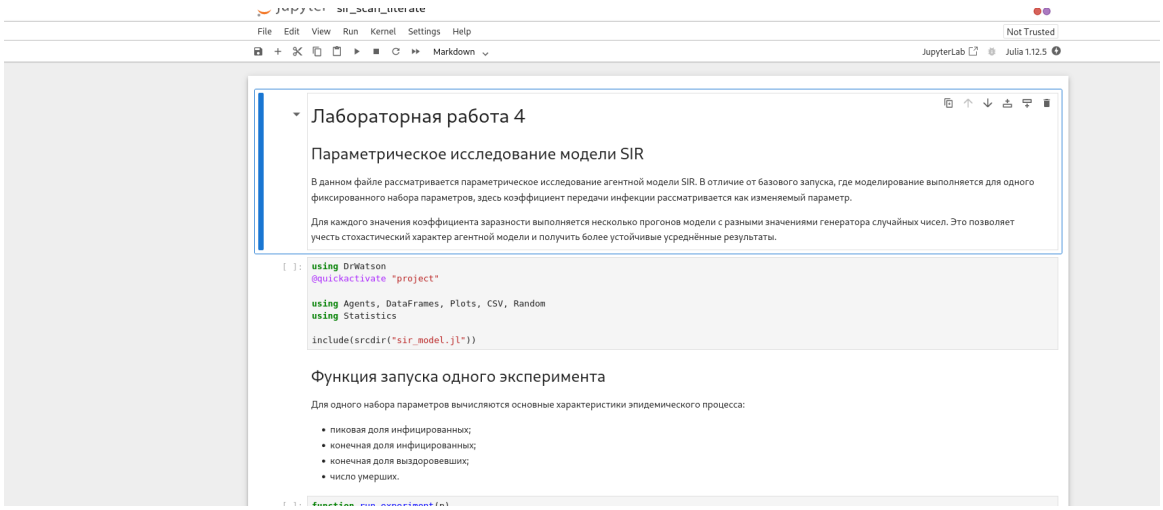
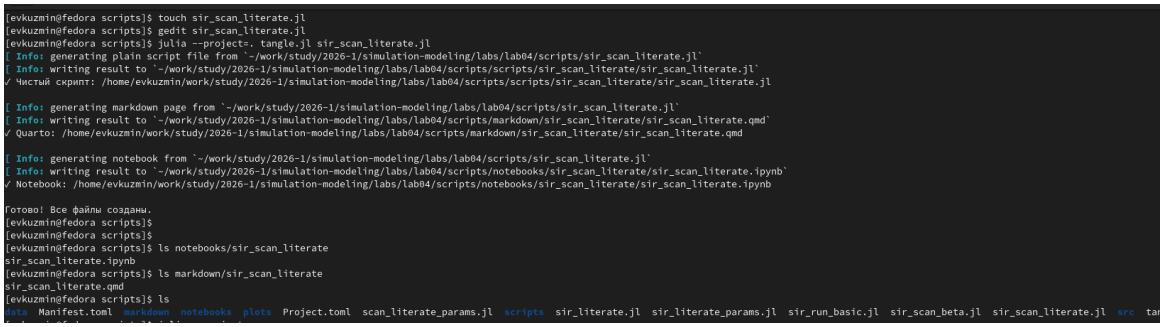


Рисунок 4.9: Notebook literate-версии второго скрипта

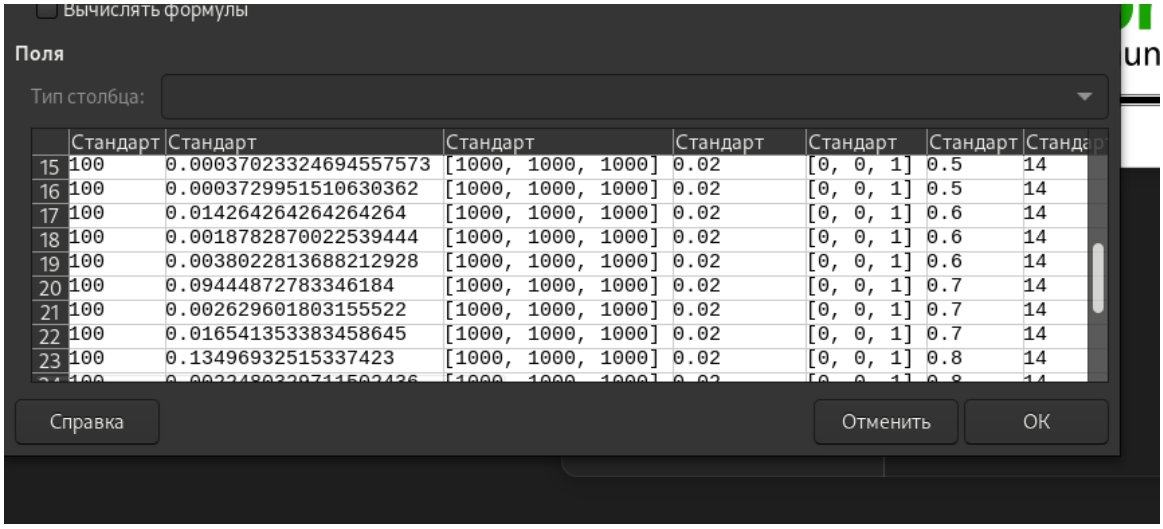
На рисунке представлен notebook literate-версии второго скрипта.

4.4.3 Генерация notebook и документации



На рисунке показан этап генерации notebook и Quarto-документации для literate-версии второго скрипта.

4.4.4 Таблица результатов



Вычислять формулы

Поля

Тип столбца:

	Стандарт	Стандарт	Стандарт	Стандарт	Стандарт	Стандарт	Станда
15	100	0.00037023324694557573	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.5	14
16	100	0.0003729951510630362	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.5	14
17	100	0.014264264264264264	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.6	14
18	100	0.0018782870022539444	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.6	14
19	100	0.0038022813688212928	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.6	14
20	100	0.09444872783346184	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.7	14
21	100	0.002629601803155522	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.7	14
22	100	0.016541353383458645	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.7	14
23	100	0.13496932515337423	[1000, 1000, 1000]	0.02	[0, 0, 1]	0.8	14

Справка Отменить ОК

Рисунок 4.10: Таблица результатов параметрического исследования

На рисунке представлена таблица результатов параметрического исследования. Она содержит значения β и соответствующие показатели: пик эпидемии, конечную долю инфицированных, долю выздоровевших и число умерших.

4.4.5 Результат параметрического исследования

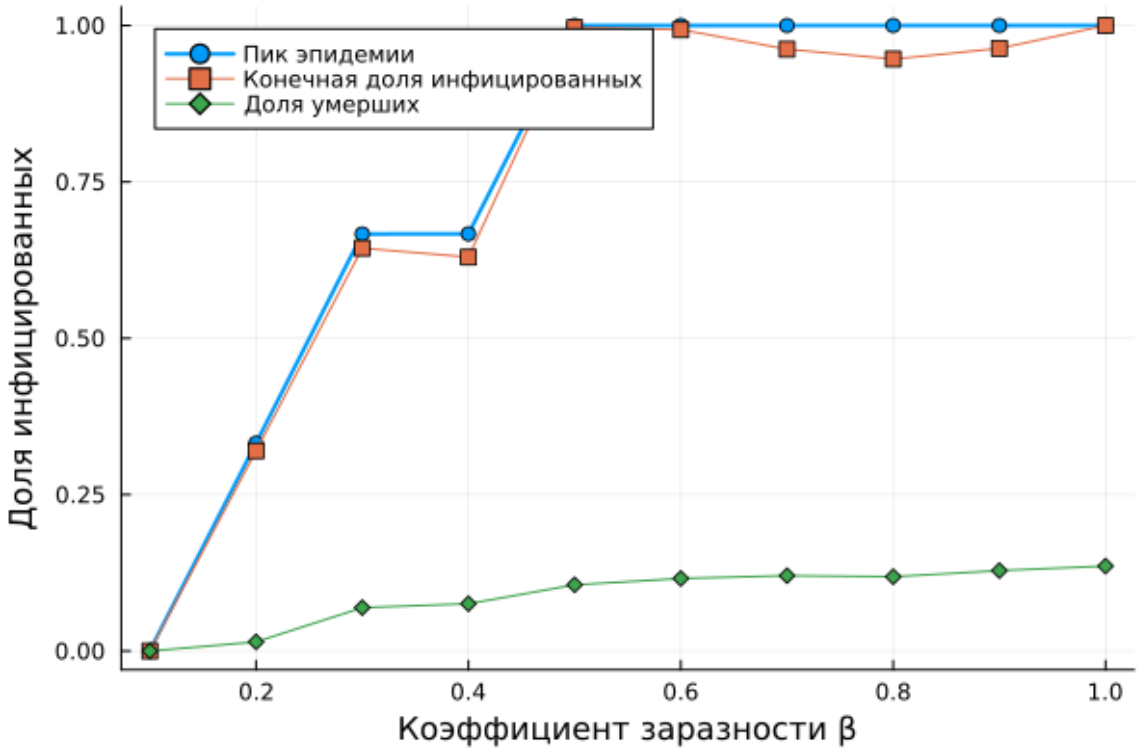


Рисунок 4.11: Зависимость характеристик эпидемии от коэффициента заражения

На рисунке показано влияние коэффициента заражения на основные характеристики эпидемии. С ростом β увеличиваются пик эпидемии, конечная доля инфицированных и смертность. Это соответствует ожидаемой интерпретации: более высокая заразность приводит к более интенсивному развитию эпидемического процесса.

4.4.6 Literate-версия второго скрипта

Листинг 4.5. Literate-версия скрипта параметрического исследования sir_scan_literate.jl

```
# # [illegible] 4
# ## [illegible] SIR
#
# [illegible]
# [illegible] SIR. [illegible], [illegible]
# [illegible]
# [illegible]
#
# [illegible]
# [illegible] [illegible]. [illegible]
# [illegible]
# [illegible].

using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Random
using Statistics

include(srcdir("sir_model.jl"))

# ## [illegible]
#
# [illegible]
# [illegible]:
#
# - [illegible];
# - [illegible];
```

```
# - [illegible] [illegible] [illegible];
# - [illegible] [illegible].

function run_experiment(p)
# [illegible] β_und β β_det [illegible] [illegible] [illegible] beta
beta = p[:beta]
β_und = fill(beta, 3)
β_det = fill(beta / 10, 3)

# [illegible] [illegible]
model = initialize_sir(;
Ns = p[:Ns],
β_und = β_und,
β_det = β_det,
infection_period = p[:infection_period],
detection_time = p[:detection_time],
death_rate = p[:death_rate],
reinfection_probability = p[:reinfection_probability],
Is = p[:Is],
seed = p[:seed],
n_steps = p[:n_steps],
)

# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
infected_fraction(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

peak_infected = 0.0
```

```
# □□□□□□□□ □□□□ □□□□□□□□□□□□□
for step = 1:p[:n_steps]
# □□□□□□□□□ □□□□□□□□□□ □□□□□□ □□□ □□ □□□□ □□□□□□□
agent_ids = collect(allids(model))
for id in agent_ids
agent = try
model[id]
catch
nothing
end

if agent !== nothing
sir_agent_step!(agent, model)
end
end

frac = infected_fraction(model)
if frac > peak_infected
peak_infected = frac
end
end

# □□□□□□□□ □□□□□□□□□□□□□□
final_infected = infected_fraction(model)
final_recovered = count(a.status == :R for a in allagents(model)) /
total_deaths = sum(p[:Ns]) - nagents(model)

return (
```

```
peak = peak_infected,
final_inf = final_infected,
final_rec = final_recovered,
deaths = total_deaths,
)
end

# ## □□□□□□□□ □□□□□□□□□□
#
# □□□□□□□□□□□□□□□ □□□□□□□□ □□□□□□□□□□□□ □□□□□□□□ □□□□□□□□ □□ 0.1 □□ 1.0
# □ □□□□□ 0.1. □□□ □□□□□□□ □□□□□□□□ □□□□□□□□□□□ □□□ □□□□□□□ □□□□□□
# □ □□□□□□□□□□ □□□□□□□□□□ seed.

beta_range = 0.1:0.1:1.0
seeds = [42, 43, 44]

# ## □□□□□□□□□□□□ □□□□□□ □□□□□□□□□□
#
# □□□ □□□□□□□ □□□□□□□□ beta □ □□□□□□□ □□□□□□□□ seed □□□□□□□□□ □□□□□□□□□
# □□□□□ □□□□□□□□□□.

params_list = []

for b in beta_range
for s in seeds
push!(
params_list,
Dict(
```

```
:beta => b,
:Ns => [1000, 1000, 1000],
:infection_period => 14,
:detection_time => 7,
:death_rate => 0.02,
:reinfection_probability => 0.1,
:Is => [0, 0, 1],
:seed => s,
:n_steps => 100,
),
)
end
end

# ## □□□□□□ □□□□□□□□□□□□□
#
# □□□ □□□□□□□ □□□□□□ □□□□□□□□□□ □□□□□□□□□□□ □□□□□□□□□□□□□, □ □□□□□
# □□□□□□□□□□ □□□□□□□□□□□ □ □□□□□ □□□□□□.

results = []

for params in params_list
data = run_experiment(params)
push!(results, merge(params, Dict(pairs(data))))
println("□□□□□□□□ □□□□□□□□□□□ □ beta = $(params[:beta]), seed = $(params
end

# ## □□□□□□□□□□ □□□□□□□□□□□
```

```
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] CSV-[illegible].

df = DataFrame(results)
CSV.write(datadir("beta_scan_all.csv"), df)

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] beta [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible].

grouped = combine(
groupby(df, [:beta]),
:peak => mean => :mean_peak,
:final_inf => mean => :mean_final_inf,
:deaths => mean => :mean_deaths,
)

# ## [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] beta.

plot(
grouped.beta,
grouped.mean_peak,
label = "[illegible] [illegible]",
```

```
xlabel = "□□□□□□□□□□□ □□□□□□□□□□□ □",
ylabel = "□□□□ □□□□□□□□□□□□□□□",
marker = :circle,
linewidth = 2,
)

plot!(
grouped.beta,
grouped.mean_final_inf,
label = "□□□□□□□□ □□□□ □□□□□□□□□□□□□□□",
marker = :square,
)

plot!(
grouped.beta,
grouped.mean_deaths ./ 3000,
label = "□□□□ □□□□□□□□",
marker = :diamond,
)

savefig(plotsdir("beta_scan.png"))

println("□□□□□□□□□□□ □□□□□□□□□□□ □ data/beta_scan_all.csv □ plots/beta_scan

# ## □□□□□
#
# □ □□□□□□□□□□□ □□□□□□□□□□□□□□□□□ □□□□□□□□□□□□□ □□□□□ □□□□□□□□□ □□□□□□□□□□□□□
# □□□□□□□□□□□□□□□□ □□□□□□□□□□□□□□□□ □□□□□□□□□ □□□ □□□□□□□□□□ □□□□□□□□□
```

```
# [illegible] [illegible]. [illegible] [illegible] [illegible] [illegible]
# beta [illegible] [illegible] [illegible], [illegible] [illegible]
# [illegible].
```

4.5 Параметризованная версия второго скрипта

На следующем этапе была подготовлена параметрическая версия второго скрипта, а также сгенерированы notebook и qmd-файлы.

```
[evkuzmin@fedora scripts]$ gedit sir_scan_literate.jl
[evkuzmin@fedora scripts]$ touch scan_literate_params.jl
[evkuzmin@fedora scripts]$ gedit scan_literate_params.jl
[evkuzmin@fedora scripts]$ julia --project=. tangle.jl scan_literate_params.jl
[ Info: generating plain script file from `~/work/study/2026-1/simulation-modeling/labs/lab04/scripts/scan_literate_params.jl`
[ Info: writing result to `~/work/study/2026-1/simulation-modeling/labs/lab04/scripts/scripts/scan_literate_params/scan_literate_params.jl`
✓ Чистый скрипт: /home/evkuzmin/work/study/2026-1/simulation-modeling/labs/lab04/scripts/scripts/scan_literate_params/scan_literate_params.jl

[ Info: generating markdown page from `~/work/study/2026-1/simulation-modeling/labs/lab04/scripts/scan_literate_params.jl`
[ Info: writing result to `~/work/study/2026-1/simulation-modeling/labs/lab04/scripts/markdown/scan_literate_params/scan_literate_params.qmd`
✓ Quarto: /home/evkuzmin/work/study/2026-1/simulation-modeling/labs/lab04/scripts/markdown/scan_literate_params/scan_literate_params.qmd

[ Info: generating notebook from `~/work/study/2026-1/simulation-modeling/labs/lab04/scripts/scan_literate_params.jl`
[ Info: writing result to `~/work/study/2026-1/simulation-modeling/labs/lab04/scripts/notebooks/scan_literate_params/scan_literate_params.ipynb`
✓ Notebook: /home/evkuzmin/work/study/2026-1/simulation-modeling/labs/lab04/scripts/notebooks/scan_literate_params/scan_literate_params.ipynb

Готово! Все файлы созданы.
[evkuzmin@fedora scripts]$
[evkuzmin@fedora scripts]$
[evkuzmin@fedora scripts]$ ls notebooks/scan_literate_params.jl
ls: невозможно получить доступ к 'notebooks/scan_literate_params.jl': Нет такого файла или каталога
[evkuzmin@fedora scripts]$ ls notebooks/scan_literate_params
scan_literate_params.ipynb
[evkuzmin@fedora scripts]$ ls markdown/scan_literate_params
scan_literate_params.qmd
[evkuzmin@fedora scripts]$ julia --project

               _
   _       _ _(_)_     |  Documentation: https://docs.julialang.org
  (_)     | (_) (_)    |
   _ _   _| |_  __ _   |  Type "?" for help, "]?" for Pkg help.
  | | | | | | |/ _` |  |
  | | |_| | | | (_| |  |  Version 1.12.5 (2026-02-09)
 _/ |\__'_|_|_|\__'_|  |  Official https://julialang.org release
|__/                   |

julia> using Pkg

julia> using IJulia

julia> notebook()
notebook = `/usr/bin/jupyter notebook`
[ Info: running `/usr/bin/jupyter notebook`
```

Рисунок 4.12: Создание параметрической версии второго скрипта и генерация файлов

На рисунке показан этап подготовки параметризованной версии второго скрипта.

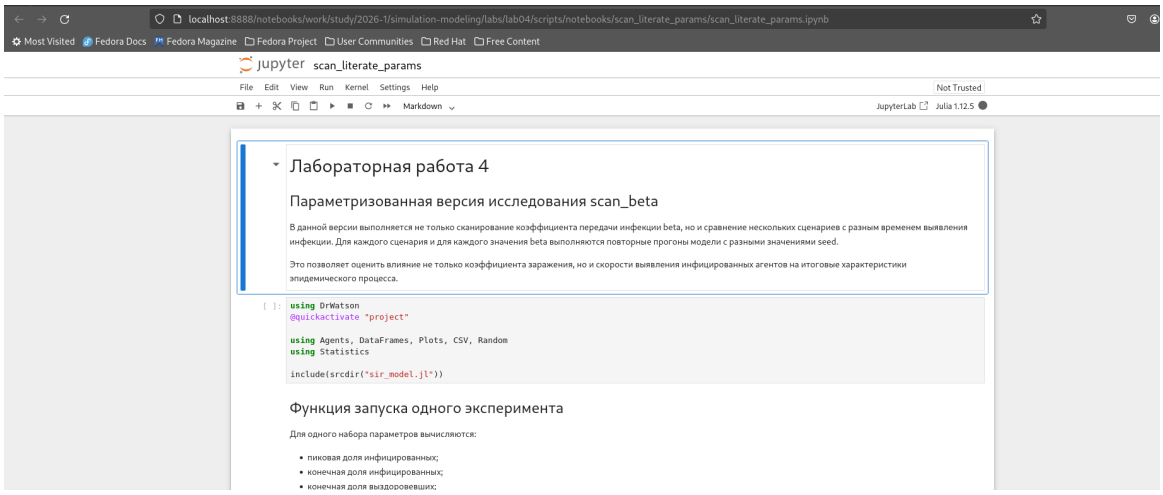


Рисунок 4.13: Notebook параметризованной версии второго скрипта

На рисунке представлен notebook параметризованной версии второго скрипта.

4.5.1 Результаты параметризованного исследования

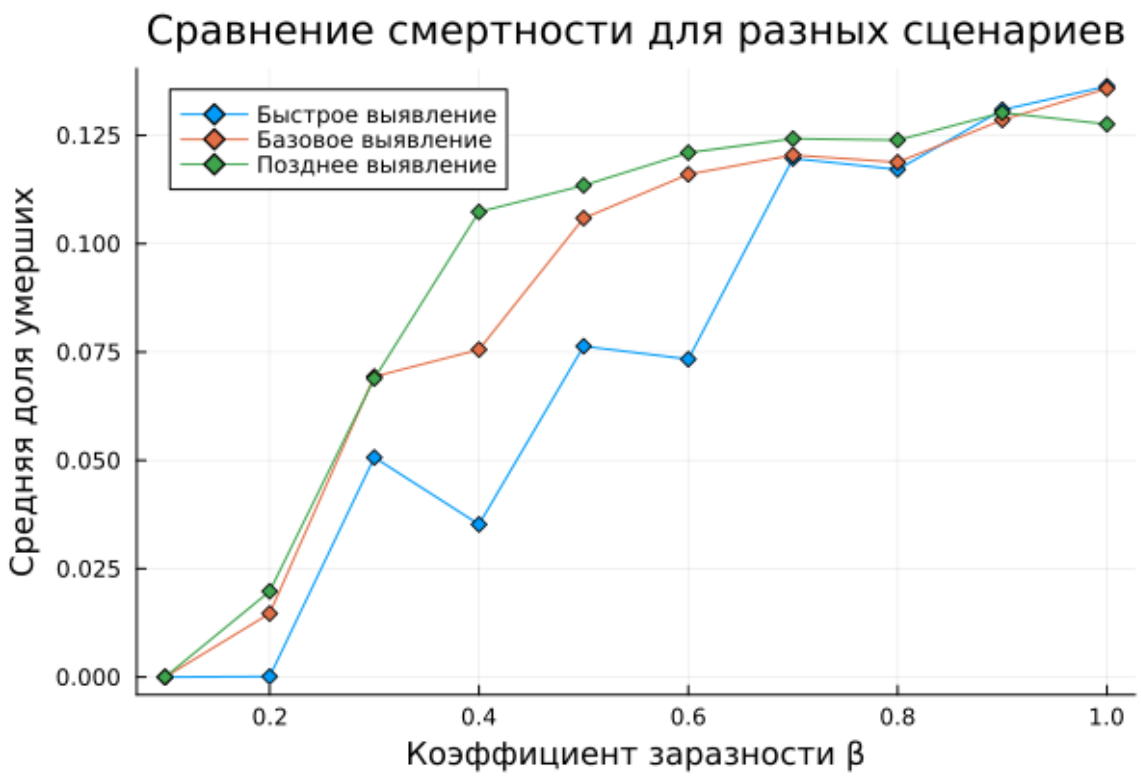


Рисунок 4.14: Сценарное исследование смертности

На рисунке показана зависимость средней доли умерших от коэффициента заражения для нескольких сценариев. Видно, что различия между сценариями усиливаются при росте заразности.

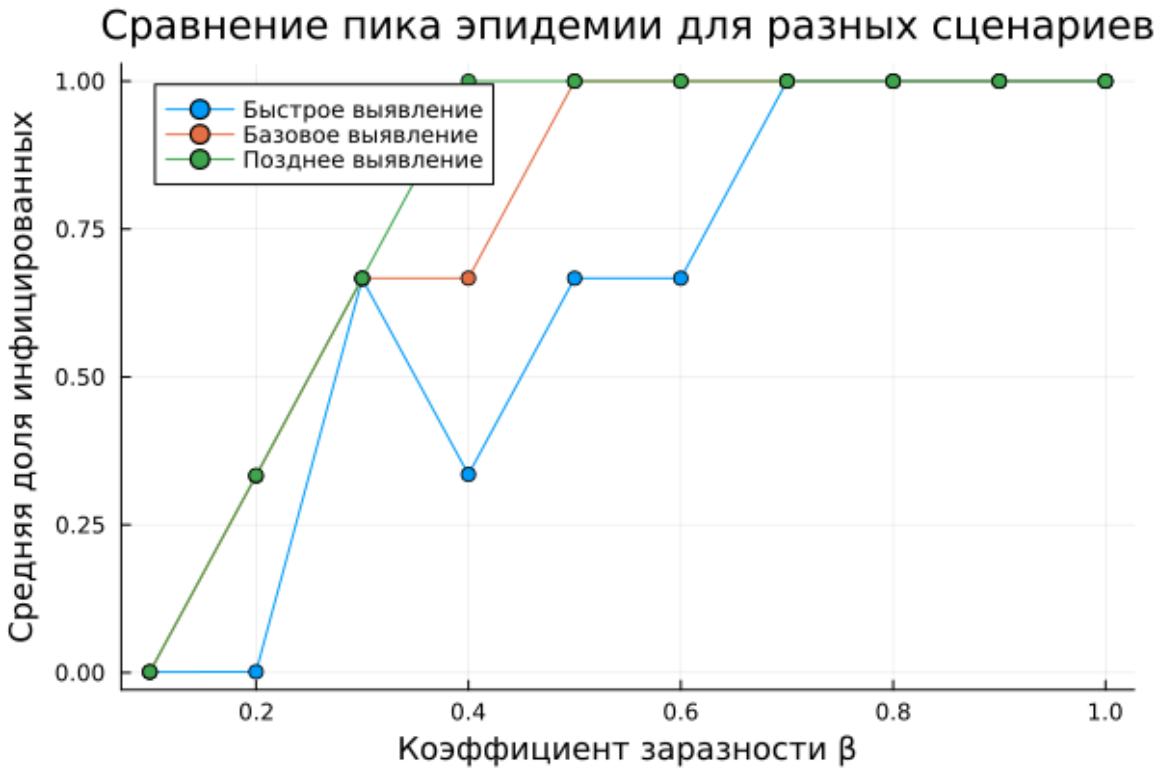


Рисунок 4.15: Сценарное исследование пика эпидемии

На рисунке сравниваются значения средней пиковой доли инфицированных в различных сценариях. Это позволяет оценить влияние дополнительных условий моделирования на развитие эпидемии.

Листинг 4.6. Параметризованная версия скрипта параметрического исследования scan_literate_params.jl

```
# # [redacted] 4
# ## [redacted] scan_beta
#
# [redacted]
```

```
# [illegible] beta, [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible]. [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] beta
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] seed.
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible], [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible].

using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Random
using Statistics

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible];
# - [illegible] [illegible].

function run_experiment(p)
beta = p[:beta]
[illegible]_und = fill(beta, 3)
```

```
β_det = fill(beta / 10, 3)

model = initialize_sir(;
Ns = p[:Ns],
β_und = β_und,
β_det = β_det,
infection_period = p[:infection_period],
detection_time = p[:detection_time],
death_rate = p[:death_rate],
reinfection_probability = p[:reinfection_probability],
Is = p[:Is],
seed = p[:seed],
n_steps = p[:n_steps],
)

infected_fraction(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

peak_infected = 0.0

for step = 1:p[:n_steps]
agent_ids = collect(allids(model))
for id in agent_ids
agent = try
model[id]
catch
nothing
end
```

```
if agent !== nothing
sir_agent_step!(agent, model)
end
end

frac = infected_fraction(model)
if frac > peak_infected
peak_infected = frac
end
end

final_infected = infected_fraction(model)
final_recovered = count(a.status == :R for a in allagents(model)) /
total_deaths = sum(p[:Ns]) - nagents(model)

return (
peak = peak_infected,
final_inf = final_infected,
final_rec = final_recovered,
deaths = total_deaths,
)
end

# ## □□□□□ □□□□□□□□□
#
# □□□□□□□□□□□□□□□ □□□ □□□□□□□□:
#
# - □□□□□□□ □□□□□□□□□;
```

```
# - □□□□□□□ □□□□□□□□□;
# - □□□□□□□ □□□□□□□□□.

scenario_sets = [
(name = "□□□□□□□ □□□□□□□□□", detection_time = 5),
(name = "□□□□□□□ □□□□□□□□□", detection_time = 7),
(name = "□□□□□□□ □□□□□□□□□", detection_time = 10),
]

# ## □□□□□□□□ □□□□□□□□ beta □ □□□□□ □□□□□□□□ seed

beta_range = 0.1:0.1:1.0
seeds = [42, 43, 44]

# ## □□□□□□□□□□□□ □□□□□□ □□□□□□□□□□

params_list = []

for scenario in scenario_sets
for b in beta_range
for s in seeds
push!(
params_list,
Dict(
:scenario => scenario.name,
:beta => b,
:Ns => [1000, 1000, 1000],
:infection_period => 14,
```

```
:detection_time => scenario.detection_time,
:death_rate => 0.02,
:reinfection_probability => 0.1,
:Is => [0, 0, 1],
:seed => s,
:n_steps => 100,
),
)
end


# ## □□□□□□ □□□□ □□□□□□□□□□□□□

results = []

for params in params_list
data = run_experiment(params)
push!(results, merge(params, Dict(pairs(data))))
println("□□□□□□□□ = $(params[:scenario]), beta = $(params[:beta]), se
end

# ## □□□□□□□□□□ □□□□ □□□□□□□□

df = DataFrame(results)
CSV.write(datadir("beta_scan_scenarios_all.csv"), df)

# ## □□□□□□□□□□ □□□□□□□□□□□
#
```

```
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] beta.

grouped = combine(
groupby(df, [:scenario, :beta]),
:peak => mean => :mean_peak,
:final_inf => mean => :mean_final_inf,
:final_rec => mean => :mean_final_rec,
:deaths => mean => :mean_deaths,
)

CSV.write(datadir("beta_scan_scenarios_grouped.csv"), grouped)

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

plot(
xlabel = "[illegible] [illegible] [illegible]",
ylabel = "[illegible] [illegible] [illegible]",
title = "[illegible] [illegible] [illegible] [illegible] [illegible] [illegible]",
linewidth = 2,
)

for scenario in scenario_sets
subset_df = grouped[grouped.scenario .== scenario.name, :]
plot!(
subset_df.beta,
subset_df.mean_peak,
```

```
label = scenario.name,
marker = :circle,
)
end

savefig(plotsdir("beta_scan_scenarios_peak.png"))

# ## [illegible]
#
# [illegible] beta.

plot(
xlabel = "[illegible]",
ylabel = "[illegible]",
title = "[illegible]",
linewidth = 2,
)

for scenario in scenario_sets
subset_df = grouped[grouped.scenario .== scenario.name, :]
plot!(
subset_df.beta,
subset_df.mean_deaths ./ 3000,
label = scenario.name,
marker = :diamond,
)
end
```

```
savefig(plotsdir("beta_scan_scenarios_deaths.png"))

println("□□□□□□□□□□ □□□□□□□□□ □ data/beta_scan_scenarios_all.csv")
println("□□□□□□□□□□□ □□□□□□□□□□ □□□□□□□□□ □ data/beta_scan_scenarios_group
println("□□□□□□□ □□□□□□□□□□ □ plots/beta_scan_scenarios_peak.png □ plots

# ## □□□□□
#
# □ □□□□□□□□□□ □□□□ □□□□□□□□ □ □□□□□□□□□ □□□□□□ □□□ □□□□□□□□□□ □□□□□□□□□
# □ □□□□□□ □□□□□□□□ □□□□□□□□□ □□□□□□□□. □□□ □□□□□□□□□ □□□□□□□□ □□□□□□□
# □□□□□□□□□ detection_time □□ □□□ □□□□□□□□ □ □□□□□□□□□□ □□□ □□□□□□□□□
# □□□□□□□□□ □□□□□□□□□□□□ □□□□□□□□□ beta.
```

4.6 Скрипт исследования миграции

Третий скрипт посвящён исследованию влияния интенсивности миграции на распространение инфекции между городами.

4.6.1 Обычная версия

Листинг 4.7. Обычная версия скрипта исследования миграции sir_migration_effect.jl

```
using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Random
using Statistics
```

```
include(srcdir("sir_model.jl"))

# □□□□□□□ □□□ □□□□□□□□ □□□□□□□ □□□□□□□□
function create_migration_matrix(C, intensity)
M = ones(C, C) .* intensity / (C - 1)
for i in 1:C
M[i, i] = 1 - intensity
end
return M
end

# □□□□□□□ □□□ □□□□□□□□ □□□□□□□ □□□□□□□□□□ □□□□
function peak_time(p)
migration_rates = create_migration_matrix(p[:C], p[:migration_intens

model = initialize_sir(;
Ns = p[:Ns],
□_und = p[:□_und],
□_det = p[:□_det],
infection_period = p[:infection_period],
detection_time = p[:detection_time],
death_rate = p[:death_rate],
reinfection_probability = p[:reinfection_probability],
Is = p[:Is],
seed = p[:seed],
migration_rates = migration_rates,
)
```

```
infected_frac(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

peak = 0.0
peak_step = 0

for step in 1:p[:n_steps]
agent_ids = collect(allids(model))
for id in agent_ids
agent = try
model[id]
catch
nothing
end

if agent !== nothing
sir_agent_step!(agent, model)
end
end

frac = infected_frac(model)
if frac > peak
peak = frac
peak_step = step
end
end

return (peak_time = peak_step, peak_value = peak)
```

```
end

# □□□□□□□□ □□□□□□□□□□□□□ □□□□□□□□
migration_intensities = 0.0:0.1:0.5
seeds = [42, 43, 44]

# □□□□□□□□□□□□□ □□□□□□□□□□□
params_list = []

for mig in migration_intensities
for s in seeds
push!(
params_list,
Dict(
:migration_intensity => mig,
:C => 3,
:Ns => [1000, 1000, 1000],
:□_und => [0.5, 0.5, 0.5],
:□_det => [0.05, 0.05, 0.05],
:infection_period => 14,
:detection_time => 7,
:death_rate => 0.02,
:reinfection_probability => 0.1,
:Is => [1, 0, 0],
:seed => s,
:n_steps => 150,
),
)
```

```
end
end

# □□□□□□ □□□□□□□□□□□□□
results = []

for params in params_list
data = peak_time(params)
push!(results, merge(params, Dict(pairs(data))))
println("□□□□□□□□ □□□□□□□□□□□ □ migration_intensity = $(params[:migratio
end

# □□□□□□□□□□ □□□□ □□□□□□□□
df = DataFrame(results)
CSV.write(datadir("migration_scan_all.csv"), df)

# □□□□□□□□□□
grouped = combine(
groupby(df, [:migration_intensity]),
:peak_time => mean => :mean_peak_time,
:peak_value => mean => :mean_peak_value,
)

# □□□□□□□□□□□□
plot(
grouped.migration_intensity,
grouped.mean_peak_time,
marker = :circle,
```

```
xlabel = "□□□□□□□□□□□□□ □□□□□□□□",
ylabel = "□□□□□ □□ □□□□ (□□□)",
label = "□□□□□ □□□□",
)

plot!(
grouped.migration_intensity,
grouped.mean_peak_value .* 3000,
marker = :square,
label = "□□□□□□□ □□□□□□□□□□□□□□□",
)

savefig(plotsdir("migration_effect.png"))

println("□□□□□□□□□□□ □□□□□□□□□□ □ data/migration_scan_all.csv □ plots/migr
```

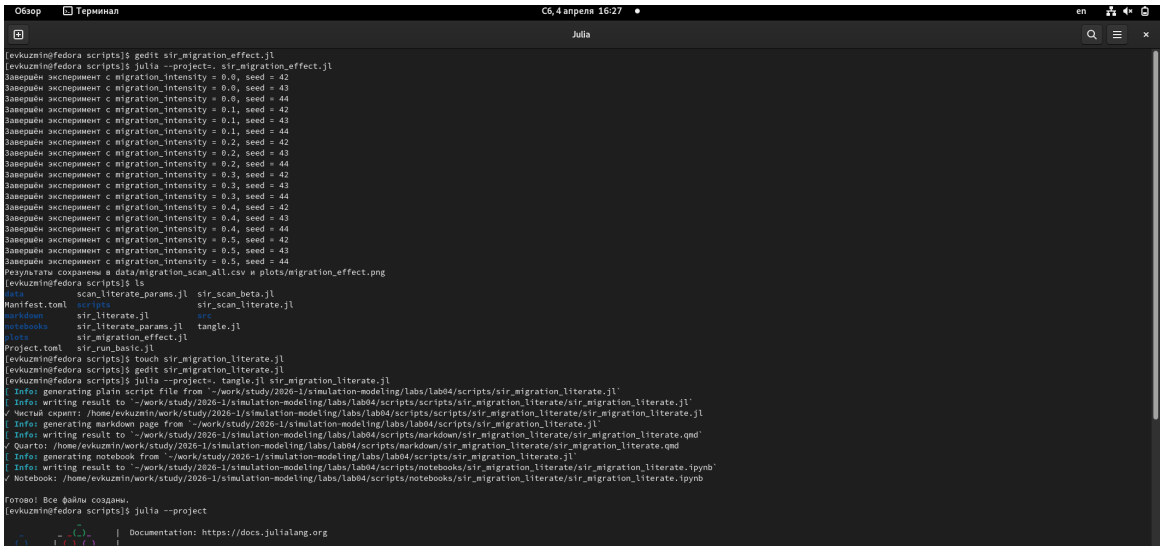


Рисунок 4.16: Создание и выполнение третьего скрипта, подготовка literate-версии

На рисунке показан запуск третьего скрипта и подготовка его literate-версии.

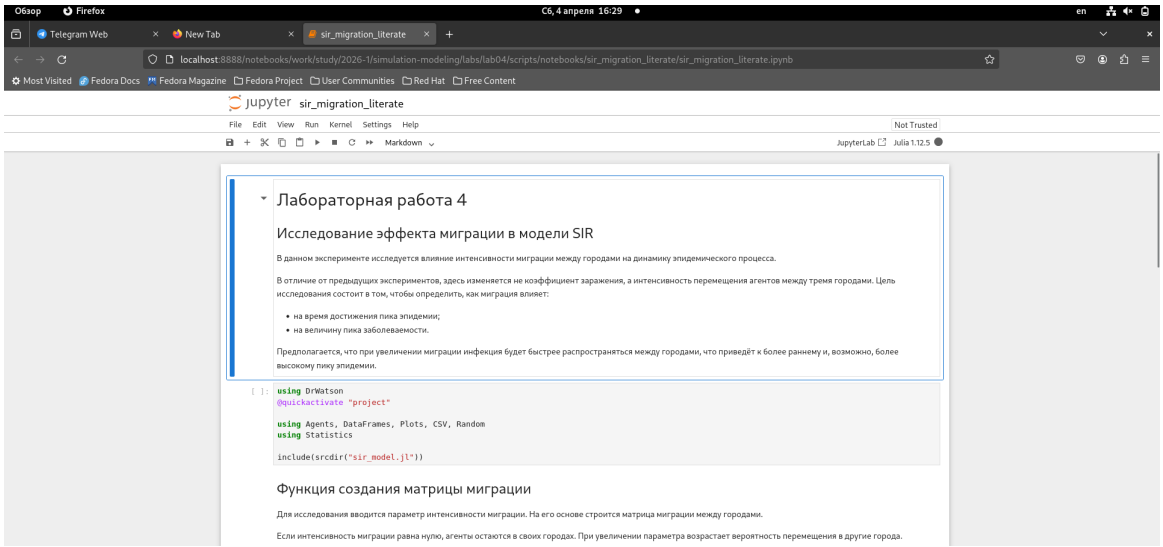


Рисунок 4.17: Notebook literate-версии третьего скрипта

На рисунке представлен notebook literate-версии третьего скрипта.

4.6.2 Результат исследования миграции

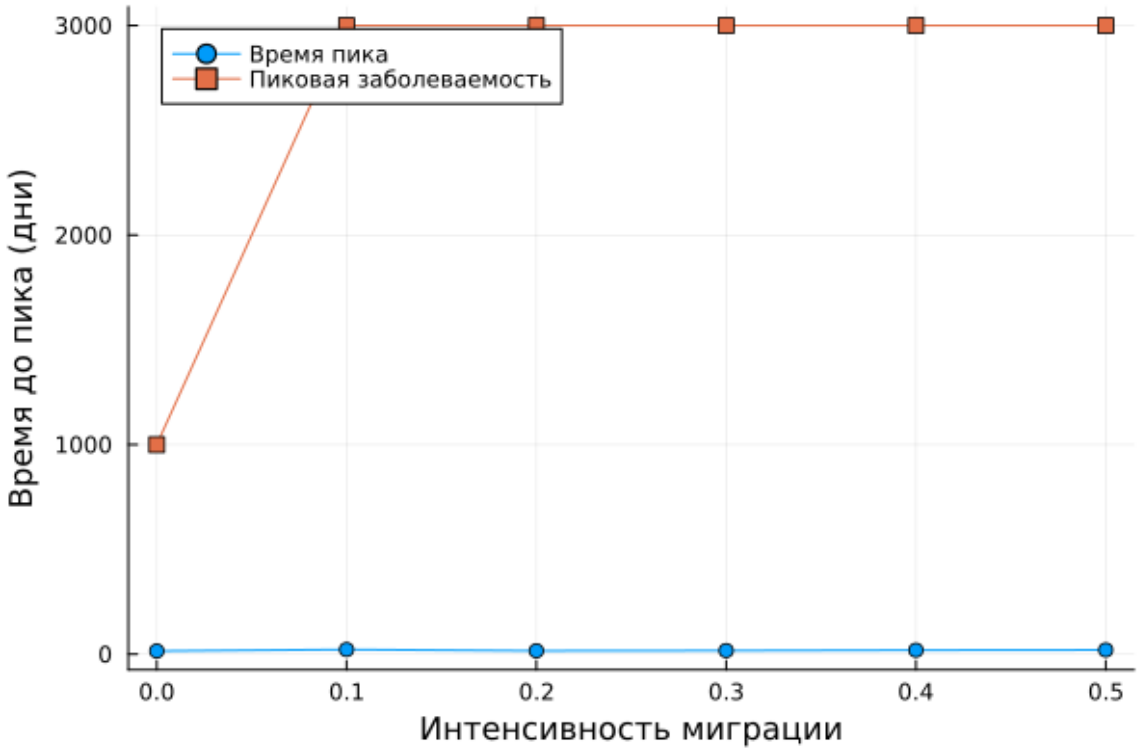


Рисунок 4.18: Влияние интенсивности миграции на динамику эпидемии

На рисунке показано влияние миграции на время достижения пика и на величину пика. При увеличении миграции инфекция распространяется между городами быстрее, что приводит к ускорению эпидемического процесса.

4.6.3 Literate-версия

Листинг 4.8. Literate-версия скрипта исследования миграции sir_migration_literate.jl

```
# # □□□□□□□□□□□□ □□□□□□ 4
# ## □□□□□□□□□□□□ □□□□□□□ □□□□□□□□ □ □□□□□□ SIR
#
```

```
# [illegible]
# [illegible].
#
# [illegible], [illegible] [illegible], [illegible] [illegible]
# [illegible], [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible], [illegible] [illegible], [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible] [illegible].
#
# [illegible], [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible],
# [illegible], [illegible] [illegible] [illegible] [illegible].

using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Random
using Statistics

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible].
```

```
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

function create_migration_matrix(C, intensity)
M = ones(C, C) .* intensity / (C - 1)
for i in 1:C
M[i, i] = 1 - intensity
end
return M
end

# ## [illegible] [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible], [illegible] [illegible]
# [illegible]:
#
# - [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible].

function peak_time(p)
migration_rates = create_migration_matrix(p[:C], p[:migration_intens

model = initialize_sir(;
Ns = p[:Ns],
[illegible]_und = p[:[illegible]_und],
[illegible]_det = p[:[illegible]_det],
infection_period = p[:infection_period],
detection_time = p[:detection_time],
death_rate = p[:death_rate],
```

```
reinfection_probability = p[:reinfection_probability],
Is = p[:Is],
seed = p[:seed],
migration_rates = migration_rates,
)

infected_frac(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

peak = 0.0
peak_step = 0

for step in 1:p[:n_steps]
agent_ids = collect(allids(model))
for id in agent_ids
agent = try
model[id]
catch
nothing
end

if agent !== nothing
sir_agent_step!(agent, model)
end
end

frac = infected_frac(model)
if frac > peak
```

```
peak = frac
peak_step = step
end
end

return (peak_time = peak_step, peak_value = peak)
end

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] 0.0 [illegible] 0.5
# [illegible] 0.1. [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible].

migration_intensities = 0.0:0.1:0.5
seeds = [42, 43, 44]

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] seed
# [illegible] [illegible] [illegible] [illegible].

params_list = []

for mig in migration_intensities
for s in seeds
push!(
params_list,
```

```
Dict(
:migration_intensity => mig,
:C => 3,
:Ns => [1000, 1000, 1000],
:β_und => [0.5, 0.5, 0.5],
:β_det => [0.05, 0.05, 0.05],
:infection_period => 14,
:detection_time => 7,
:death_rate => 0.02,
:reinfection_probability => 0.1,
:Is => [1, 0, 0],
:seed => s,
:n_steps => 150,
),
)
end
end

# ## □□□□□□ □□□□□□□□□□□□□
#
# □□□ □□□□□□□ □□□□□□ □□□□□□□□□□ □□□□□□□□□□□ □□□□□□□□□ □□□□□□□□□□□□□,
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results = []

for params in params_list
data = peak_time(params)
push!(results, merge(params, Dict(pairs(data))))
```

```
println("□□□□□□□□ □□□□□□□□□□□ □ migration_intensity = $(params[:migratio
end

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□□□ □□□□ □□□□□□□□ □□□□□□□□□□□ □ CSV-□□□□ □□□ □□□□□□□□□□□□ □□□□□□□.

df = DataFrame(results)
CSV.write(datadir("migration_scan_all.csv"), df)

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□ □□□□□□□□ □□□□□□□□ □□□□□□□□□□□□□ □□□□□□□□ □□□□□□□□□□□ □□□□□□□ □□□□□□□□:
#
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# - □□□□□□□□ □□□□ □□□□□□□□□□□□□□.

grouped = combine(
groupby(df, [:migration_intensity]),
:peak_time => mean => :mean_peak_time,
:peak_value => mean => :mean_peak_value,
)

# ## □□□□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□□ □□□□□□ □□□□□□□□□□□ □□□□□□□□ □□ □□□□ □ □□□□□□□□□ □□□□
# □□ □□□□□□□□□□□□□ □□□□□□□□□.
```

```
plot(
grouped.migration_intensity,
grouped.mean_peak_time,
marker = :circle,
xlabel = "□□□□□□□□□□□□□ □□□□□□□□",
ylabel = "□□□□□□□□ □□□□□□□□□□",
label = "□□□□□ □□□□",
)

plot!(
grouped.migration_intensity,
grouped.mean_peak_value .* 3000,
marker = :square,
label = "□□□□□□□ □□□□□□□□□□□□□□",
)

savefig(plotsdir("migration_effect.png"))

println("□□□□□□□□□□ □□□□□□□□□ □ data/migration_scan_all.csv □ plots/migr

# ## □□□□□
#
# □ □□□□□□□□□□ □□□□□□□□□□□□□ □□□□ □□□□□□□□□□ □□□□□□□□□□ □□□□□□□
# □□□□□□□□□□ □□□□ □□□□□□□□ □ □□□□□□□□ □□□□ □□□□□□□□□□□□□□ □□ □□□□□□□□□□□□□
# □□□□□□□□ □□□□□ □□□□□□□□.
#
# □□□□□□□□□□ □□□□□□□□□□□□□ □□□□□□□□ □□□□□□□□ □ □□□□□ □□□□□□□□ □□□□□□□□□□□□□□□
# □□□□□□□□ □□□□□ □□□□□□□□, □□□, □□□ □□□□□□□, □□□□□□□□□ □□□□□ □□ □□□□□□□□□□
```

```
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
```

4.7 Параметризованная версия скрипта миграции

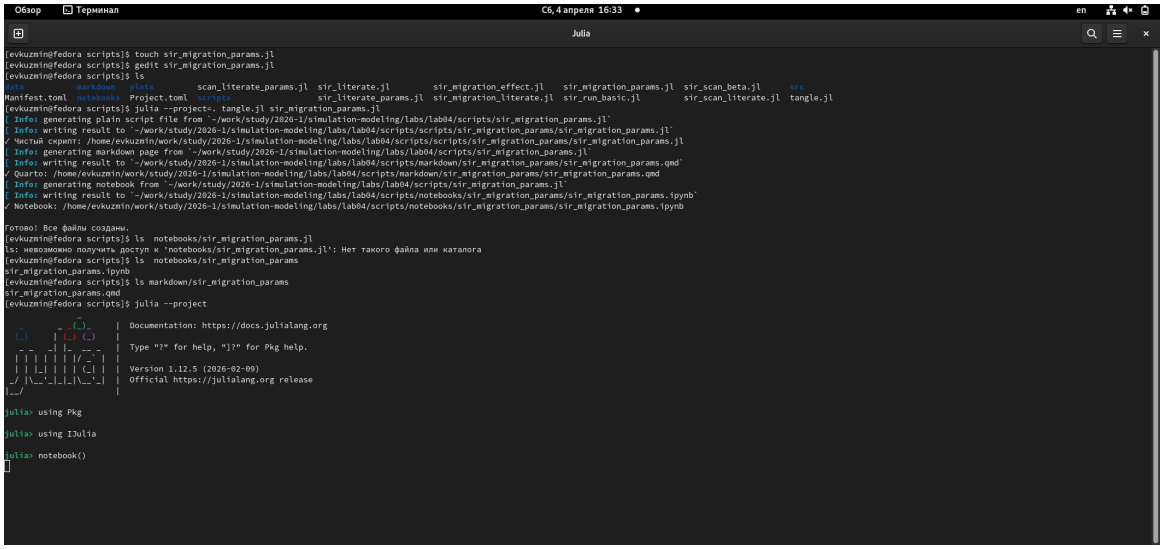

Рисунок 4.19: Создание параметрической версии третьего скрипта

На рисунке показан этап создания параметрической версии третьего скрипта.

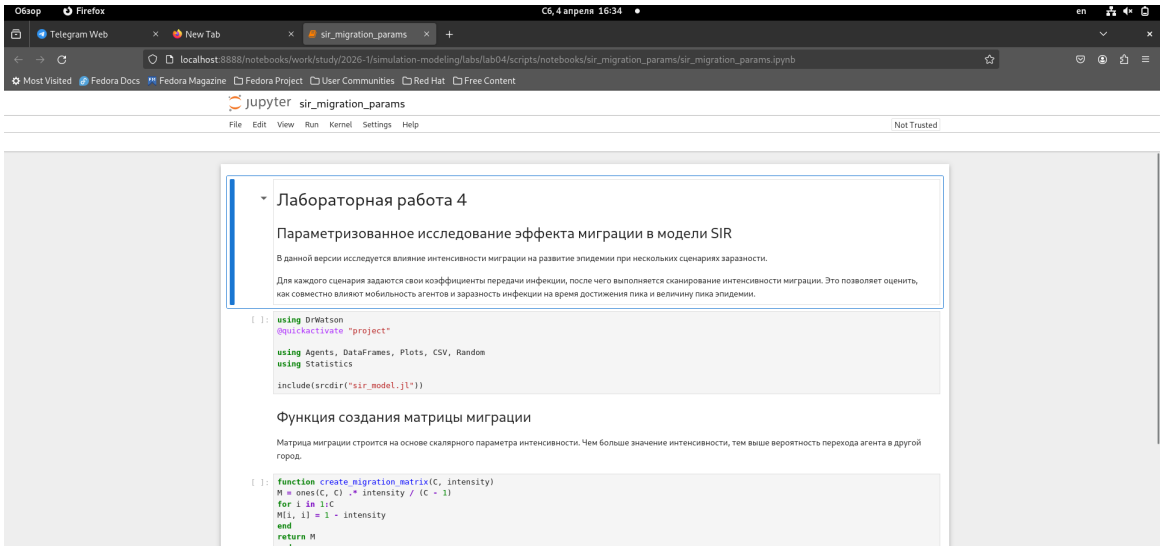

Рисунок 4.20: Notebook параметрической версии третьего скрипта

На рисунке показан notebook параметрической версии третьего скрипта.

4.7.1 Результаты параметризованного исследования миграции

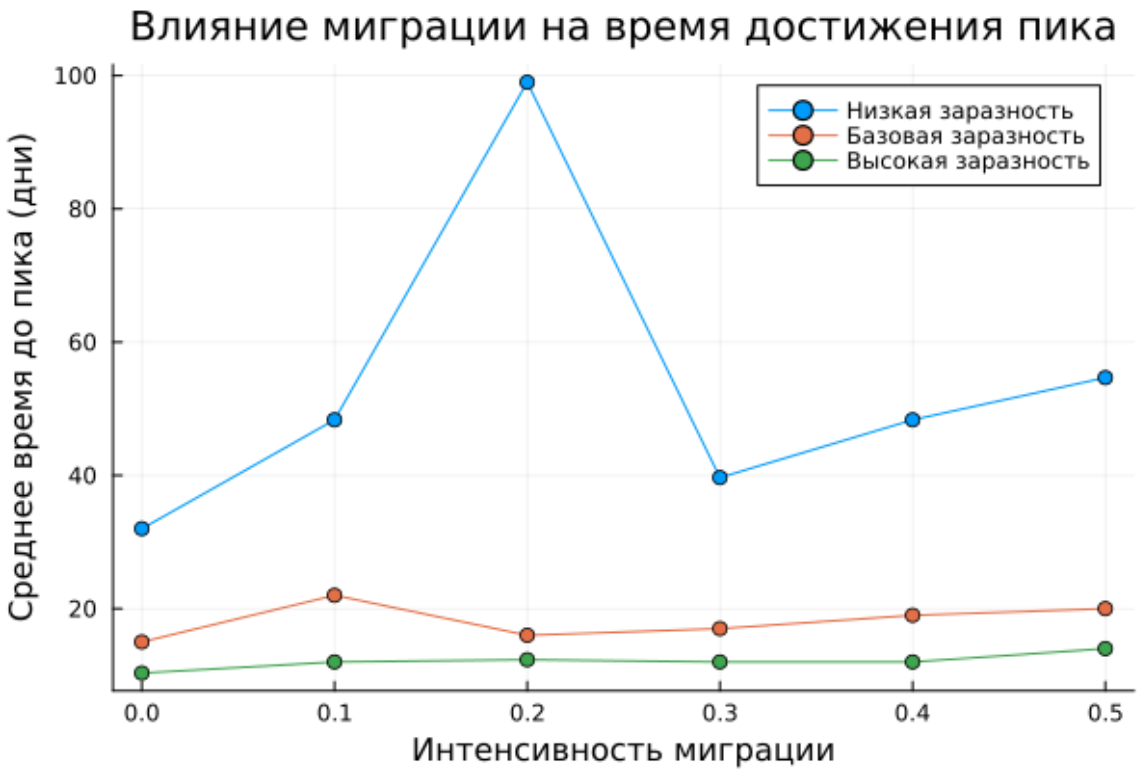

Рисунок 4.21: Сценарное исследование времени до пика при миграции

На рисунке представлена зависимость времени достижения пика от интенсивности миграции в разных сценариях. Это позволяет сравнить скорость распространения инфекции при различных условиях.

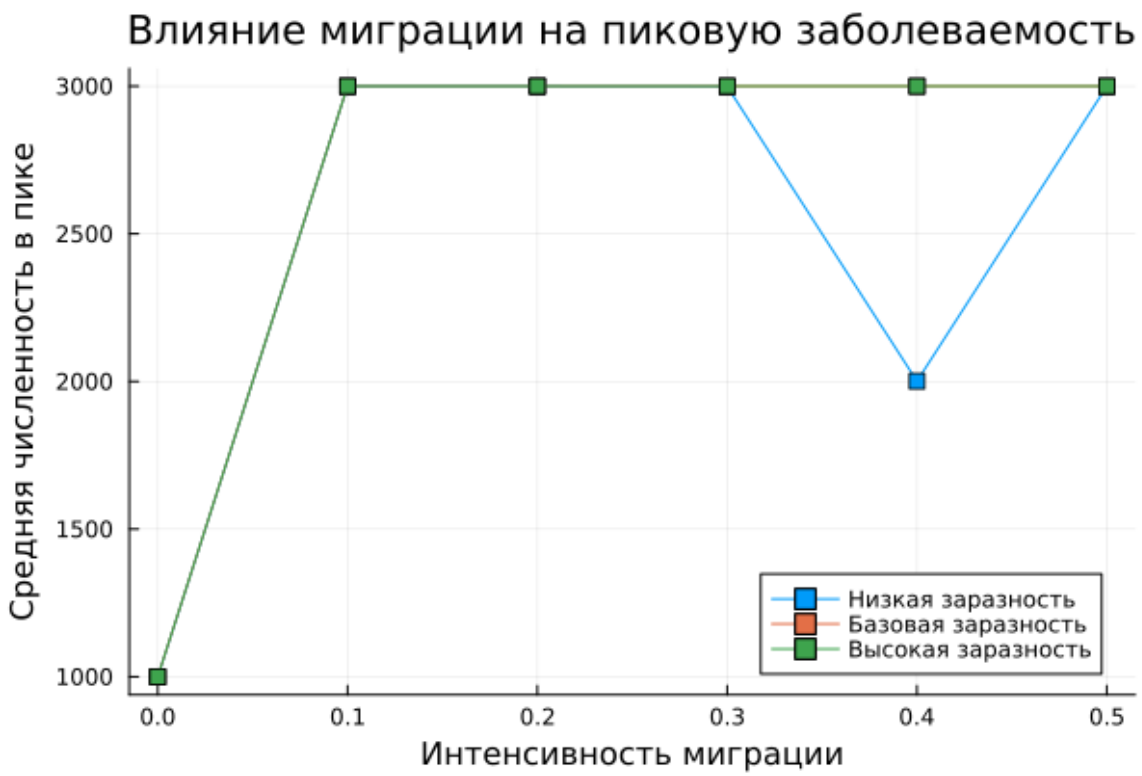

Рисунок 4.22: Сценарное исследование пикового уровня инфицирования при миграции

На рисунке показано, как в разных сценариях меняется величина пика эпидемии. Рост миграции, как правило, способствует более быстрому перемешиванию популяции и усилению распространения инфекции.

Листинг 4.9. Параметризованная версия скрипта исследования миграции sir_migration_params.jl

```
# # [illegible] 4
# ## [illegible] [illegible] [illegible] [illegible] [illegible] SIR
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible],
```

```
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]. [illegible] [illegible]
# [illegible], [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Random
using Statistics

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible].

function create_migration_matrix(C, intensity)
M = ones(C, C) .* intensity / (C - 1)
for i in 1:C
M[i, i] = 1 - intensity
end
return M
end

# ## [illegible] [illegible] [illegible] [illegible]
#
```

```
# □□□ □□□□□□□□□ □□□□□□ □□□□□□□□□□ □□□□□□□□□□□:
#
# - □□□□□ □□□□□□□□□□ □□□□ □□□□□□□□;
# - □□□□□□□□ □□□□ □□□□□□□□.

function peak_time(p)
migration_rates = create_migration_matrix(p[:C], p[:migration_intens

model = initialize_sir(;
Ns = p[:Ns],
□_und = p[:□_und],
□_det = p[:□_det],
infection_period = p[:infection_period],
detection_time = p[:detection_time],
death_rate = p[:death_rate],
reinfection_probability = p[:reinfection_probability],
Is = p[:Is],
seed = p[:seed],
migration_rates = migration_rates,
)

infected_frac(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

peak = 0.0
peak_step = 0

for step in 1:p[:n_steps]
```

```
agent_ids = collect(allids(model))
for id in agent_ids
agent = try
model[id]
catch
nothing
end

if agent !== nothing
sir_agent_step!(agent, model)
end
end

frac = infected_frac(model)
if frac > peak
peak = frac
peak_step = step
end
end

return (peak_time = peak_step, peak_value = peak)
end

# ## □□□□□ □□□□□□□□□
#
# □□□□□□□□□□□□□□□ □□□ □□□□□□□□:
#
# - □□□□□□ □□□□□□□□□□;
```

```
# - [illegible];
# - [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] 10 [illegible], [illegible] [illegible].

scenario_sets = [
(name = "[illegible]", [illegible]_und = [0.3, 0.3, 0.3], [illegible]_det = [0.03, 0.
(name = "[illegible]", [illegible]_und = [0.5, 0.5, 0.5], [illegible]_det = [0.05, 0
(name = "[illegible]", [illegible]_und = [0.7, 0.7, 0.7], [illegible]_det = [0.07, 0
]

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] 0.0 [illegible] 0.5 [illegible] [illegible] 0.1.

migration_intensities = 0.0:0.1:0.5
seeds = [42, 43, 44]

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] seed
# [illegible] [illegible] [illegible] [illegible].

params_list = []

for scenario in scenario_sets
```

```
for mig in migration_intensities
for s in seeds
push!(
params_list,
Dict(
:scenario => scenario.name,
:migration_intensity => mig,
:C => 3,
:Ns => [1000, 1000, 1000],
:□_und => scenario.□_und,
:□_det => scenario.□_det,
:infection_period => 14,
:detection_time => 7,
:death_rate => 0.02,
:reinfection_probability => 0.1,
:Is => [1, 0, 0],
:seed => s,
:n_steps => 150,
),
)
end
end
end

# ## □□□□□□ □□□□□□□□□□□□□
#
# □□□ □□□□ □□□□□□□ □□□□□□□□□□ □□□□□□□□□□□ □□□□□□□□□□□□□.
```

```
results = []

for params in params_list
data = peak_time(params)
push!(results, merge(params, Dict(pairs(data))))
println("□□□□□□□□ = $(params[:scenario]), migration = $(params[:migra
end

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□ □□□□□□ □□□□□□□□□□ □□□□ □□□□□□□□.

df = DataFrame(results)
CSV.write(datadir("migration_scenarios_all.csv"), df)

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□ □□□□□□□□□□ □□ □□□□□□□□□□ □□□□□□□□□ □□□□□□□□ □ □□□□□□□□□□□□□ □□□□□□□□.

grouped = combine(
groupby(df, [:scenario, :migration_intensity]),
:peak_time => mean => :mean_peak_time,
:peak_value => mean => :mean_peak_value,
)

CSV.write(datadir("migration_scenarios_grouped.csv"), grouped)

# ## □□□□□□□□□□ □□□□□□□□ □□□□□□□□ □□ □□□□
```

```
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible].

plot(
xlabel = "[illegible] [illegible]",
ylabel = "[illegible] [illegible] [illegible] [illegible] ([illegible])",
title = "[illegible] [illegible] [illegible] [illegible] [illegible] [illegible]",
linewidth = 2,
)

for scenario in scenario_sets
subset_df = grouped[grouped.scenario .== scenario.name, :]
plot!(
subset_df.migration_intensity,
subset_df.mean_peak_time,
label = scenario.name,
marker = :circle,
)
end

savefig(plotsdir("migration_scenarios_peak_time.png"))

# ## [illegible] [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

plot(
```

```
xlabel = "□□□□□□□□□□□□□ □□□□□□□□",
ylabel = "□□□□□□□ □□□□□□□□□□□ □ □□□□",
title = "□□□□□□□ □□□□□□□□ □□ □□□□□□□ □□□□□□□□□□□□□□",
linewidth = 2,
)

for scenario in scenario_sets
subset_df = grouped[grouped.scenario .== scenario.name, :]
plot!(
subset_df.migration_intensity,
subset_df.mean_peak_value .* 3000,
label = scenario.name,
marker = :square,
)
end

savefig(plotsdir("migration_scenarios_peak_value.png"))

println("□□□□□□□□□□ □□□□□□□□□ □ data/migration_scenarios_all.csv")
println("□□□□□□□□□□□ □□□□□□□□□□ □□□□□□□□□ □ data/migration_scenarios_group
println("□□□□□□□ □□□□□□□□□□ □ plots/migration_scenarios_peak_time.png □ p

# ## □□□□□
#
# □ □□□□□□□□□□ □□□□ □□□□□□□□□□□ □□□□□□□□□ □□□□□□□□□ □ □□□□□□□□□ □□□□□□□□□□□
# □□□□□□□□□ □□□ □□□□□□ □□□□□□□□□ □□□□□□□□□□□□□ □□□□□□□□. □□□ □□□□□□□□□ □□□□□□□,
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# □□□□□□□ □□ □□□□□□□□ □□□□□□□□ □□□□□□□□ □ □□□□□□□□ □□ □□□□.
```

4.8 Скрипт оптимизации параметров модели

Четвёртый скрипт решает задачу оптимизации параметров модели SIR.

4.8.1 Обычная версия

Листинг 4.10. Обычная версия скрипта оптимизации sir_optimize_parameters.jl

```
using DrWatson
@quickactivate "project"

using BlackBoxOptim, Random, Statistics
using Agents
using JLD2

include(srcdir("sir_model.jl"))

function cost_fast(x)
infected_frac(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

dead_count(model) = 1500 - nagents(model)

peak_vals = Float64[]
dead_vals = Float64[]

for rep in 1:2
```

```
model = initialize_sir(;
Ns = [500, 500, 500],
β_und = fill(x[1], 3),
β_det = fill(x[1] / 10, 3),
infection_period = 10,
detection_time = round(Int, x[2]),
death_rate = x[3],
reinfection_probability = 0.1,
Is = [0, 0, 1],
seed = 42 + rep,
n_steps = 50,
)

peak_infected = 0.0

for step in 1:50
Agents.step!(model, 1)
frac = infected_frac(model)
if frac > peak_infected
peak_infected = frac
end
end

push!(peak_vals, peak_infected)
push!(dead_vals, dead_count(model) / 1500)
end

mean_peak = mean(peak_vals)
```

```
mean_dead = mean(dead_vals)

return mean_peak + mean_dead
end

result = bboptimize(
cost_fast;
Method = :random_search,
SearchRange = [
(0.1, 1.0),
(3.0, 14.0),
(0.01, 0.1),
],
NumDimensions = 3,
MaxTime = 20,
TraceMode = :silent,
)

best = best_candidate(result)
fitness = best_fitness(result)

println("□□□□□□□□□□□ □□□□□□□□□:")
println("□_und = $(best[1])")
println("□□□□□ □□□□□□□□□ = $(round(Int, best[2])) □□□□")
println("□□□□□□□□□□ = $(best[3])")

println("□□□□□□□□ □□□□□□□ □□□□□□□: $(fitness)")
```

```
save(
datadir("optimization_fast_result.jld2"),
Dict(
"best" => best,
"fitness" => fitness,
),
)
```

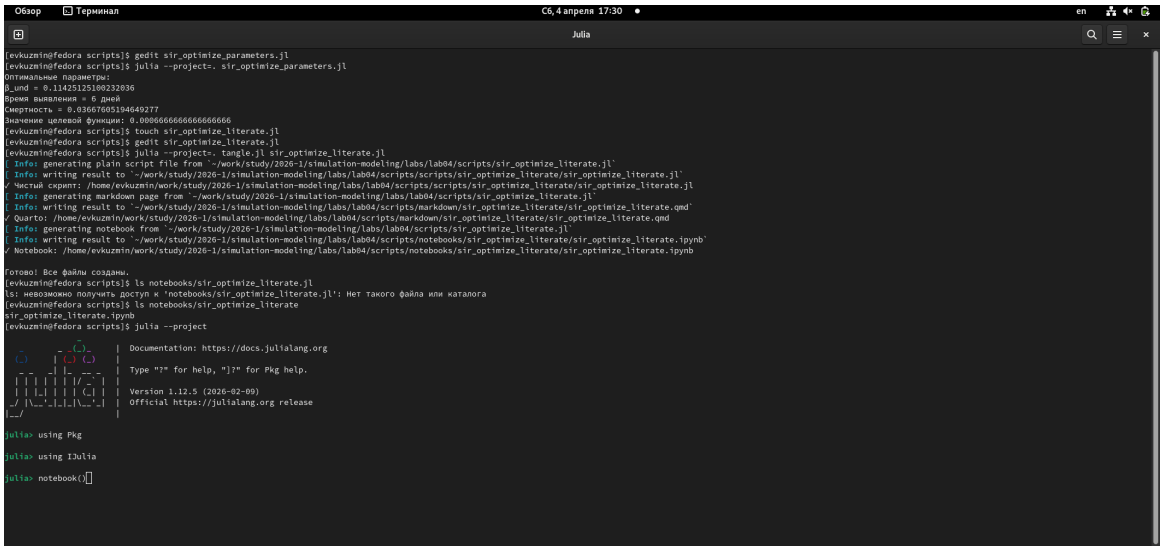

Рисунок 4.23: Создание и выполнение четвёртого скрипта, подготовка literate-версии

На рисунке показан запуск четвёртого скрипта и создание его literate-версии.

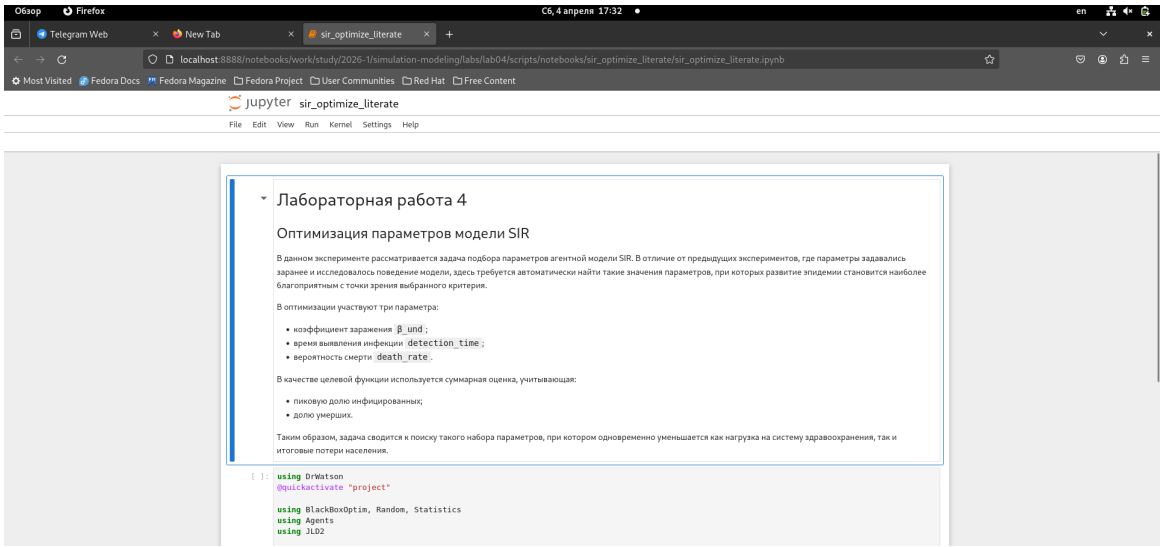

Рисунок 4.24: Notebook literate-версии четвёртого скрипта

На рисунке представлен notebook literate-версии четвёртого скрипта.

4.8.2 Literate-версия

Листинг 4.11. Literate-версия скрипта оптимизации sir_optimize_literate.jl

```
# # [redacted] 4
# ## [redacted] [redacted] [redacted] SIR
#
# [redacted] [redacted] [redacted] [redacted] [redacted] [redacted]
# [redacted] [redacted] SIR. [redacted] [redacted] [redacted] [redacted], [redacted]
# [redacted] [redacted] [redacted] [redacted] [redacted] [redacted],
# [redacted] [redacted] [redacted] [redacted] [redacted] [redacted],
# [redacted] [redacted] [redacted] [redacted] [redacted] [redacted]
# [redacted] [redacted] [redacted] [redacted].
#
# [redacted] [redacted] [redacted] [redacted]:
```

```
#
# - [illegible] [illegible] `[illegible]_und`;
# - [illegible] [illegible] [illegible] `detection_time`;
# - [illegible] [illegible] `death_rate`.
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible],
# [illegible]:
#
# - [illegible] [illegible] [illegible];
# - [illegible] [illegible].
#
# [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible] [illegible],
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible], [illegible] [illegible] [illegible] [illegible] [illegible].

using DrWatson
@quickactivate "project"

using BlackBoxOptim, Random, Statistics
using Agents
using JLD2

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] `x`, [illegible]:
#
```

```
# - `x[1]` — □□□□□□□□□□□ □□□□□□□□□ `□_und`;
# - `x[2]` — □□□□□ □□□□□□□□□ □□□□□□□□;
# - `x[3]` — □□□□□□□□□□□ □□□□□□.
#
# □□□ □□□□□□□□□□ □□□□□□□ □□□□□□□□□□□ □□□□□□□□□ □□□□□□□□□□□
# □□ □□□□□□□□□□ □□□□□□□□ □□□□□□.

function cost_fast(x)
infected_frac(model) =
count(a.status == :I for a in allagents(model)) / nagents(model)

dead_count(model) = 1500 - nagents(model)

peak_vals = Float64[]
dead_vals = Float64[]

for rep in 1:2
model = initialize_sir(;
Ns = [500, 500, 500],
□_und = fill(x[1], 3),
□_det = fill(x[1] / 10, 3),
infection_period = 10,
detection_time = round(Int, x[2]),
death_rate = x[3],
reinfection_probability = 0.1,
Is = [0, 0, 1],
seed = 42 + rep,
n_steps = 50,
```

```
)

peak_infected = 0.0

for step in 1:50
Agents.step!(model, 1)
frac = infected_frac(model)
if frac > peak_infected
peak_infected = frac
end
end

push!(peak_vals, peak_infected)
push!(dead_vals, dead_count(model) / 1500)
end

mean_peak = mean(peak_vals)
mean_dead = mean(dead_vals)

return mean_peak + mean_dead
end

# ## □□□□□□ □□□□□□□□□□□
#
# □□□ □□□□□□ □□□□□□□□□□□ □□□□□□□□ □□□□□□□□□□□ □□□□□□□□ □□□□□□□□□□ □□□□□□.
# □□ □□□□□□□□ □□□□□□□ □□□□□ □□□□□□□ □□□□□□□□□□□□□□□□□□ □□□□□□□ □ □□□□□□□□
# □□□ □□□□□□□□□□□ □□□□□□□□□□□□□□□□ □□□□□□ □□□□□□.
```

```
result = bboptimize(
cost_fast;
Method = :random_search,
SearchRange = [
(0.1, 1.0),
(3.0, 14.0),
(0.01, 0.1),
],
NumDimensions = 3,
MaxTime = 20,
TraceMode = :silent,
)

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□ □□□□□□□□□□ □□□□□□□□□□□ □□□□□□□□□□□ □□□□□□□□□ □□□□□□□□□
# □ □□□□□□□□ □□□□□□□ □□□□□□□.

best = best_candidate(result)
fitness = best_fitness(result)

println("□□□□□□□□□□□ □□□□□□□□□:")
println("□_und = $(best[1])")
println("□□□□□ □□□□□□□□□ = $(round(Int, best[2])) □□□□")
println("□□□□□□□□□□ = $(best[3])")

println("□□□□□□□□ □□□□□□□ □□□□□□□: $(fitness)")
```

```
# ## [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible].

save(
datadir("optimization_fast_result.jld2"),
Dict(
"best" => best,
"fitness" => fitness,
),
)

# ## [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible],
# [illegible] [illegible] [illegible] [illegible].
# [illegible], [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible], [illegible] [illegible] [illegible] [illegible],
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible].
```

4.9 Параметризованная версия скрипта оптимизации

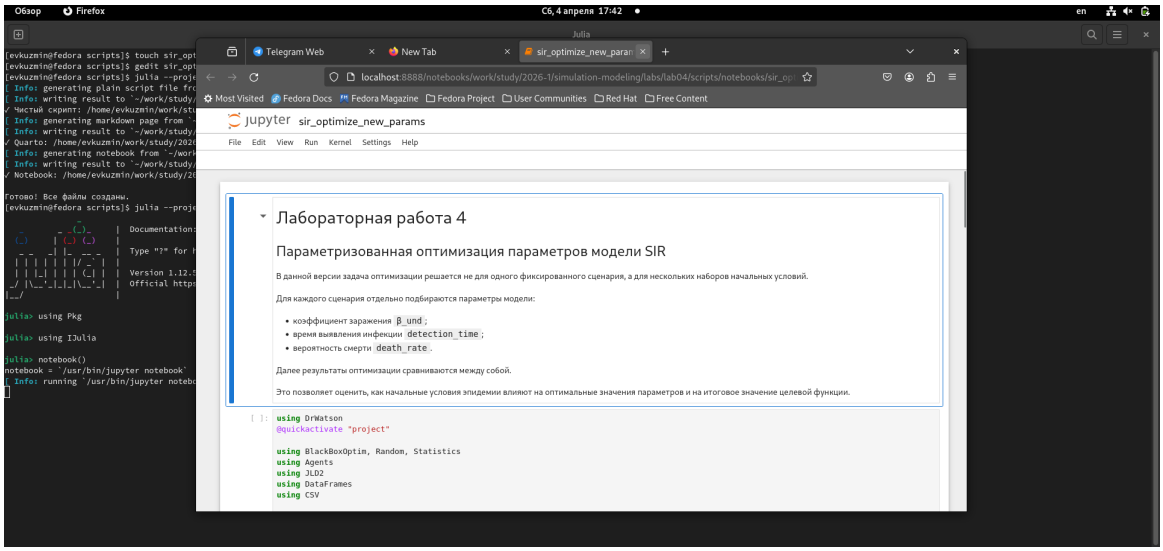

Рисунок 4.25: Генерация файлов и notebook для параметризованной версии четвёртого скрипта

На рисунке показан этап генерации артефактов для параметризованной версии четвёртого скрипта.

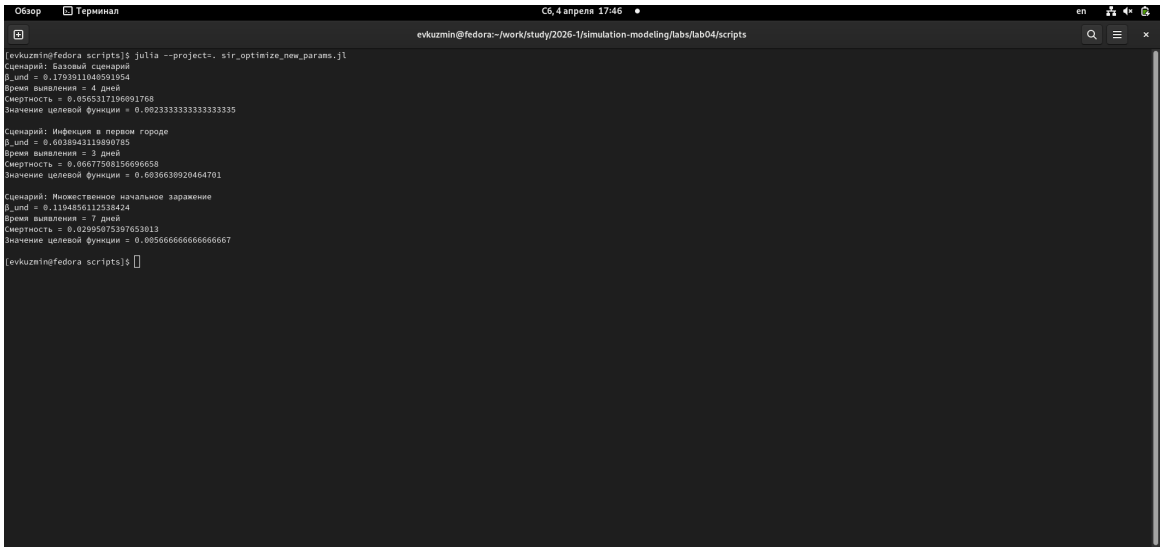

Рисунок 4.26: Выполненная параметризованная версия четвёртого скрипта

На рисунке показан запуск параметризованной версии четвёртого скрипта.

4.9.1 Параметризованная версия

Листинг 4.12. Параметризованная версия скрипта оптимизации sir_optimize_new_params.jl

```
# # [illegible] 4
# ## [illegible] SIR
#
# [illegible]
# [illegible], [illegible].
#
# [illegible]:
#
# - [illegible] `[illegible]_und`;
# - [illegible] `detection_time`;
# - [illegible] `death_rate`.
#
# [illegible].
#
# [illegible], [illegible]
# [illegible] [illegible].

using DrWatson
@quickactivate "project"

using BlackBoxOptim, Random, Statistics
using Agents
using JLD2
```

```
using DataFrames
using CSV

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible]
#
# [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

scenario_sets = [
(name = "[illegible] [illegible]", Is = [0, 0, 1], Ns = [500, 500, 500]),
(name = "[illegible] [illegible] [illegible]", Is = [1, 0, 0], Ns = [500, 500, 500]
(name = "[illegible] [illegible] [illegible]", Is = [5, 0, 0], Ns = [500, 50
]

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible], [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

function make_cost_function(scenario)
    function cost_fast(x)
        infected_frac(model) =
            count(a.status == :I for a in allagents(model)) / nagen
```

```
        total_population = sum(scenario.Ns)
        dead_count(model) = total_population - nagents(model)

        peak_vals = Float64[]
        dead_vals = Float64[]

        for rep in 1:2
            model = initialize_sir(;
                Ns = scenario.Ns,
                β_und = fill(x[1], 3),
                β_det = fill(x[1] / 10, 3),
                infection_period = 10,
                detection_time = round(Int, x[2]),
                death_rate = x[3],
                reinfection_probability = 0.1,
                Is = scenario.Is,
                seed = 42 + rep,
                n_steps = 50,
            )

            peak_infected = 0.0

            for step in 1:50
                Agents.step!(model, 1)
                frac = infected_frac(model)
                if frac > peak_infected
                    peak_infected = frac
                end
```

```
            end

            push!(peak_vals, peak_infected)
            push!(dead_vals, dead_count(model) / total_population)
        end

        mean_peak = mean(peak_vals)
        mean_dead = mean(dead_vals)

        return mean_peak + mean_dead
    end

    return cost_fast
end

# ## □□□□□□□□□□ □□□□□□□□□□□ □□□ □□□□ □□□□□□□□□
#
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# □□□□□□□□□ □□□□□□□□□.

results = DataFrame(
    scenario = String[],
    beta_und = Float64[],
    detection_time = Int[],
    death_rate = Float64[],
    fitness = Float64[],
)
```

```
for scenario in scenario_sets
    cost_fun = make_cost_function(scenario)

    result = bboptimize(
        cost_fun;
        Method = :random_search,
        SearchRange = [
            (0.1, 1.0),
            (3.0, 14.0),
            (0.01, 0.1),
        ],
        NumDimensions = 3,
        MaxTime = 20,
        TraceMode = :silent,
    )

    best = best_candidate(result)
    fitness = best_fitness(result)

    push!(
        results,
        (
            scenario.name,
            best[1],
            round(Int, best[2]),
            best[3],
            fitness,
        ),
```

```
    )

    println("□□□□□□□□: $(scenario.name)")
    println("□_und = $(best[1])")
    println("□□□□□ □□□□□□□□□ = $(round(Int, best[2])) □□□□")
    println("□□□□□□□□□□ = $(best[3])")
    println("□□□□□□□□ □□□□□□□ □□□□□□□ = $(fitness)")
    println()
end

# ## □□□□□□□□ □□□□□□□□ □□□□□□□

results

# ## □□□□□□□□□□ □□□□□□□□□□□
#
# □□□□□□□□ □□□□□□□ □□ □□□□□ □□□□□□□□□□.

CSV.write(datadir("optimization_scenarios.csv"), results)

save(
    datadir("optimization_scenarios.jld2"),
    Dict("results" => results),
)

# ## □□□□□
#
# □ □□□□□□□□□□ □□□□ □□□□□□□□ □□□□□□□□□□□ □□□□□□□□ □□□□□□ □□□ □□□□□□□□□□
```

```
# [illegible] [illegible] [illegible]. [illegible] [illegible], [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible].
```

4.10 Скрипт комплексной визуализации результатов

Пятый скрипт используется для построения составного рисунка по уже рассчитанным данным.

4.10.1 Обычная версия и literate-версия

Листинг 4.13. Скрипт комплексной визуализации sir_visualize_dynamics.jl

```
using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV

include(srcdir("sir_model.jl"))

# [illegible] [illegible] [illegible]
df = CSV.read(datadir("beta_scan_all.csv"), DataFrame)

# [illegible] [illegible]: [illegible] [illegible] [illegible] [illegible]
p1 = plot(
```

```
    df.beta,
    df.peak,
    label = "□□□",
    xlabel = "□",
    ylabel = "□□□□ □□□□□□□□□□□□□□",
)

plot!(
    p1,
    df.beta,
    df.final_inf,
    label = "□□□□□□□□",
)

# □□□□□□ □□□□□□: □□□□□ □□□□□□□
p2 = plot(
    df.beta,
    df.deaths,
    xlabel = "□",
    ylabel = "□□□□□ □□□□□□□",
    label = "□□□□□□□",
)

# □□□□□□ □□□□□□: □□□□ □□□□□□□□□□□□□
p3 = plot(
    df.beta,
    df.final_rec,
    xlabel = "□",
```

```
    ylabel = "□□□□ □□□□□□□□□□□□□",
    label = "□□□□□□□□□□□□□□",
)

# □□□□□□□□□□ □□□□□□□
plot(
    p1,
    p2,
    p3,
    layout = (3, 1),
    size = (800, 900),
)

savefig(plotsdir("comprehensive_analysis.png"))
```

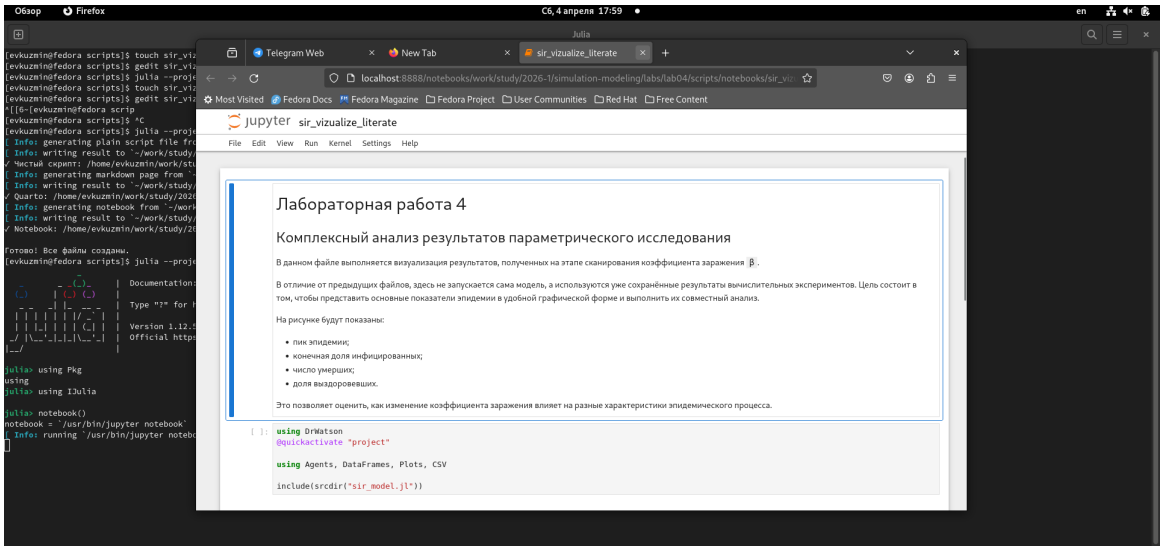

Рисунок 4.27: Создание и выполнение пятого скрипта, генерация literate-версии и notebook

На рисунке показан этап выполнения пятого скрипта и генерации для него notebook и literate-версии.

4.10.2 Результат комплексного анализа

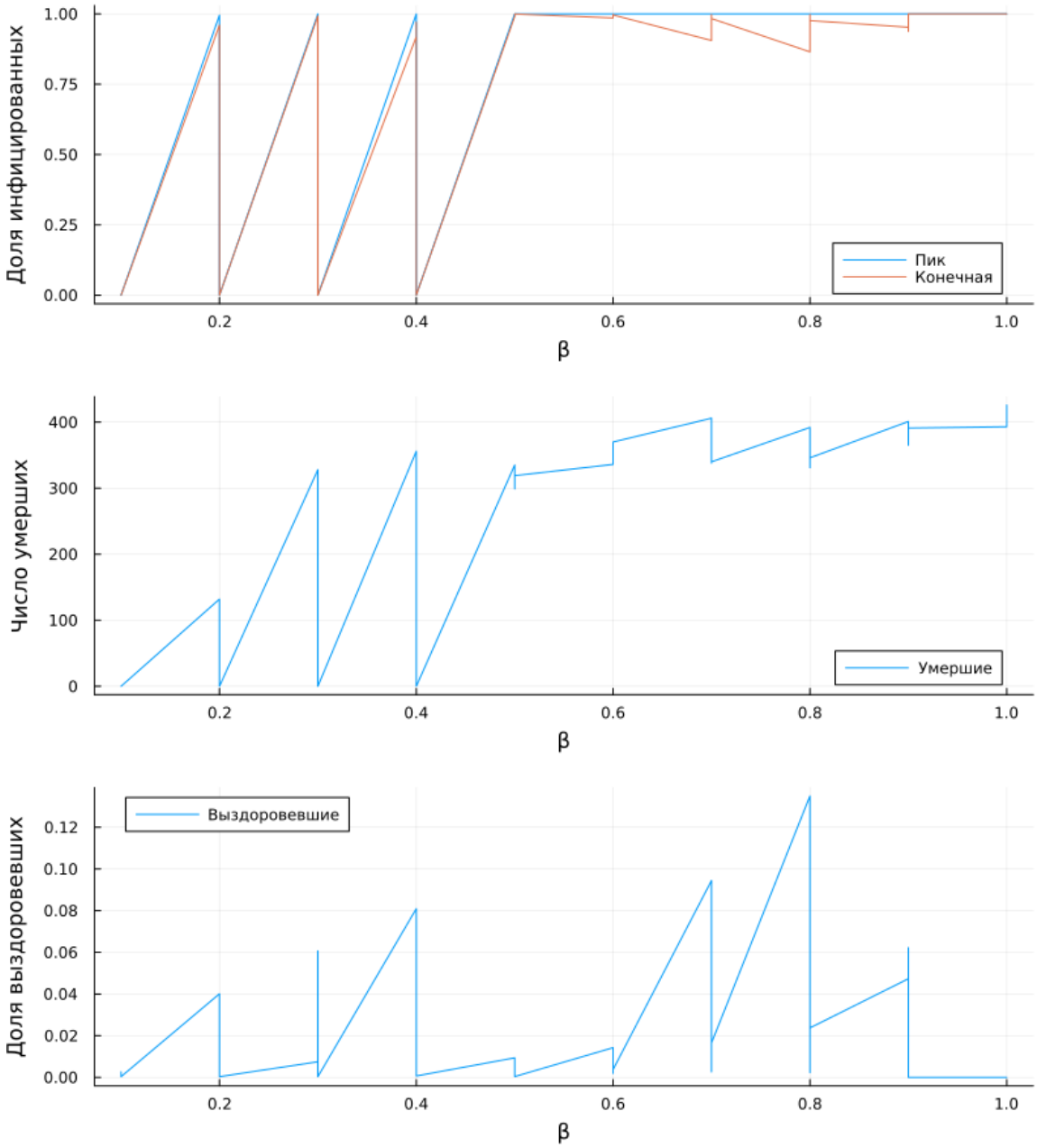

Рисунок 4.28: Комплексный анализ результатов моделирования

На рисунке объединены несколько итоговых зависимостей: пик эпидемии, конечная доля инфицированных, число умерших и доля выздоровевших. Такой

составной график позволяет одновременно анализировать несколько ключевых характеристик модели.

Листинг 4.14. Literate-версия скрипта комплексной визуализации sir_visualize_literate.jl

```
# # [illegible] 4
# ## [illegible]
#
# [illegible], [illegible]
# [illegible] `[illegible]`.
#
# [illegible], [illegible],
# [illegible].
# [illegible], [illegible]
# [illegible].
#
# [illegible]:
#
# - [illegible];
# - [illegible];
# - [illegible];
# - [illegible].
#
# [illegible], [illegible]
# [illegible].

using DrWatson
@quickactivate "project"
```

```julia
using Agents, DataFrames, Plots, CSV

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] CSV-[illegible].

df = CSV.read(datadir("beta_scan_all.csv"), DataFrame)

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible];
# - [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible].

p1 = plot(
    df.beta,
    df.peak,
    label = "[illegible]",
    xlabel = "[illegible]",
    ylabel = "[illegible] [illegible]",
)
```

```
plot!(
    p1,
    df.beta,
    df.final_inf,
    label = "□□□□□□□□",
)

# ## □□□□□□□□□□ □□□□□□□ □□□□□□□
#
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p2 = plot(
    df.beta,
    df.deaths,
    xlabel = "□",
    ylabel = "□□□□□ □□□□□□□",
    label = "□□□□□□□",
)

# ## □□□□□□□□□□ □□□□□□□□ □□□□□□□
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p3 = plot(
    df.beta,
    df.final_rec,
```

```
    xlabel = "□",
    ylabel = "□□□□ □□□□□□□□□□□□□",
    label = "□□□□□□□□□□□□□",
)

# ## □□□□□□□□□□□□ □□□□□□□□□□ □□□□□□□
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plot(
    p1,
    p2,
    p3,
    layout = (3, 1),
    size = (800, 900),
)

savefig(plotsdir("comprehensive_analysis.png"))

# ## □□□□□
#
# □ □□□□□□□□□□ □□□ □□□□□□□□ □□□□□□□□□ □□□□□□□, □□□□□□□□□□ □□□□□□□
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# □□□□□□□□□□ □ □□□□□□□□□□□□□□.
```

5 Дополнительные задания

5.1 Дополнительные задания 1–3

Дополнительные задания 1–3 объединены в один скрипт, так как они связаны с базовой динамикой модели, исследованием порога эпидемии и анализом гетерогенности коэффициента заражения.

Листинг 5.1. Скрипт дополнительных заданий 1–3

extra_1_2_3.jl

```
# # [redacted] 1–3
# ## [redacted], [redacted] [redacted] [redacted] [redacted]
#
# [redacted] [redacted] [redacted] [redacted] [redacted]:
#
# - [redacted] [redacted] [redacted] [redacted] [redacted] [redacted] [redacted];
# - [redacted] [redacted];
# - [redacted] [redacted] [redacted] [redacted] [redacted].
#
# [redacted] [redacted] [redacted], [redacted] [redacted] [redacted] [redacted]
# [redacted] [redacted] [redacted] `[redacted]` [redacted] [redacted] [redacted] [redacted] [redacted] SIR.

using DrWatson
@quickactivate "project"
```

```
using Agents, DataFrames, Plots, CSV, Statistics
using JLD2

include(srcdir("sir_model.jl"))

function main()

# ## 1. □□□□□□□ □□□□□□□
#
# □□□□□□□ □□□□□□□□ □□□□□□ □□□□□□ □ □□□□□□□□□□□ □□ □□□□□□□□□□,
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# □ □□□□□□□□ □□□□□□□ □□□□□□□□□□□□□□ □□□□□:
#
# $$ R_0 = \frac{\beta}{\gamma}, \quad \gamma = \frac{1}{infection\

params_basic = Dict(
    :Ns => [1000, 1000, 1000],
    :□_und => [0.5, 0.5, 0.5],
    :□_det => [0.05, 0.05, 0.05],
    :infection_period => 14,
    :detection_time => 7,
    :death_rate => 0.02,
    :reinfection_probability => 0.1,
    :Is => [0, 0, 1],
    :seed => 42,
    :n_steps => 100,
)
```

```
model = initialize_sir(; params_basic...)

times = Int[]
S_vals = Int[]
I_vals = Int[]
R_vals = Int[]

for step in 1:params_basic[:n_steps]
    Agents.step!(model, 1)
    push!(times, step)
    push!(S_vals, susceptible_count(model))
    push!(I_vals, infected_count(model))
    push!(R_vals, recovered_count(model))
end

basic_df = DataFrame(
    time = times,
    susceptible = S_vals,
    infected = I_vals,
    recovered = R_vals,
)

□ = 1 / params_basic[:infection_period]
R0 = params_basic[:□_und][1] / □

p_basic = plot(
    basic_df.time,
    basic_df.susceptible,
```

```
    label = "S",
    xlabel = "□□□",
    ylabel = "□□□□□□□□□□□",
    title = "□□□□□□□ □□□□□□□□ SIR",
)
plot!(p_basic, basic_df.time, basic_df.infected, label = "I")
plot!(p_basic, basic_df.time, basic_df.recovered, label = "R")
savefig(p_basic, plotsdir("extra_1_basic_sir.png"))

println("□□□□□□□ □□□□□□□□□□□□□□ □□□□□ R0 = $(round(R0, digits=3))")

# ## 2. □□□□□□□□□□□ □□□□□□
#
# □□□□□□ □□□□□□□□□, □□□ □□□□□ □□□□□□□□□□□ □□□□□□□□ `□`
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#
# $$ R_0 = 1 \Rightarrow \beta = \gamma. $$

beta_range = 0.05:0.05:1.0
threshold_beta = nothing
threshold_peak = nothing
population_total = sum(params_basic[:Ns])

threshold_results = DataFrame(
    beta = Float64[],
```

```
    peak_fraction = Float64[],
)

for beta in beta_range
    model_thr = initialize_sir(;
        Ns = params_basic[:Ns],
        β_und = fill(beta, 3),
        β_det = fill(beta / 10, 3),
        infection_period = params_basic[:infection_period],
        detection_time = params_basic[:detection_time],
        death_rate = params_basic[:death_rate],
        reinfection_probability = params_basic[:reinfection_probabi
        Is = params_basic[:Is],
        seed = params_basic[:seed],
        n_steps = params_basic[:n_steps],
    )

    peak_fraction = 0.0

    for step in 1:params_basic[:n_steps]
        Agents.step!(model_thr, 1)
        frac = infected_count(model_thr) / population_total
        if frac > peak_fraction
            peak_fraction = frac
        end
    end

    push!(threshold_results, (beta, peak_fraction))
```

```
    if threshold_beta === nothing && peak_fraction > 0.05
        threshold_beta = beta
        threshold_peak = peak_fraction
    end
end

theoretical_beta = □

p_threshold = plot(
    threshold_results.beta,
    threshold_results.peak_fraction,
    label = "□□□□□□□ □□□□ I",
    xlabel = "□",
    ylabel = "□□□□ □□□□□□□□□□□□□□",
    title = "□□□□□□□□□□□□ □□□□□□ □□□□□□□□",
)
hline!(p_threshold, [0.05], label = "□□□□□ 5%")
vline!(p_threshold, [theoretical_beta], label = "□□□□□□□□□□□□□ □□□□□ R₀
savefig(p_threshold, plotsdir("extra_2_threshold.png"))

println("□□□□□□□□□□□□□ □□□□□ beta = $(round(theoretical_beta, digits=3)
if threshold_beta !== nothing
    println("□□□□□□□□□ □□□□□ beta = $(threshold_beta), □□□ = $(round(th
else
    println("□ □□□□□□□□□ beta □□□□□ □□ □□□□□□")
end

CSV.write(datadir("extra_2_threshold_results.csv"), threshold_resul
```

```
# ## 3. □□□□□□ □□□□□□□□□□□□□□□
#
# □□ □□□□□ □□□□□□ □□□□□□□□ □□□□□□□ □□□□□□□□□□□□□ □□□□□□□□□□ □□□ □□□□□□ □□□□□□□□
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#
# - □□□□□□ 1: `□ = 0.2`
# - □□□□□□ 2: `□ = 0.5`
# - □□□□□□ 3: `□ = 0.8`

params_hetero = Dict(
    :Ns => [1000, 1000, 1000],
    :□_und => [0.2, 0.5, 0.8],
    :□_det => [0.02, 0.05, 0.08],
    :infection_period => 14,
    :detection_time => 7,
    :death_rate => 0.02,
    :reinfection_probability => 0.1,
    :Is => [0, 0, 1],
    :seed => 42,
    :n_steps => 100,
)

model_hetero = initialize_sir(; params_hetero...)

hetero_total = DataFrame(
    time = Int[],
```

```
    infected = Int[],
)

hetero_city = DataFrame(
    time = Int[],
    city = Int[],
    infected = Int[],
)

for step in 1:params_hetero[:n_steps]
    Agents.step!(model_hetero, 1)

    push!(hetero_total, (step, infected_count(model_hetero)))

    for city in 1:3
        city_inf = count(a.status == :I && a.pos == city for a in a
        push!(hetero_city, (step, city, city_inf))
    end
end

p_total = plot(
    hetero_total.time,
    hetero_total.infected,
    label = "□□□□□ □□□□□□□□ I",
    xlabel = "□□□",
    ylabel = "□□□□□ □□□□□□□□□□□□□□",
    title = "□□□□□□□□□□□□□□: □□□□□ □□□□□□□□",
)
```

```
savefig(p_total, plotsdir("extra_3_heterogeneity_total.png"))

p_city = plot(
    xlabel = "□□□",
    ylabel = "□□□□□ □□□□□□□□□□□□□□",
    title = "□□□□□□□□□□□□□□: □□□□□□□□ □□ □□□□□□□",
)
for city in 1:3
    subdf = hetero_city[hetero_city.city .== city, :]
    plot!(p_city, subdf.time, subdf.infected, label = "□□□□□ $city")
end
savefig(p_city, plotsdir("extra_3_heterogeneity_by_city.png"))

CSV.write(datadir("extra_3_heterogeneity_total.csv"), hetero_total)
CSV.write(datadir("extra_3_heterogeneity_by_city.csv"), hetero_city

save(datadir("extra_1_basic_result.jld2"), Dict(
    "R0" => R0,
    "basic_df" => basic_df,
    "threshold_beta" => threshold_beta,
    "threshold_peak" => threshold_peak,
))

# ## □□□□□
#
# □ □□□□□□□□□□ □□□□□□□□□□ □□□□□□□□□□□□□□ □□□□□□□ 1-3 □□□□:
#
# - □□□□□□□□ □□□□□□□ □□□□□□□□□□ `S`, `I`, `R`;
```

```
# - [illegible] [illegible] [illegible] [illegible] `R₀`;
# - [illegible] [illegible] [illegible] [illegible] [illegible] `[illegible]`;
# - [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible].

end

main()
```

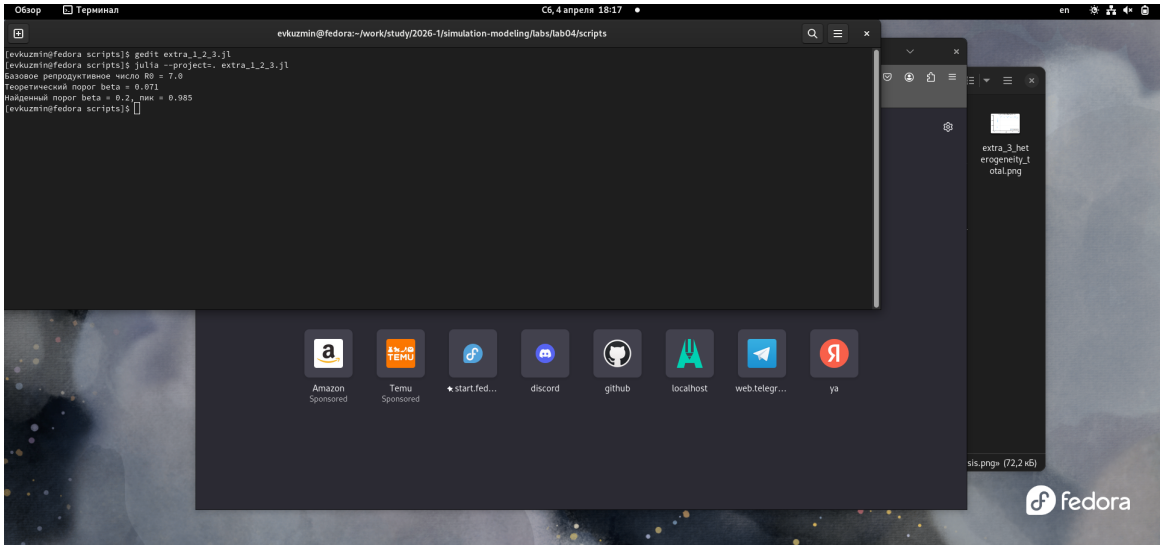

Рисунок 5.1: Создание и выполнение скрипта дополнительных заданий 1–3

На рисунке показан запуск скрипта, объединяющего дополнительные задания 1–3.

5.1.1 Базовая динамика

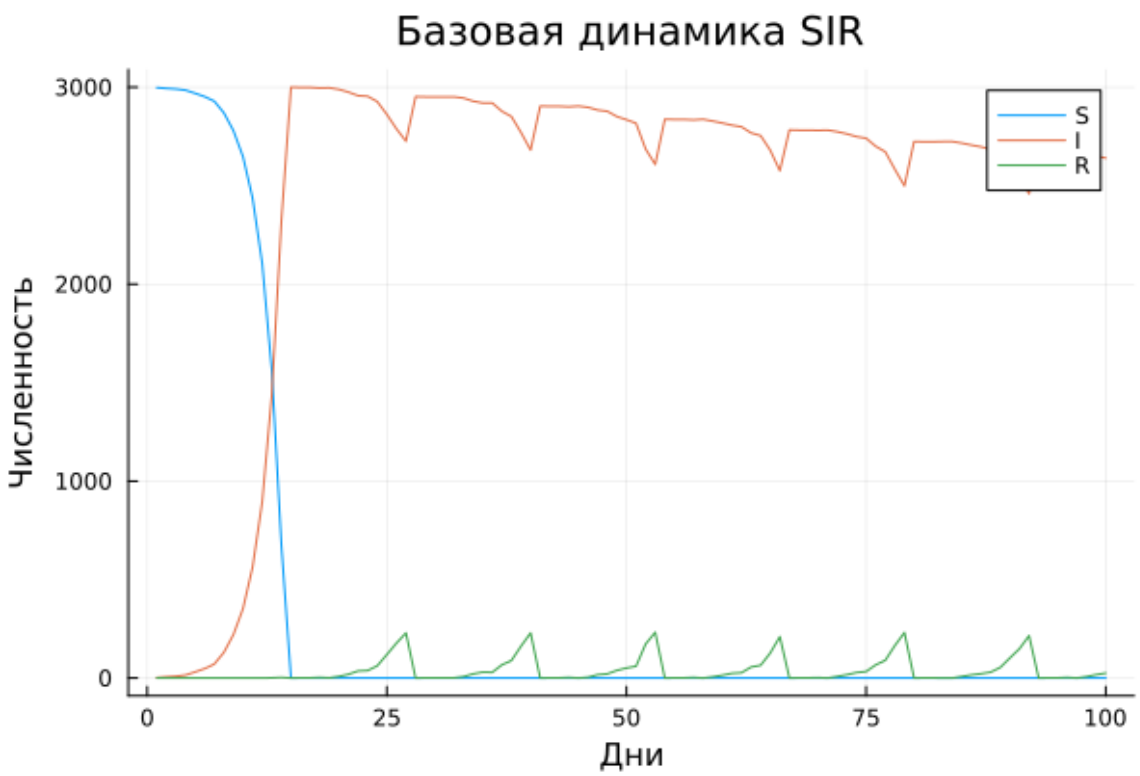

Рисунок 5.2: Базовая динамика SIR для дополнительных заданий

На рисунке показана базовая динамика системы SIR для дополнительных заданий. Видно, что эпидемический процесс проходит стадию роста, достигает пика и затем затухает за счёт уменьшения числа восприимчивых и накопления выздоровевших.

5.1.2 Исследование порога

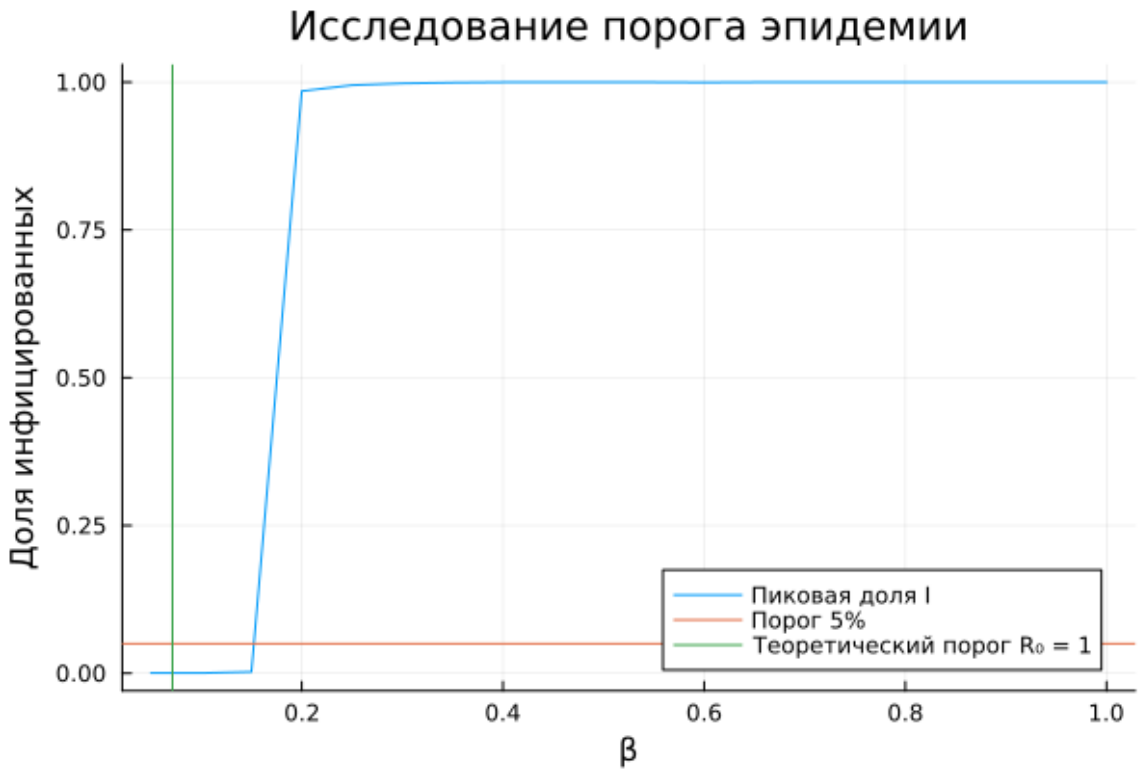

Рисунок 5.3: Исследование порога эпидемии

На рисунке показано исследование эпидемического порога. Горизонтальная линия соответствует уровню 5% популяции, а вертикальная — теоретическому порогу R_0 = 1. Сравнение позволяет сопоставить теоретические оценки и наблюдаемые результаты моделирования.

5.1.3 Гетерогенность

Рисунок 5.4: Динамика инфицированных по городам при гетерогенных параметрах

На рисунке показаны траектории числа инфицированных в отдельных городах при различных значениях β. Более высокая заразность в отдельном городе приводит к более интенсивному локальному развитию эпидемии.

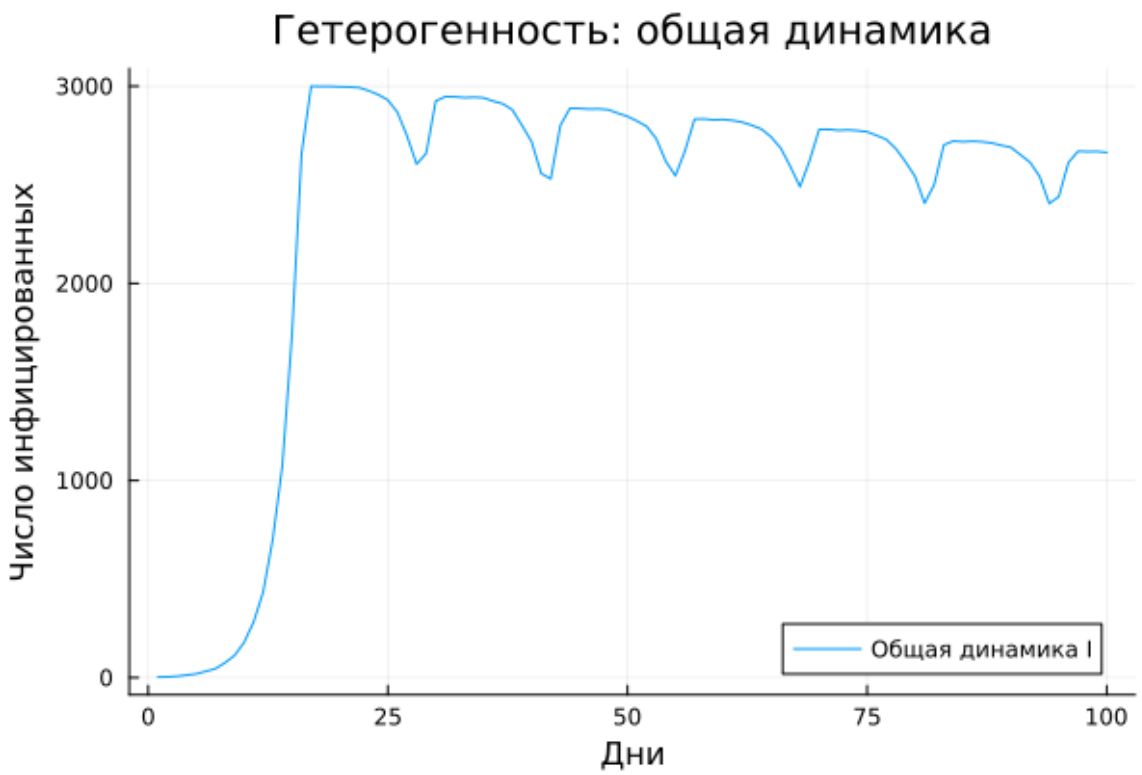

Рисунок 5.5: Общая динамика при гетерогенных параметрах

На рисунке представлена общая динамика инфицированных при гетерогенных параметрах. Введение неоднородности делает поведение системы более сложным по сравнению с однородным случаем.

5.2 Дополнительные задания 4–5

Задания 4 и 5 объединены в один скрипт, так как обе постановки связаны с миграцией и ограничением перемещений между городами.

Листинг 5.2. Скрипт дополнительных заданий 4–5

extra_4_5.jl

```
# # [illegible] 4-5
# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible] [illegible] [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]: [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible], [illegible] [illegible] [illegible].

using DrWatson
@quickactivate "project"

using Agents, DataFrames, Plots, CSV, Statistics
using JLD2

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible].

function create_migration_matrix(C, intensity)
```

```
    M = ones(C, C) .* intensity / (C - 1)
    for i in 1:C
        M[i, i] = 1 - intensity
    end
    return M
end

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible], [illegible] [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

function peak_time_without_quarantine(p)
    migration_rates = create_migration_matrix(p[:C], p[:migration_i

    model = initialize_sir(;
        Ns = p[:Ns],
        [illegible]_und = p[:[illegible]_und],
        [illegible]_det = p[:[illegible]_det],
        infection_period = p[:infection_period],
        detection_time = p[:detection_time],
        death_rate = p[:death_rate],
        reinfection_probability = p[:reinfection_probability],
        Is = p[:Is],
```

```
        seed = p[:seed],
        migration_rates = migration_rates,
    )

    infected_frac(model) =
        count(a.status == :I for a in allagents(model)) / nagents(m

    peak = 0.0
    peak_step = 0

    for step in 1:p[:n_steps]
        agent_ids = collect(allids(model))
        for id in agent_ids
            agent = try
                model[id]
            catch
                nothing
            end
            if agent !== nothing
                sir_agent_step!(agent, model)
            end
        end

        frac = infected_frac(model)
        if frac > peak
            peak = frac
            peak_step = step
        end
```

```
    end

    return (peak_time = peak_step, peak_value = peak)
end

# ## □□□□□□□□ □ □□□□□□□□□□□
#
# □ □□□□ □□□□□□□□ □□□□□□□□□□□□ □□□□□□□ □□□□□□□□□□□ □□□□:
# □□□□ □□□□ □□□□□□□□□□□□□□□ □ □□□□□□ □□□□□□□□□ □□□□□□□□ □□□□□,
# □□□□□□□□□ □□ □□□□□ □□□□□□ □□□□□□□□□□□.

function peak_time_with_quarantine(p)
    migration_rates = create_migration_matrix(p[:C], p[:migration_i

    model = initialize_sir(;
        Ns = p[:Ns],
        □_und = p[:□_und],
        □_det = p[:□_det],
        infection_period = p[:infection_period],
        detection_time = p[:detection_time],
        death_rate = p[:death_rate],
        reinfection_probability = p[:reinfection_probability],
        Is = p[:Is],
        seed = p[:seed],
        migration_rates = copy(migration_rates),
    )

    infected_frac(model) =
```

```
        count(a.status == :I for a in allagents(model)) / nagents(m

    peak = 0.0
    peak_step = 0

    quarantine_threshold = p[:quarantine_threshold]
    quarantined_cities = falses(p[:C])

    for step in 1:p[:n_steps]
        for city in 1:p[:C]
            city_population = count(a.pos == city for a in allagent
            city_infected = count(a.status == :I && a.pos == city f

            if city_population > 0
                city_frac = city_infected / city_population
                if city_frac > quarantine_threshold && !quarantined
                    model.migration_rates[city, :] .= 0.0
                    model.migration_rates[city, city] = 1.0
                    quarantined_cities[city] = true
                end
            end
        end

        agent_ids = collect(allids(model))
        for id in agent_ids
            agent = try
                model[id]
            catch
```

```
                nothing
            end
            if agent !== nothing
                sir_agent_step!(agent, model)
            end
        end

        frac = infected_frac(model)
        if frac > peak
            peak = frac
            peak_step = step
        end
    end

    return (peak_time = peak_step, peak_value = peak)
end

function main()

# ## [illegible] [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] 0.0 [illegible] 0.5
# [illegible] 0.1. [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible].

    migration_intensities = 0.0:0.1:0.5
    seeds = [42, 43, 44]
```

```
    params_list = []

    for mig in migration_intensities
        for s in seeds
            push!(
                params_list,
                Dict(
                    :migration_intensity => mig,
                    :C => 3,
                    :Ns => [1000, 1000, 1000],
                    :□_und => [0.5, 0.5, 0.5],
                    :□_det => [0.05, 0.05, 0.05],
                    :infection_period => 14,
                    :detection_time => 7,
                    :death_rate => 0.02,
                    :reinfection_probability => 0.1,
                    :Is => [1, 0, 0],
                    :seed => s,
                    :n_steps => 150,
                    :quarantine_threshold => 0.1,
                ),
            )
        end
    end

# ## □□□□□□ □□□□□□□□□□□□□
#
# □□□ □□□□□□□ □□□□□□ □□□□□□□□□□ □□□□□□□□□□□ □□□ □□□□□□□:
```

```
#
# - [illegible] [illegible];
# - [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].

    results = DataFrame(
        migration_intensity = Float64[],
        seed = Int[],
        mode = String[],
        peak_time = Float64[],
        peak_value = Float64[],
    )

    for params in params_list
        res_no_q = peak_time_without_quarantine(params)
        push!(results, (
            params[:migration_intensity],
            params[:seed],
            "[illegible] [illegible]",
            res_no_q.peak_time,
            res_no_q.peak_value,
        ))

        res_q = peak_time_with_quarantine(params)
        push!(results, (
            params[:migration_intensity],
            params[:seed],
```

```
            "□ □□□□□□□□□□",
            res_q.peak_time,
            res_q.peak_value,
        ))

        println("□□□□□□□□ □□□□□□□□□□□□: migration = $(params[:migration_i
    end

# ## □□□□□□□□□□ □□□□□□□□□□□

#
# □□□□□□ □□□□□□□ □□□□□□□□□□□ □□□□□□□□□□□ □ CSV-□□□□.

    CSV.write(datadir("extra_4_5_results.csv"), results)

# ## □□□□□□□□□□ □□□□□□□□□□□

#
# □□□ □□□□□□□□ □□□□□□□□ □□□□□□□□□□□□□ □□□□□□□□ □ □□□ □□□□□□□ □□□□□□
# (□ □□□□□□□□□□ □ □□□ □□□□□□□□□) □□□□□□□□□□□ □□□□□□□ □□□□□□□□:
#
# - □□□□□□□ □□ □□□□;
# - □□□□□□□□ □□□□.

    grouped = combine(
        groupby(results, [:migration_intensity, :mode]),
        :peak_time => mean => :mean_peak_time,
        :peak_value => mean => :mean_peak_value,
    )
```

```
# ## [illegible]
#
# [illegible]
# [illegible] [illegible].

    p_time = plot(
        xlabel = "[illegible]",
        ylabel = "[illegible]",
        title = "[illegible]: [illegible]",
    )

    for mode in unique(grouped.mode)
        subdf = grouped[grouped.mode .== mode, :]
        plot!(p_time, subdf.migration_intensity, subdf.mean_peak_ti
    end
    savefig(p_time, plotsdir("extra_4_5_peak_time.png"))

# ## [illegible]
#
# [illegible]
# [illegible] [illegible].

    p_peak = plot(
        xlabel = "[illegible]",
        ylabel = "[illegible]",
        title = "[illegible]: [illegible]",
    )
```

```
    for mode in unique(grouped.mode)
        subdf = grouped[grouped.mode .== mode, :]
        plot!(p_peak, subdf.migration_intensity, subdf.mean_peak_va
    end
    savefig(p_peak, plotsdir("extra_4_5_peak_value.png"))

# ## [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] JLD2.

    save(datadir("extra_4_5_results.jld2"), Dict(
        "results" => results,
        "grouped" => grouped,
    ))
end

main()

# ## [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] 4-5 [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible],
# [illegible] [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible],
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
```

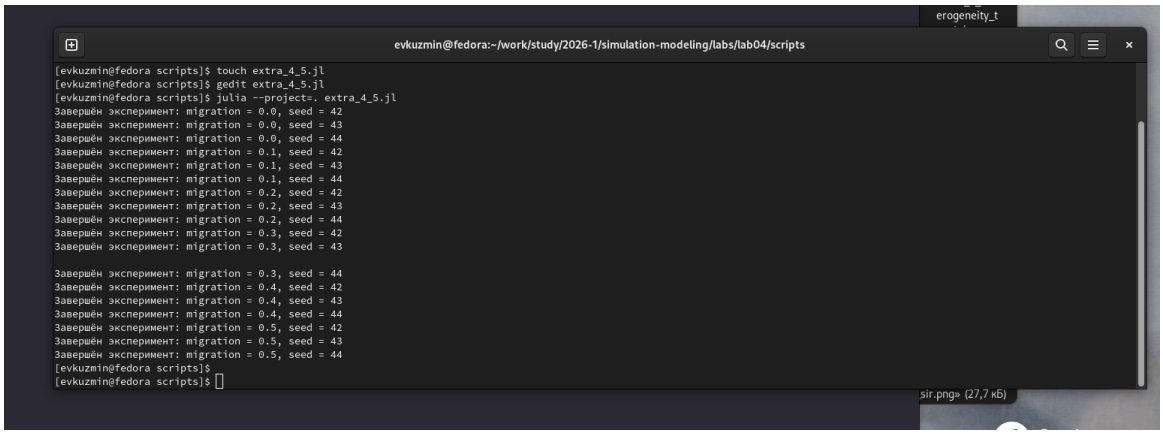

Рисунок 5.6: Создание и выполнение скрипта дополнительных заданий 4–5

На рисунке показан запуск скрипта дополнительных заданий 4–5.

5.2.1 Влияние миграции и карантина на время до пика

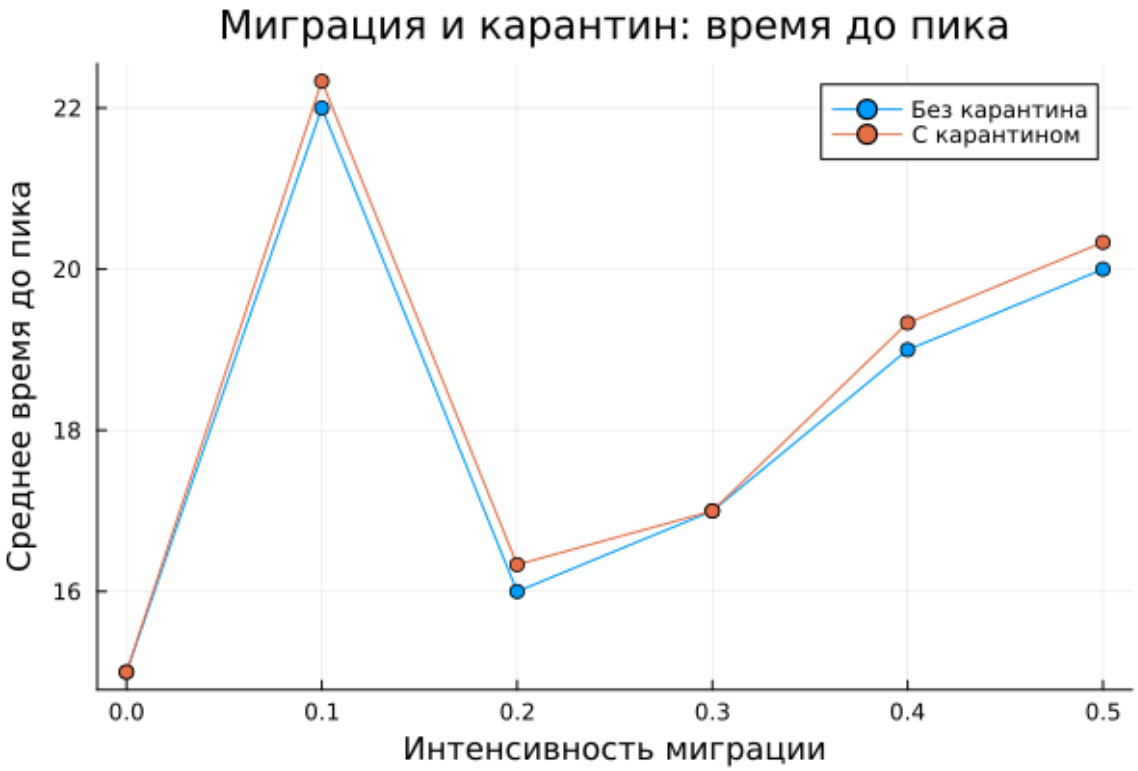

Рисунок 5.7: Сравнение времени достижения пика с карантином и без карантина

На рисунке показано, как меняется среднее время достижения пика при различных значениях миграции. Сравнение режимов с карантином и без карантина позволяет оценить, насколько ограничение перемещений замедляет развитие эпидемии.

5.2.2 Влияние миграции и карантина на величину пика

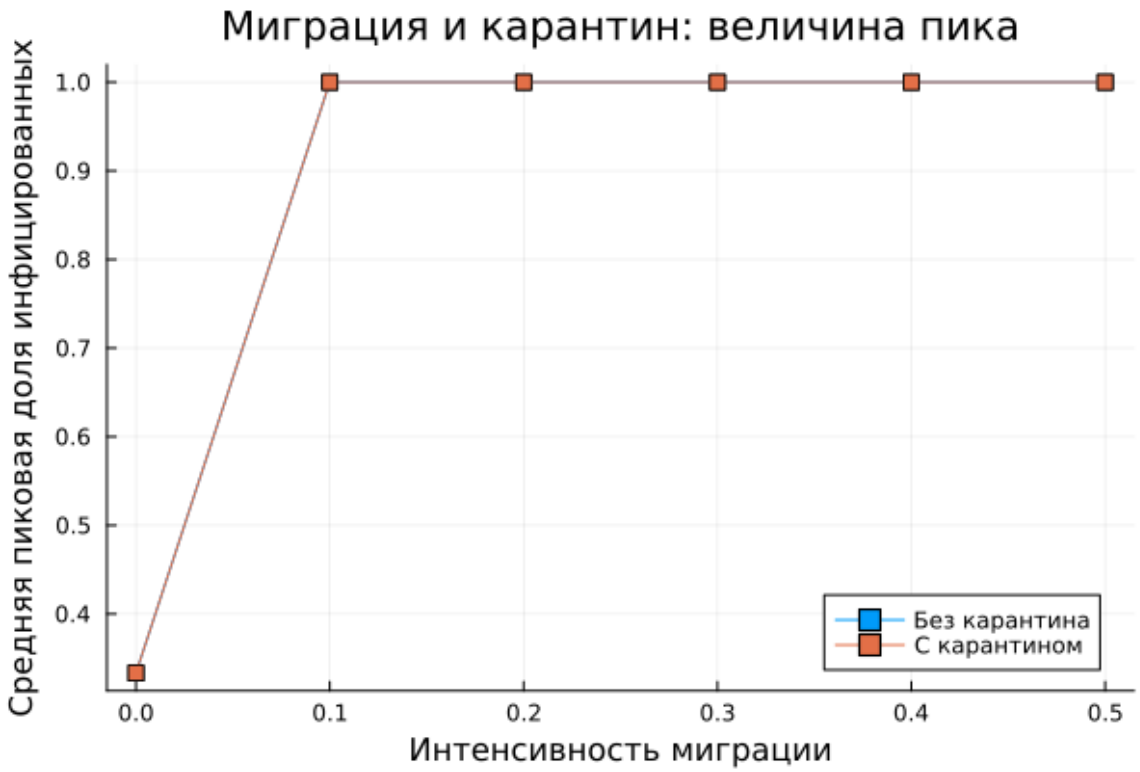

Рисунок 5.8: Сравнение величины пика с карантином и без карантина

На рисунке показана зависимость величины пика эпидемии от интенсивности миграции для режимов с карантином и без карантина. Это позволяет оценить эффективность карантинных мер по снижению максимальной нагрузки.

5.3 Дополнительное задание 6

В дополнительном задании 6 решалась задача оптимизации параметров модели при ограничении на пиковую долю инфицированных.

Листинг 5.3. Скрипт дополнительного задания 6

extra_6.jl

```
# # [illegible] 6
# ## [illegible] SIR
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible] [illegible], [illegible]:
#
# - [illegible] [illegible] [illegible];
# - [illegible] [illegible] [illegible] 30% [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible]:
#
# - [illegible] [illegible] `[illegible]_und`;
# - [illegible] [illegible] [illegible] `detection_time`;
# - [illegible] [illegible] `death_rate`.
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible], [illegible] [illegible] [illegible] [illegible] [illegible].

using DrWatson
@quickactivate "project"

using BlackBoxOptim, Random, Statistics
```

```
using Agents
using JLD2
using DataFrames
using CSV
using Plots

include(srcdir("sir_model.jl"))

# ## [illegible] [illegible]
#
# [illegible] [illegible] [illegible] [illegible] `x`, [illegible]:
#
# - `x[1]` — [illegible] [illegible] `[illegible]_und`;
# - `x[2]` — [illegible] [illegible] [illegible];
# - `x[3]` — [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] 30% [illegible],
# [illegible] [illegible] [illegible] [illegible] [illegible].

function cost_with_constraint(x)
    infected_frac(model) =
        count(a.status == :I for a in allagents(model)) / nagents(m

    total_population = 1500
    dead_frac(model) = (total_population - nagents(model)) / total_
```

```
peak_vals = Float64[]
dead_vals = Float64[]

for rep in 1:2
    model = initialize_sir(;
        Ns = [500, 500, 500],
        β_und = fill(x[1], 3),
        β_det = fill(x[1] / 10, 3),
        infection_period = 10,
        detection_time = round(Int, x[2]),
        death_rate = x[3],
        reinfection_probability = 0.1,
        Is = [0, 0, 1],
        seed = 42 + rep,
        n_steps = 50,
    )

    peak_infected = 0.0

    for step in 1:50
        Agents.step!(model, 1)
        frac = infected_frac(model)
        if frac > peak_infected
            peak_infected = frac
        end
    end

    push!(peak_vals, peak_infected)
```

```
        push!(dead_vals, dead_frac(model))
    end

    mean_peak = mean(peak_vals)
    mean_dead = mean(dead_vals)

    penalty = 0.0
    if mean_peak > 0.30
        penalty = 10.0 * (mean_peak - 0.30)
    end

    return mean_dead + penalty
end

function main()

# ## □□□□□□ □□□□□□□□□□□
#
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    result = bboptimize(
        cost_with_constraint;
        Method = :random_search,
        SearchRange = [
            (0.1, 1.0),
            (3.0, 14.0),
            (0.01, 0.1),
```

```
        ],
        NumDimensions = 3,
        MaxTime = 20,
        TraceMode = :silent,
    )

# ## □□□□□□□□□□ □□□□□□□□□ □□□□□□□□□□
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# □ □□□□□□□□ □□□□□□□ □□□□□□□.

    best = best_candidate(result)
    fitness = best_fitness(result)

    println("□□□□□□□□□□□ □□□□□□□□□:")
    println("□_und = $(best[1])")
    println("□□□□□ □□□□□□□□□ = $(round(Int, best[2])) □□□□")
    println("□□□□□□□□□□ = $(best[3])")
    println("□□□□□□□□ □□□□□□□ □□□□□□□ = $(fitness)")

# ## □□□□□□□□□□□ □□□□□□
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    model_check = initialize_sir(;
        Ns = [500, 500, 500],
        □_und = fill(best[1], 3),
```

```
        ⊠_det = fill(best[1] / 10, 3),
        infection_period = 10,
        detection_time = round(Int, best[2]),
        death_rate = best[3],
        reinfection_probability = 0.1,
        Is = [0, 0, 1],
        seed = 123,
        n_steps = 50,
    )

    times = Int[]
    infected_vals = Float64[]
    dead_vals = Float64[]

    total_population = 1500
    peak_check = 0.0

    for step in 1:50
        Agents.step!(model_check, 1)

        current_infected = infected_count(model_check) / total_popu
        current_dead = (total_population - total_count(model_check)

        push!(times, step)
        push!(infected_vals, current_infected)
        push!(dead_vals, current_dead)

        if current_infected > peak_check
```

```
            peak_check = current_infected
        end
    end

    check_df = DataFrame(
        time = times,
        infected_fraction = infected_vals,
        dead_fraction = dead_vals,
    )

    println("□□□□□□□□□□□ □□□ □□□□□□□□□□□□□□ = $(round(peak_check, digits=3
    println("□□□□□ 30% □□□□□□□□: $(peak_check <= 0.30)")

# ## □□□□□□□□□□ □□□□□□□ □□□□□□□□□□□□ □□□□□□□
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    p = plot(
        check_df.time,
        check_df.infected_fraction,
        label = "□□□□ □□□□□□□□□□□□□□",
        xlabel = "□□□",
        ylabel = "□□□□",
        title = "□□□□□□□□ □□□□□□□□□□□□ □□□□□□□",
```

```
    )

    plot!(p, check_df.time, check_df.dead_fraction, label = "□□□□ □□□
    hline!(p, [0.30], label = "□□□□□□□□□□□ 30%")

    savefig(p, plotsdir("extra_6_optimization_check.png"))

# ## □□□□□□□□□□ □□□□□□□□□□□
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# □ □□□□□□□□□□ □□□□□□□□□□□□ □□□□□□□.

    CSV.write(datadir("extra_6_check.csv"), check_df)

    save(
        datadir("extra_6_optimization_result.jld2"),
        Dict(
            "best" => best,
            "fitness" => fitness,
            "peak_check" => peak_check,
            "check_df" => check_df,
        ),
    )

end

main()
```

```
# ## [illegible]
#
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible],
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
# [illegible]. [illegible] [illegible] [illegible], [illegible] [illegible]
# [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible].
```

5.3.1 Проверка найденного оптимального решения

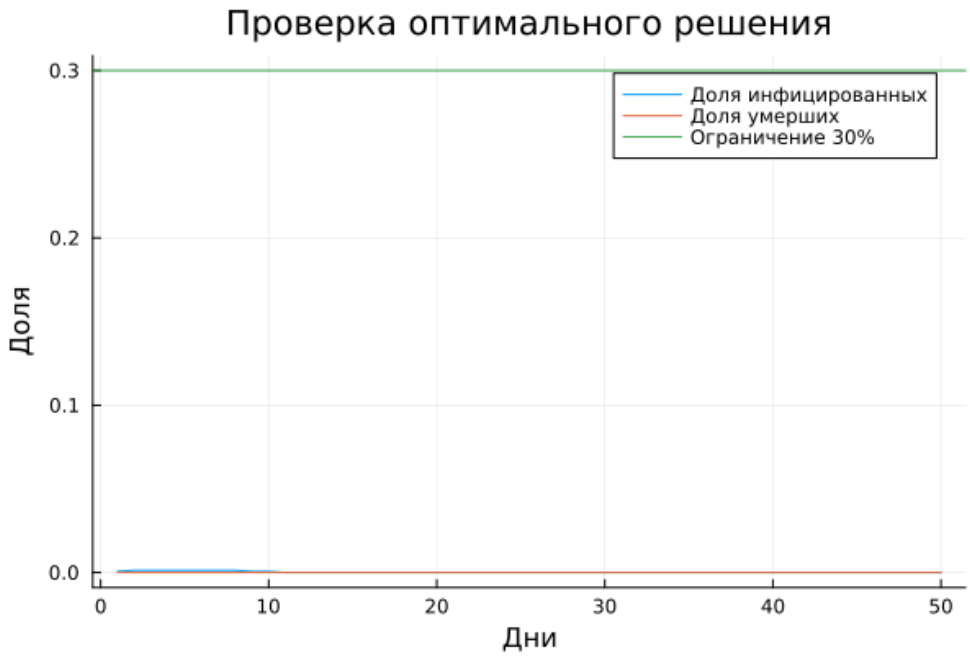

Рисунок 5.9: Проверка оптимального решения для дополнительного задания 6

На рисунке показана проверка найденного оптимального решения. Горизонтальная линия соответствует ограничению на пиковую долю инфицированных. По графику можно оценить, удовлетворяет ли найденное решение заданному ограничению.

6 Итоговые выводы

В ходе выполнения лабораторной работы была реализована агентная модель SIR и проведено её подробное исследование.

В работе были выполнены:

- построение базовой модели;
- подготовка обычных и literate-версий скриптов;
- генерация notebook и Quarto-документации;
- параметрические исследования коэффициента заражения;
- анализ миграции между городами;
- решение задачи оптимизации параметров;
- выполнение дополнительных заданий, связанных с порогом эпидемии, гетерогенностью, карантинными мерами и ограниченной оптимизацией.

Полученные результаты показывают, что агентная модель SIR позволяет исследовать широкий круг эпидемиологических сценариев. Изменение параметров модели существенно влияет на время достижения пика, число инфицированных, число умерших и характер распространения инфекции между городами.

7 Список литературы

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