Index

A
Action potentials, 49–51
Activating gates, 43, 44
Activator-inhibitor system, 109, 110, 118, 147
Adaptive dynamics model, 172
Adaptive significance, 171
Ad-hoc rules, 149
Anisotropic growth, 1, 7
Approximate Bayesian computation (ABC), 204
Arabidopsis thaliana inflorescence shoot apical meristems (SAMs), 90
Auxin, 6, 8, 99, 100, 110–112
Axiom, 113, 141, 148

B
Bifurcation theory, 62
Boolean models, 71
Bottom-up approach, 72
Boundary conditions, 19–20
B-spline surfaces, 121–123

C
Canalization model, 111, 112
Cavitation bubbles, 25
Cell division
  growing cell disk, 115, 116
  model of, 114, 115
  Voronoi regions, 114, 115
Cellerator, 72
Cell expansion, 15
Cell geometry, 64
Cellular automata, 140, 141
Cellular membrane excitability
  action potentials, 49–51
  membrane currents, 47–49
  Nernst potential, 47
Cellular Potts model (CPM), 6, 131–133
Cellular spaces, *see* Cellular automata
Cell wall, 3
Cell wall mechanical properties, 3, 7
Channel dynamics, 39–40
Chemical Langevin equation, 96
Circular tube flow, 23–24
Classical (von Neumann) model, 140
Claude-Louis Navier equation, 19
Climate change, 182, 186
Clonal analysis, 3
Computational models, 140
Computational Morphodynamics, 88, 89
Conservation of mass, 17–18, 27
Context sensitive rules, 113
Continuous concentration-based approach, 96, 97
Continuous model, 5–6, 198
Continuum hypothesis, 17
Convection-diffusion equation, 29
Coordinate system, 124–125
Corner-flow analysis, 28
Cortical array (CA), *see* Plant cortical microtubule array
Coupling biochemical process, 8
Coupling biomechanical process, 8
Creeping flow, 21
Cyclin-dependent kinase (CDK) activity, 90

© Springer Nature Switzerland AG 2018

R. J. Morris (ed.), *Mathematical Modelling in Plant Biology*,
https://doi.org/10.1007/978-3-319-99070-5

D
Data driven growth, 123–125
De novo pattern formation, 111
Diffusion
  of ionic species, 38–39
  prospective framework, 200–201, 204, 207
  shear-enhanced diffusion, 32–35
Discrete time steps, 58
Diurnal Reference Cycles, 75
Dormancy, 198
Dynamic self-organization, 54
Dynamics instability, 54–56

E
E-Cell, 72
Ecology, 172, 173, 188, 190, 197
Effective diffusivity, 34, 35
Elastic modulus, 7, 9, 10
Eulerian approach, 131, 141
Event-driven simulations, 58
Expression dynamics, 88, 185

F
Fickian flux rules, 38
Fick's law, 29, 33, 147
Filamentous blue-green bacterium *Anabaena catenula,* 142
Finite element method (FEM), 6, 129–131
Finite hydraulic permeability, 74
First-generation OnGuard software, 75, 76
FitzHugh-Nagumo model, 38
Fixed templates
  activator-inhibitor system, 109
  auxin, feedback of, 111, 112
  boundary conditions, 108
  de novo pattern formation, 111
  Mitchison's polar transport model, 111
  reaction-diffusion patterning, 110
  realistic templates, 112, 113
  rectangular, hex and Voronoi regions, 112
  Sachs' canalization mechanism, 110
  Turing mechanism, 108
FLOWERING LOCUS C (*FLC*), 174
Flowering phenology
  climate change, 182–183
  model construction and parameterization, 184–187
  prediction, 185–188
Flowering time
  evolution of, 180–182
  FLC generates diversity
    monocarpic annuals, 179–180
    monocarpic perennials, 180
    polycarpic-intermittent flowering, 180
    polycarpic-yearly flowering, 180
  forecasting flowering phenology
    flowering phenology and climate change, 182–183
    model construction and parameterization, 184–187
    prediction, 185–188
  genetic-physiological model
    allelic variations, 178
    bistability of cellular systems, 176
    chromatin remodeling, 176
    floral integrator gene, 175–176
    genetic component, 175
    leaf biomass, 177
    optimal flowering strategy, 178
    physiological component, 175
    repression state, 176
    stored resource (S) changes, 178
    temperature-dependent pathway, 175
    vernalization-specific genes, 175–176
  natural variation, vernalization responses, 173–175
  proximate causes, 171–173
  ultimate causes, 171–173
Fluid transport
  physical principles and mathematical equations
    boundary conditions, 19–20
    conservation of mass, 17–18
    continuum hypothesis, 17
    Navier-Stokes equation, 18–19
    Newtonian fluid, 17
    non-Newtonian fluid, 17
    Reynolds number, 20–21
  plant hydraulics
    flow in a straight tube, 21–25
    flow in a tube with varying diameter, 26–28
    geometrical complications, 21
    Münch hypothesis, 21
    osmosis, 15
    pits, 21
    tracheids and vessels, 21
    transport routes for fluids, 16
    water influx, 15
  solute transport
    convection, 30–32
    diffusion equation, 29–31
    shear-enhanced diffusion, 32–35
    transport equation, 28–29
Formal language theory, 145
Forward Euler method, 149

Fraction of channels, 45
FRIGIDA (FRI), 174

G
Game theory, 172
Gating, 39
Gene expression analysis, 186
Genetic-physiological model
  allelic variations, 178
  bistability of cellular systems, 176
  chromatin remodeling, 176
  floral integrator gene, 175–176
  genetic component, 175
  leaf biomass, 177
  optimal flowering strategy, 178
  physiological component, 175
  repression state, 176
  stored resource (S) changes, 178
  temperature-dependent pathway, 175
  vernalization-specific genes, 175–176
Genetic regulatory network (GRN)
  activator-inhibitor model, 147
  bistable behaviour (hysteresis), 151
  cell division, 149, 150
  data structures, 148
  external PatS, 151
  Fick's law, 147
  flux of PatS, 149
  heterocyst differentiation, 146
  HetR and PatS interactions, 146, 147
  module types and initial state, 148
  production for walls, 148–149
  reaction-diffusion model, 147
  refractory behaviour of heterocysts, 151
  simulation parameter values, 147, 150
Genomic data analysis, 201–202
Geometric concept, 140
Geometric template model, 112, 113
George Gabriel Stokes equation, 19
Gibb's free energy, 39
Gillespie algorithm, 41–42, 96
GRN, *see* Genetic regulatory network
Growth anisotropy, 1, 7, 134
Growth rate, 1, 7
Guard cells, 49, 70–75, 81

H
Hamiltonian based methods, 131–134
Hejnowicz coordinate system, 118–120
Hill-Robertson effect, 196, 197, 208
Hodgkin-Huxley formalism, 49
Hodgkin-Huxley model, 38
Homogeneous arrays, 65
Humidity, 75–80
Hybrid algorithms, 96
Hydraulic transport routes, 16
Hydromechanical model, 71

I
Inactivating gates, 43, 44
Incomplete Lineage Sorting (ILS), 205
Integral projection model, 172
Ion channels
  activating gates, 43, 44
  averaging, 45–46
  cellular membrane excitability
    action potentials, 49–51
    membrane currents, 47–49
    Nernst potential, 47
  Gillespie algorithm, 41–42
  inactivating gates, 43, 44
  master equation, 44–45
  single ion channel dynamics
    channel dynamics, 39–40
    ionic species diffusion, 38–39
    Markov processes, 40–41
  transition probabilities, 42–43
Ion flux, 73, 77
Ionic species diffusion, 38–39
Isotropic solution, 62
Iterative computational modelling, 74

K
Kirchoff's second law, 49

L
Lagrangian approach, 131, 141
Lewontin paradox, 197
Linkage disequilibrium (LD), 196
Linked selection, 196, 197
Lockhart's model growth, 127
L-systems, 113, 114
  cellular automata, 140, 141
  genetic regulatory network
    activator-inhibitor model, 147
    bistable behaviour (hysteresis), 151
    cell division, 149, 150
    data structures, 148
    external PatS, 151
    Fick's law, 147
    flux of PatS, 149
    heterocyst differentiation, 146
    HetR and PatS interactions, 146, 147

L-systems (*cont.*)
    module types and initial state, 148
    production for walls, 148–149
    reaction-diffusion model, 147
    refractory behaviour of heterocysts, 151
    simulation, 150
    simulation parameter values, 147
  geometric interpretation, 151–153
  modeling cell division patterns
    developmental sequence, 144
    L-system-based simulator CELIA, 143
    numerical parameter, 143
    vegetative segments of *Anabaena,* 142, 143
  modeling phenotypic plasticity, 159–161
  operation of, 141, 142
  plant architecture models
    age of internodes, 155
    `br_angle(t)`, 156
    decomposition rule, 155
    descriptive and mechanistic models, 153–154, 158
    interpretation rule, 155, 156, 158
    `leaf_length(t)`, 156
    Lychnis coronaria shoot, 159
    Lychnis model, 156, 157
    mature *Lychnis coronaria* plant, 154
    modules, 155
    `nproduce` statement, 158
    `produce` statement, 158
    simple branching structure model, 154
    turtle command
      Surface(`LEAF_SURFACE`, `leaf_length(t)`), 156
  programming, 145
  trees modeling
    components, 161
    `E1` and `GetHead`, 162
    elements, 163–165
    plant and environment, 165
    recursive branching pattern, 161
Lychnis model, 156, 157

M
Mapping function, 116
Markov processes, 40–41
Mass-spring model, 125–129
Master equation, 44–45
Maximal growth direction, 1, 7
Mechanical signals, 9–10
Meinhardt activator-inhibitor system, 127
Membrane currents, 47–49
Metropolis algorithm, 131
Microtubule associated proteins (MAPs), 53
Microtubule (MT) cytoskeleton, *see* Plant cortical microtubule array
Mitchison's polar transport model, 111
Morphogens, 130
MorphoGraphX, 2
Münch hypothesis, 21

N
Natural variation, vernalization responses, 173–175
Navier-Stokes equation, 18–19
Nernst potential, 47
Neutral and selective genetic diversity, 196
Neutral evolutionary processes
  constant population size, 203
  past demographic events, 203–204
  recombination rate, 205, 206
  speciation, 204–205
Newtonian fluid, 17
Newton's law of viscosity, 17
Non-circular tube flow, 24–25
Non-isotropic solutions, 51
Non-Newtonian fluids, 17
Non-persistent seed bank, 198
Non-SB Wright–Fisher model, 204

O
OnGuard2 Arabidopsis model, 82
OnGuard platform
  elements, 72–74
  macro-and microscopic processes, 81
  modelling stomata
    biophysical and kinetic features, 72
    Boolean models, 71
    effective modelling efforts, 70
    guard cell outward-rectifying K^+ channel, 72
    guard cell physiology, 70
    macroscopic approaches, 71
    microscopic level, 71
    reverse-engineering, 71
    robust models of gas exchange, 71
    stomatal function, 70, 71
    true mechanistic models, 71
  OnGuard2 Arabidopsis model, 82
  outputs, 80
  simulating stomatal physiology and response, 75–80
  whole-plant water relations
    diurnal Reference Cycles, 75
    finite hydraulic permeability, 74

iterative computational modelling, 74
Reference State, 75
Reference State Wizard, 74
Open and closed states, 39
Optimal control theory, 172
Order parameters, 60–63
Organ-centric coordinate system, 116, 117, 121
Organ growth, 3, 10, 156
Osmosis, 15

P
Passage/escape times, 40
PatS external to it ([PatS]*ext*), 151
Péclet number, 33, 35
Phenotypic diversity, 195
Photosynthesis process, 16
Phyllotaxis, 118
Phytohormone auxin, 98
Pits, 21
Plant architecture
age of internodes, 155
`br_angle(t)`, 156
decomposition rule, 155
descriptive and mechanistic models, 153–154, 158
interpretation rule, 155, 156, 158
`leaf_length(t)`, 156
Lychnis coronaria shoot, 159
Lychnis model, 156, 157
mature *Lychnis coronaria* plant, 154
modules, 155
nproduce statement, 158
produce statement, 158
simple branching structure model, 154
turtle command Surface(`LEAF_SURFACE`, `leaf_length(t)`), 156
Plant cortical microtubule array
behaviour levels
in *A. thaliana* hypocotyl cell, 56
coarse graining, 56–57
dynamic instability, 54–55
interactions, 55–56
consensus model of dynamics, 57
dynamic self-organization, 54
order parameters, 60–63
orientation, 63–64
plant cell growth and development, 53–54
severing enzyme katanin, 65
time steps *vs.* event driven simulations, 57–59
Plant hydraulics, 15–16
flow in a straight tube
circular tube flow, 23–24
non-circular tube flow, 24–25
Poiseuille velocity profile, 22
pressure gradient drives flow, 22
tube collapse and cavitation, 25
flow in a tube with varying diameter, 26–28
geometrical complications, 21
Münch hypothesis, 21
osmosis, 15
pits, 21
tracheids and vessels, 21
transport routes for fluids, 16
water influx, 15
Plant life history
evolution of, 180–182
FLC generates diversity
monocarpic annuals, 179–180
monocarpic perennials, 180
polycarpic-intermittent flowering, 180
polycarpic-yearly flowering, 180
genetic-physiological model
allelic variations, 178
bistability of cellular systems, 176
chromatin remodeling, 176
floral integrator gene, 175–176
genetic component, 175
leaf biomass, 177
optimal flowering strategy, 178
physiological component, 175
repression state, 176
stored resource (S) changes, 178
temperature-dependent pathway, 175
vernalization-specific genes, 175–176
natural variation, vernalization responses, 173–175
Plant morphogenesis, 108
cellular Potts model, 6
continuous model, 5–6
elementary transformations, 1
forces
simple rheological behaviors and plant growth, 4–5
tissues and cells, 3–4
growth implementation, 7
parameters, 1
physical model
isolated plant cell, 7–8
mechanical feedback, 9–10
organ elongation, 8
sheet-like organs, 8–9
variability, 10–11
quantifying cell growth, 2
quantifying organ growth, 3
vertex-based model, 6

Plant's flowering behaviors, 172, 173
Plant shoot apex, 116, 117
Poiseuille velocity profile, 22
Polarizer gradient, 130
Pressure gradient drives flow, 22
Protofilaments, 55

Q
Quantifying cell growth, 2
Quantifying morphogenesis, 1, 2
Quantitative image analysis
cellular size and morphology parameters, 93
deconvolution, 92
gene expression, 92, 93
live imaging mCitrine-ATML1 expression data, 93, 94
microscopy parameters, 92
SAM, block matching algorithm, 92, 94
spatiotemporal single cell data, 94
3D nuclear segmentation, 92, 93
time sampling, 92
topological features, quantification of, 93, 95
watershed algorithm, 92, 93
Quantitative measure, 60

R
Rate constants, 41
Reaction-diffusion system, 118, 122, 128, 147
Reference State Wizard, 74
Refractory behaviour of heterocysts, 151
Relative elemental rate of growth (RERG), 117
Residual stress, 9
Reynolds number, 20–21
Rheological model, 4–5
Root apex, 118–120

S
Sachs' canalization mechanism, 110
Selective processes
linked sites, 207–208
unlinked sites, 206, 207
Sensing mechanisms, 10
Shear-enhanced diffusion, 32–35
Shedding, 163
Shoot apex surface, 117
Shoot meristem, 116
Shortest wall rule, 114, 115
Single-cell approaches
Arabidopsis thaliana inflorescence SAMs, 90
cell division rules, 89–90
Computational Morphodynamics workflow, 88, 89
dynamic pattern formation, 88
experimental and computational tools, 88
functional tissue formation, 87
growth and division properties, 90
modelling tissue morphogenesis
bridging simulated data with experimental data, 98–100
cell fate decisions, 95–97
cell-to-cell interactions, 95–96, 98
cellular growth and division patterns, 96–98
chemical Langevin equation, 96
deterministic and stochastic processes, 96
hybrid algorithms, 96
regulatory networks, 95
quantitative image analysis
cellular size and morphology parameters, 93
deconvolution, 92
gene expression, 92, 93
live imaging mCitrine-ATML1 expression data, 93, 94
microscopy parameters, 92
SAM, block matching algorithm, 92, 94
spatiotemporal single cell data, 94
3D nuclear segmentation, 92, 93
time sampling, 92
topological features, quantification of, 93, 95
watershed algorithm, 92, 93
signalling and gene regulatory mechanisms, 88
spatiotemporal description, 89
time-lapse microscopy methods, 88, 89
Single ion channel dynamics
channel dynamics, 39–40
ionic species diffusion, 38–39
Markov processes, 40–41
Soft sweeps, 207
Soil seed banks
effective population size, 196, 197
genetic diversity, 196
linked selection, 196, 197
mutation rate, 196, 197
neutral evolutionary processes
constant population size, 203
past demographic events, 203–204

recombination rate, 205, 206
speciation, 204–205
prospective diffusion framework, 200–201
retrospective coalescent view, 199–200
selective processes
linked sites, 207–208
unlinked sites, 206, 207
statistical measure, 201–202
Solute transport
convection, 30–32
diffusion equation, 29–31
shear-enhanced diffusion, 32–35
transport equation, 28–29
Spatial models, 108
Stochasticity, 95, 96
Stokes flow, 21
Stomata
biophysical and kinetic features, 72
Boolean models, 71
effective modelling efforts, 70
guard cell outward-rectifying K^+ channel, 72
guard cell physiology, 70
macroscopic approaches, 71
microscopic level, 71
reverse-engineering, 71
robust models of gas exchange, 71
stomatal function, 70, 71
true mechanistic models, 71
Strain, 10, 17, 97, 100, 127
Stress, 3–5, 9–11, 16–18, 51

T
Taylor-Aris dispersion, 28
Temperature-dependent pathway, 175
Theoretical and empirical evolutionary genetics, 196
Tissue deformation, 7
Tissue morphogenesis
bridging simulated data with experimental data, 98–100
cell fate decisions, 95–97
cell-to-cell interactions, 95–96, 98
cellular growth and division patterns, 96–98
chemical Langevin equation, 96
deterministic and stochastic processes, 96
hybrid algorithms, 96
regulatory networks, 95
Tissue polarity, 130
Transition probabilities, 42–43
Transport equation, 28–29
Transport-feedback patterning mechanism, 118
True mechanistic models, 71
Tube collapse and cavitation, 25
Turgor pressure, 3
Turing mechanism, 108
Turing patterns, 108
Turtle commands, 152

V
Vein-based model, 11
Vernalization, 174
Vertex-based model, 6
Virtual Cell, 72
Volvox, 8

W
Water influx, 15
Wright–Fisher model, 198

Z
Zero Reynolds number flow, 21