

Plantando anomalias de densidade com gradiometria gravimétrica

Leonardo Uieda

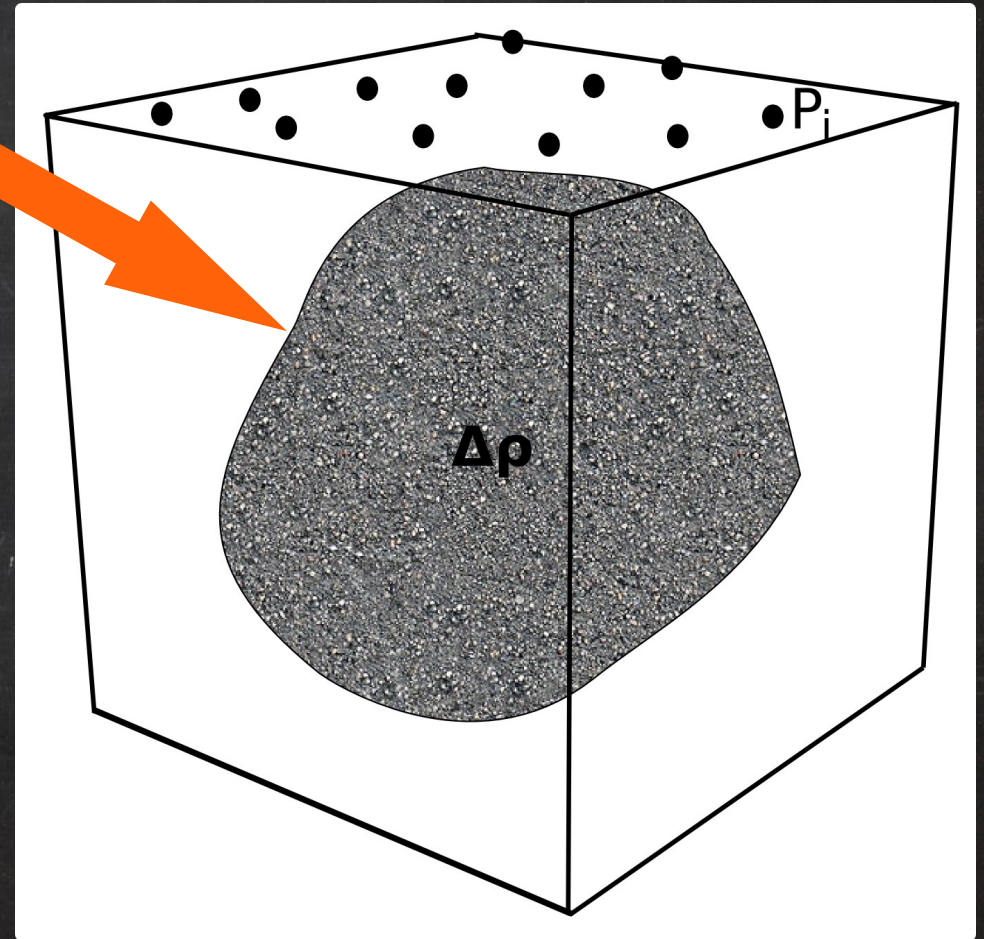
Observatório Nacional

2010

Modelagem Direta

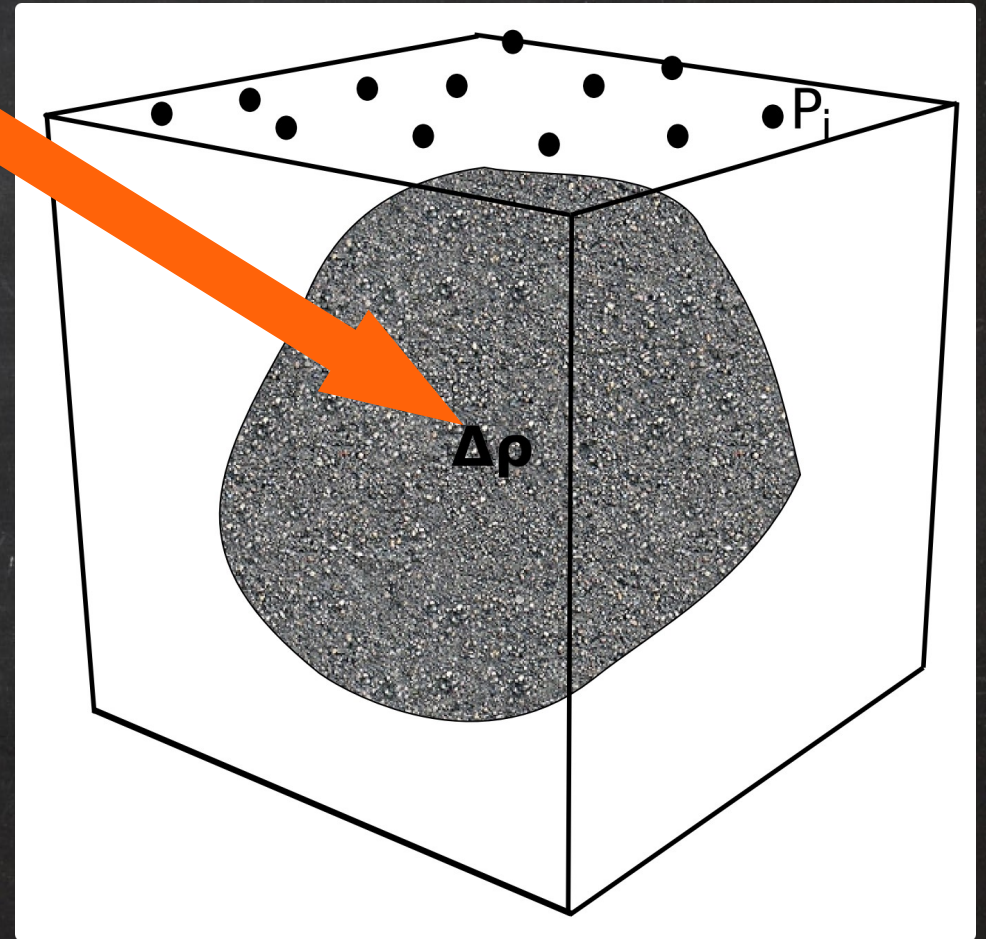
Modelagem direta

✓ Corpo anômalo



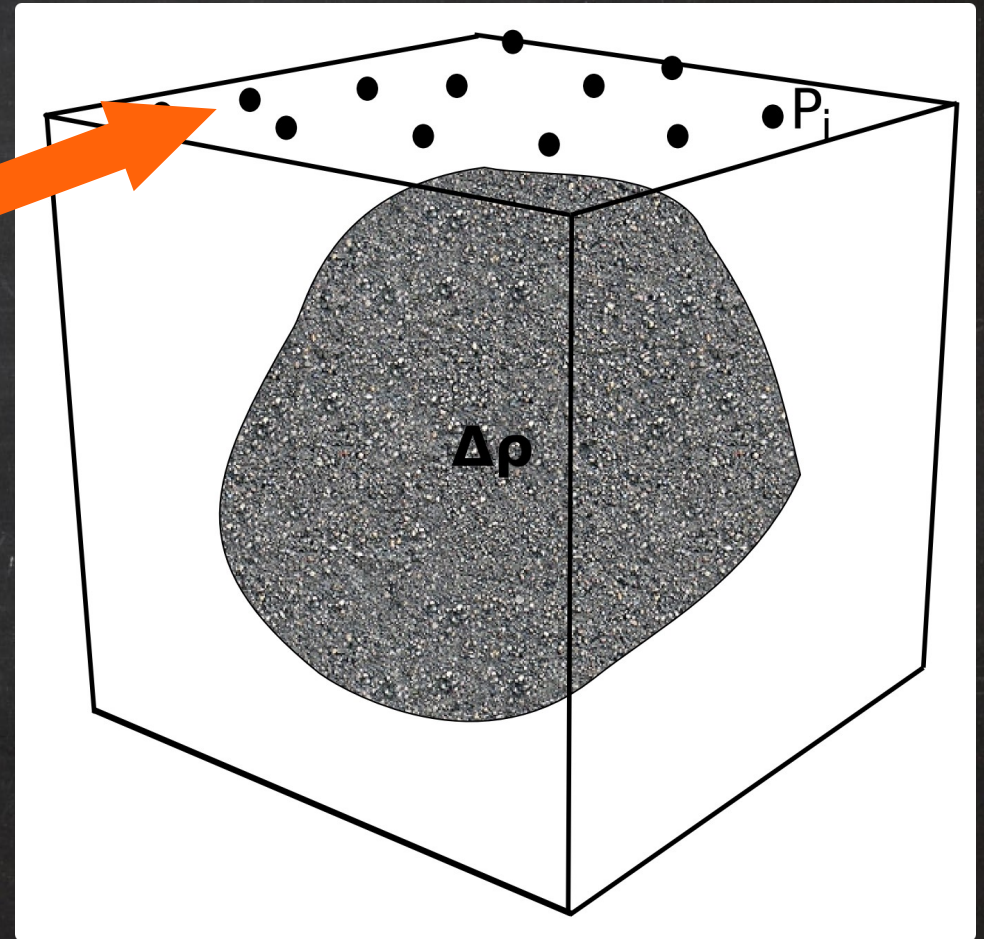
Modelagem direta

- ✓ Corpo anômalo
- ✓ Contraste de densidade



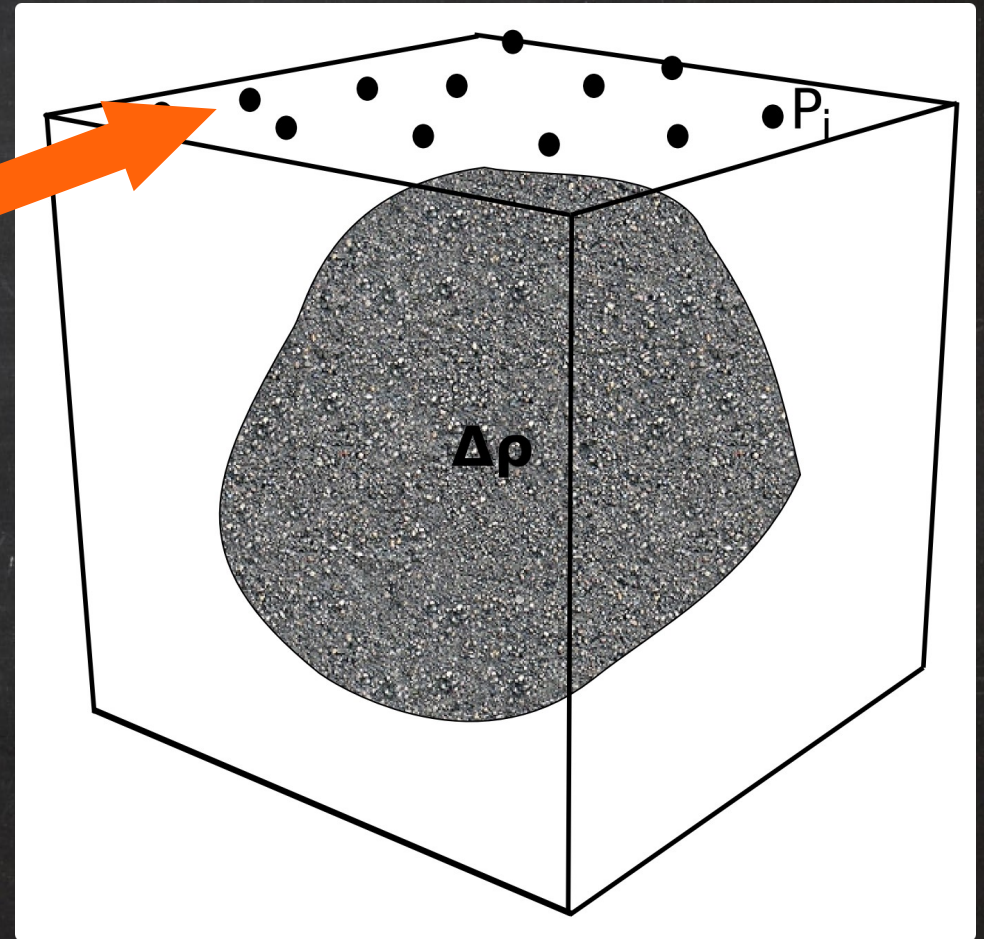
Modelagem direta

- ✓ Corpo anômalo
- ✓ Contraste de densidade
- ✓ Medidas em pontos



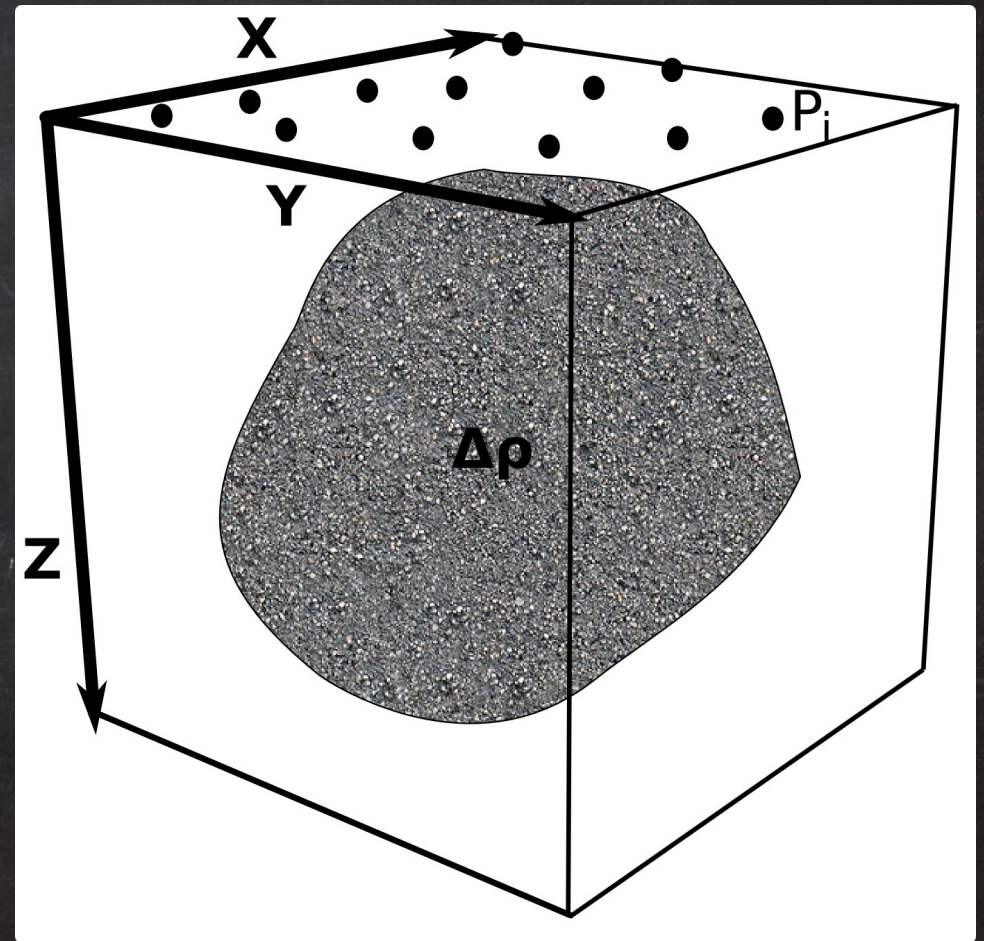
Modelagem direta

- ✓ Corpo anômalo
- ✓ Contraste de densidade
- ✓ Medidas em pontos
- ✓ Gradientes de gravidade
- ✓ 6 componentes



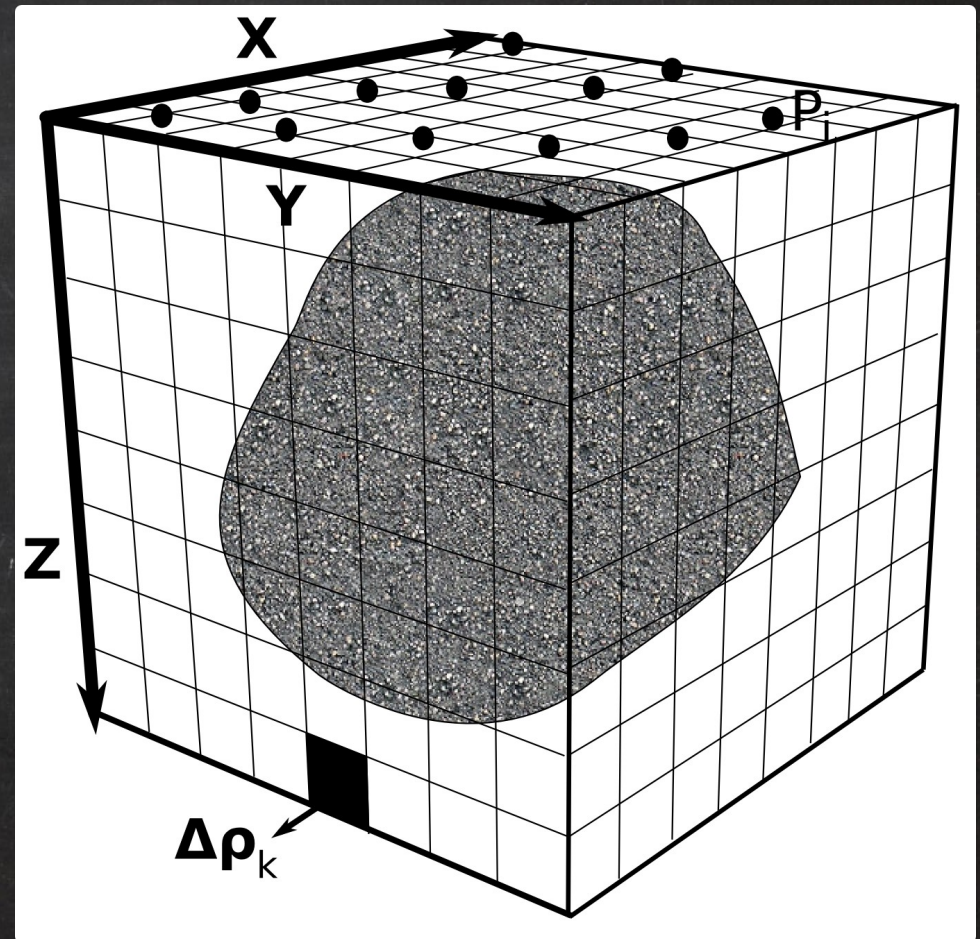
Modelagem direta

- ✓ Corpo anômalo
- ✓ Contraste de densidade
- ✓ Medidas em pontos
 - ✓ Gradientes de gravidade
 - ✓ 6 componentes
- ✓ Sistema de coordenadas



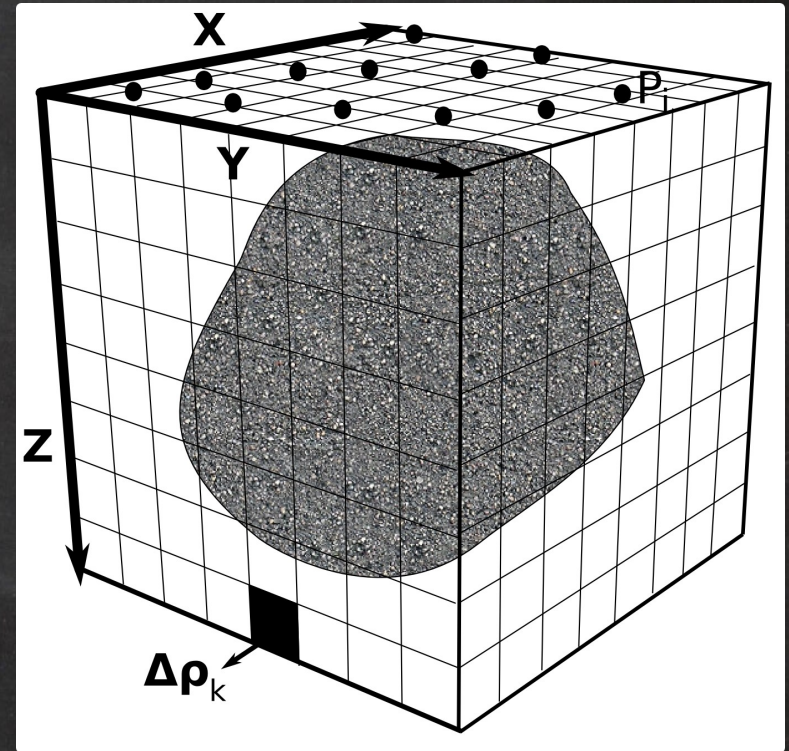
Modelagem direta

- ✓ Corpo anômalo
- ✓ Contraste de densidade
- ✓ Medidas em pontos
- ✓ Gradientes de gravidade
- ✓ 6 componentes
- ✓ Sistema de coordenadas
- ✓ Discretizar em prismas



Modelagem direta

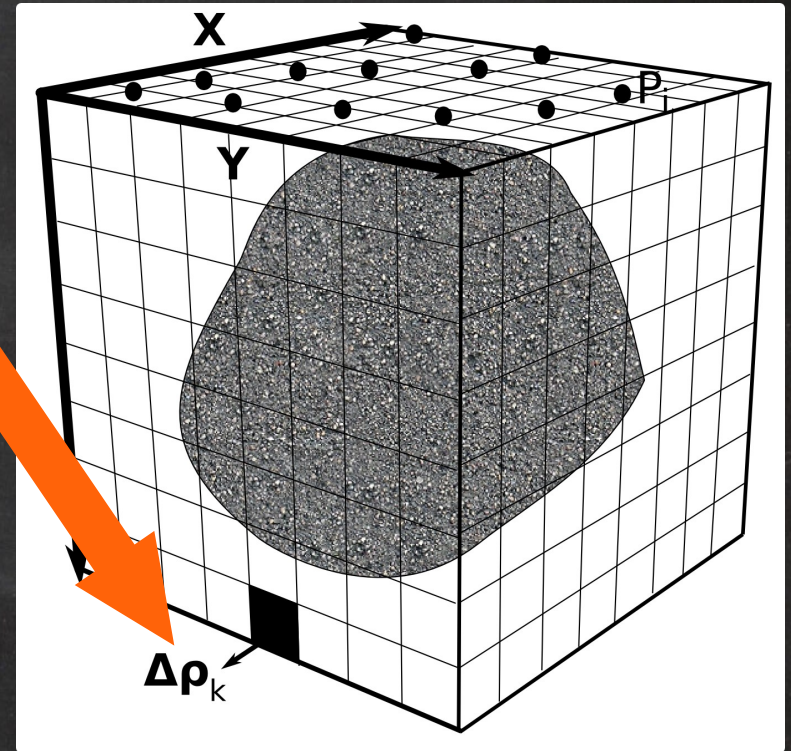
Cada prisma:



Modelagem direta

Cada prisma:

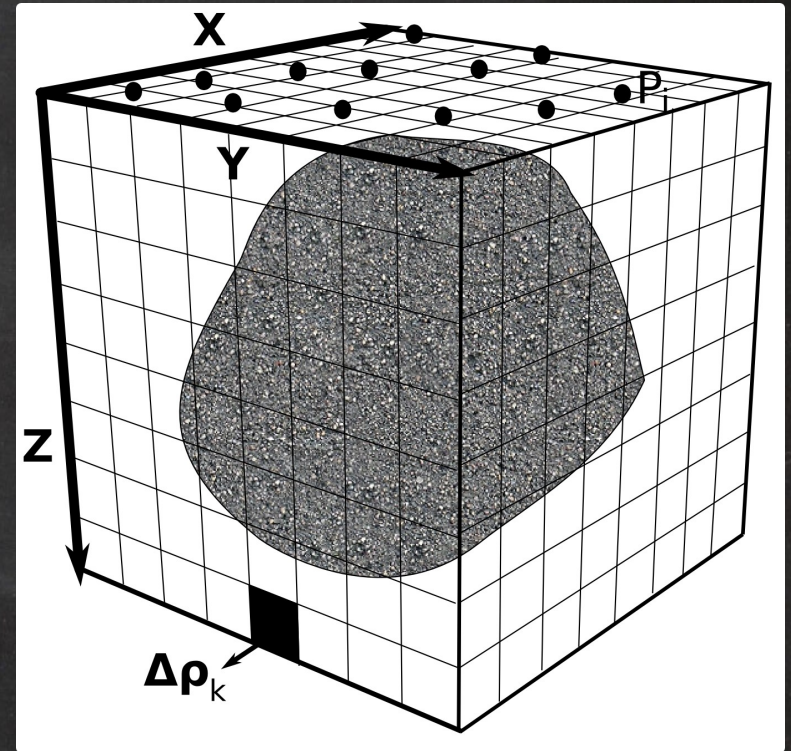
✓ Contraste de densidade $\Delta \rho_k$



Modelagem direta

Cada prisma:

- ✓ Contraste de densidade $\Delta \rho_k$
- ✓ Volume V_k



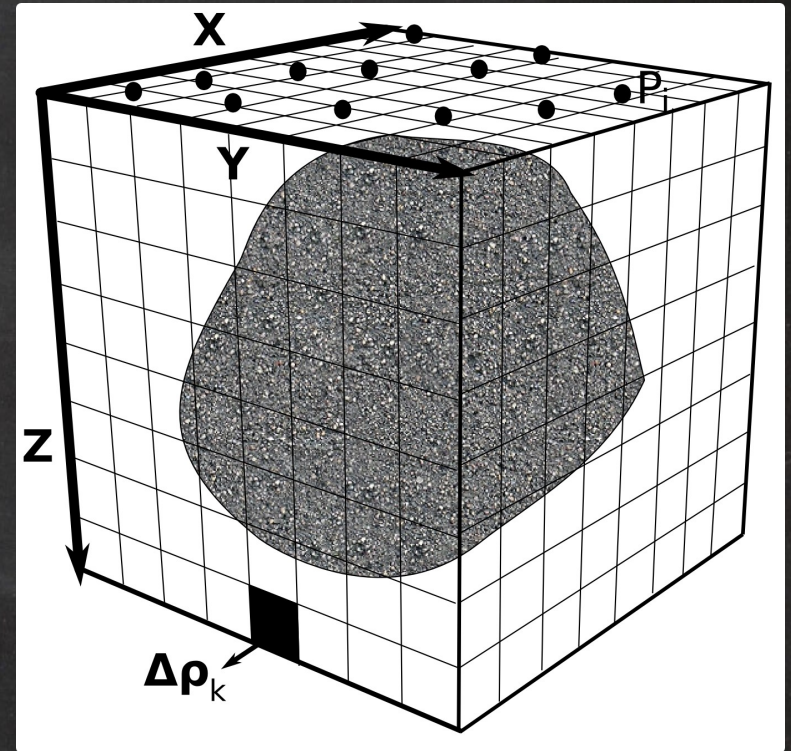
Modelagem direta

Cada prisma:

- ✓ Contraste de densidade $\Delta \rho_k$
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Componente α, β do gradiente:

$$g_{\alpha, \beta}(P_i) = \gamma \sum_{k=0}^{M-1} \Delta \rho_k \int_{V_k} K_{\alpha, \beta} dV$$



Modelagem direta

Cada prisma:

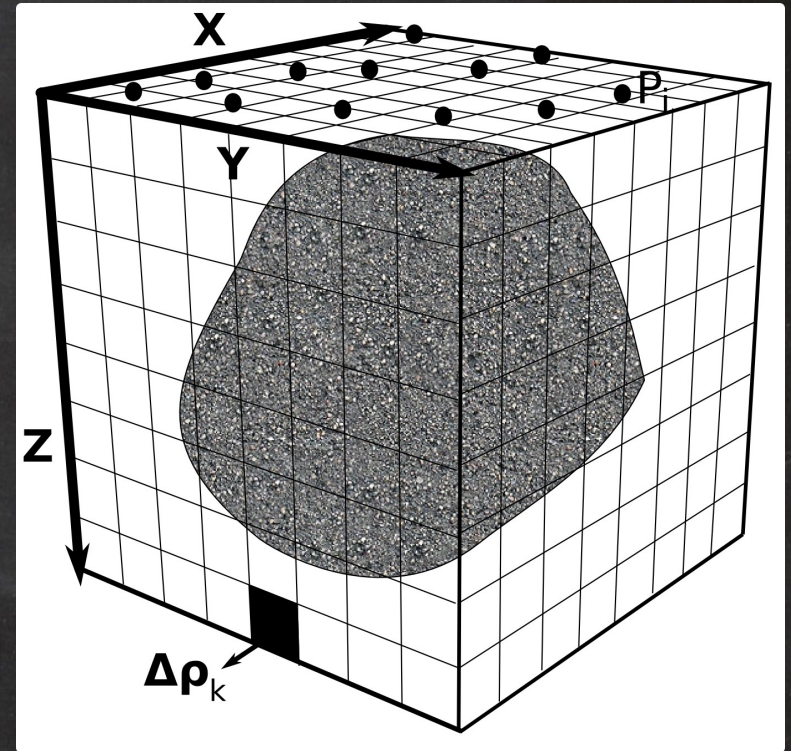
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Medido



Modelagem direta

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- ✓ Contraste de densidade $\Delta \rho_k$
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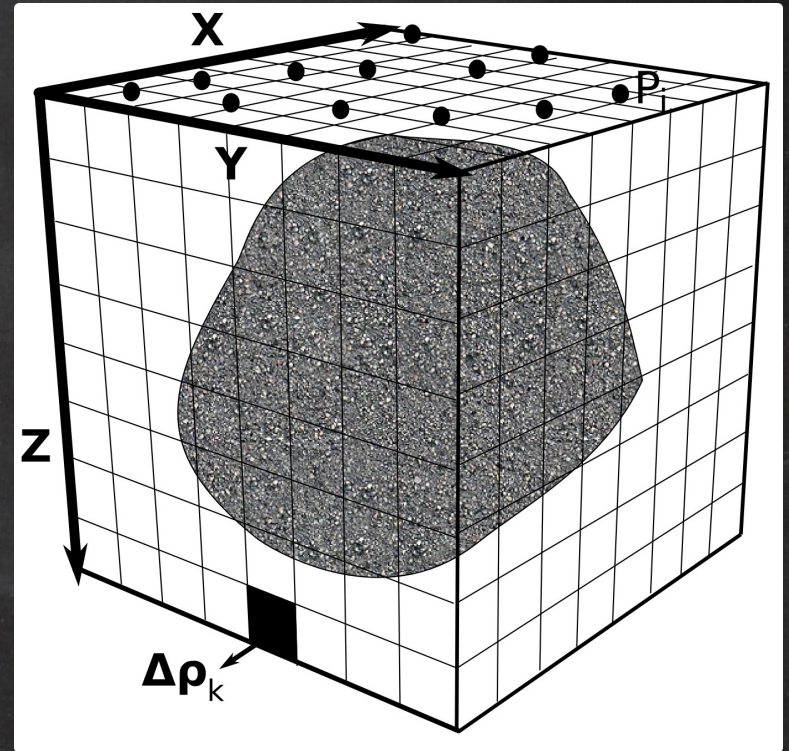
$$g_{\alpha, \beta}(P_i) = \gamma \sum_{k=0}^{M-1} \Delta \rho_k \int_{V_k} K_{\alpha, \beta} dV$$



Medido



Quero saber



Modelagem Inversa

Modelagem inversa

Medições em diversos pontos:

$$g_{xx}(P_1) = \Delta \rho_1 \gamma \int_{V_1} K_{xx} dV + \Delta \rho_2 \gamma \int_{V_2} K_{xx} dV + \cdots + \Delta \rho_M \gamma \int_{V_M} K_{xx} dV$$

\vdots

$$g_{xx}(P_{N_{xx}}) = \Delta \rho_1 \gamma \int_{V_1} K_{xx} dV + \Delta \rho_2 \gamma \int_{V_2} K_{xx} dV + \cdots + \Delta \rho_M \gamma \int_{V_M} K_{xx} dV$$

\vdots

$$g_{zz}(P_{N_{zz}}) = \Delta \rho_1 \gamma \int_{V_1} K_{zz} dV + \Delta \rho_2 \gamma \int_{V_2} K_{zz} dV + \cdots + \Delta \rho_M \gamma \int_{V_M} K_{zz} dV$$

Modelagem inversa

Medições em diversos pontos:

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Medições em diversos pontos:

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$$\begin{array}{c}
 \boxed{\begin{bmatrix} g_{xx}(P_1) \\ \vdots \\ g_{xx}(P_{N_{xx}}) \\ \vdots \\ g_{zz}(P_{N_{zz}}) \end{bmatrix}} \\
 \bar{d}_0 =
 \end{array}
 =
 \begin{array}{c}
 \begin{bmatrix}
 \gamma \int_{V_1} K_{xx} dV & \gamma \int_{V_2} K_{xx} dV & \cdots & \gamma \int_{V_M} K_{xx} dV \\
 \vdots & \vdots & & \vdots \\
 \gamma \int_{V_1} K_{xx} dV & \gamma \int_{V_2} K_{xx} dV & \cdots & \gamma \int_{V_M} K_{xx} dV \\
 \vdots & \vdots & & \vdots \\
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 \end{bmatrix} \\
 \bar{\bar{G}}
 \end{array}
 \begin{array}{c}
 \boxed{\begin{bmatrix} \Delta \rho_1 \\ \vdots \\ \Delta \rho_N \\ \vdots \\ \Delta \rho_M \end{bmatrix}} \\
 \bar{p}
 \end{array}$$

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 \end{array}
 =
 \begin{array}{c}
 \left[\begin{array}{cccc}
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 \vdots & \vdots & & \vdots \\
 \gamma \int_{V_1} K_{xx} dV & \gamma \int_{V_2} K_{xx} dV & \cdots & \gamma \int_{V_M} K_{xx} dV \\
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 \end{array} \right]
 \end{array}
 \begin{array}{c}
 \boxed{\begin{bmatrix} \Delta \rho_1 \\ \vdots \\ \Delta \rho_N \\ \vdots \\ \Delta \rho_M \end{bmatrix}} \\
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 \end{array}$$

$\bar{\bar{G}} \Rightarrow \text{Jacobiana}$

Modelagem inversa

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$\bar{d}_0 =$

$\bar{G} \Rightarrow$ Jacobiana

\bar{p}

Dados preditos pelos parâmetros

Modelagem inversa

✓ Vetor de dados medidos: \bar{d}

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Dados preditos
pelos parâmetros

$$\bar{r} = \bar{d} - \bar{G} \bar{p}$$

Qual valor dos parâmetros que minimizam
uma determinada norma dos resíduos?

Modelagem inversa

- ✓ Minimizar uma função objetivo

$$\Gamma = \phi + \mu \theta$$

Modelagem inversa

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- ✓ ϕ = Norma dos resíduos

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Modelagem inversa

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✓ Busca sistemática

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Utilizada neste
trabalho



Modelagem inversa

- ✓ Solução analítica $\hat{\bar{p}} = (\bar{G}^T \bar{G} + \mu \bar{W})^{-1} \bar{G}^T \bar{d}$
- ✓ Resolver um sistema NxN ou MxM

Modelagem inversa

- ✓ Solução analítica $\hat{\bar{p}} = (\bar{G}^T \bar{G} + \mu \bar{W})^{-1} \bar{G}^T \bar{d}$
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 - ✓ Testar diversos parâmetros aleatoriamente

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 - ✓ Testar diversos parâmetros aleatoriamente
- ✓ Busca sistemática
 - ✓ Testar diversos parâmetros sistematicamente
 - ✓ Rene (1986)
 - ✓ Camacho *et al.* (2000)

Modelagem inversa

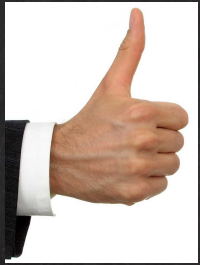
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Desenvolvido um
híbrido

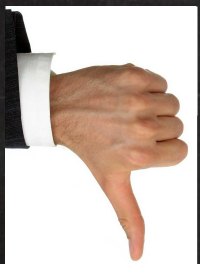


Modelagem inversa

Rene (1986): Open-Reject-Fill



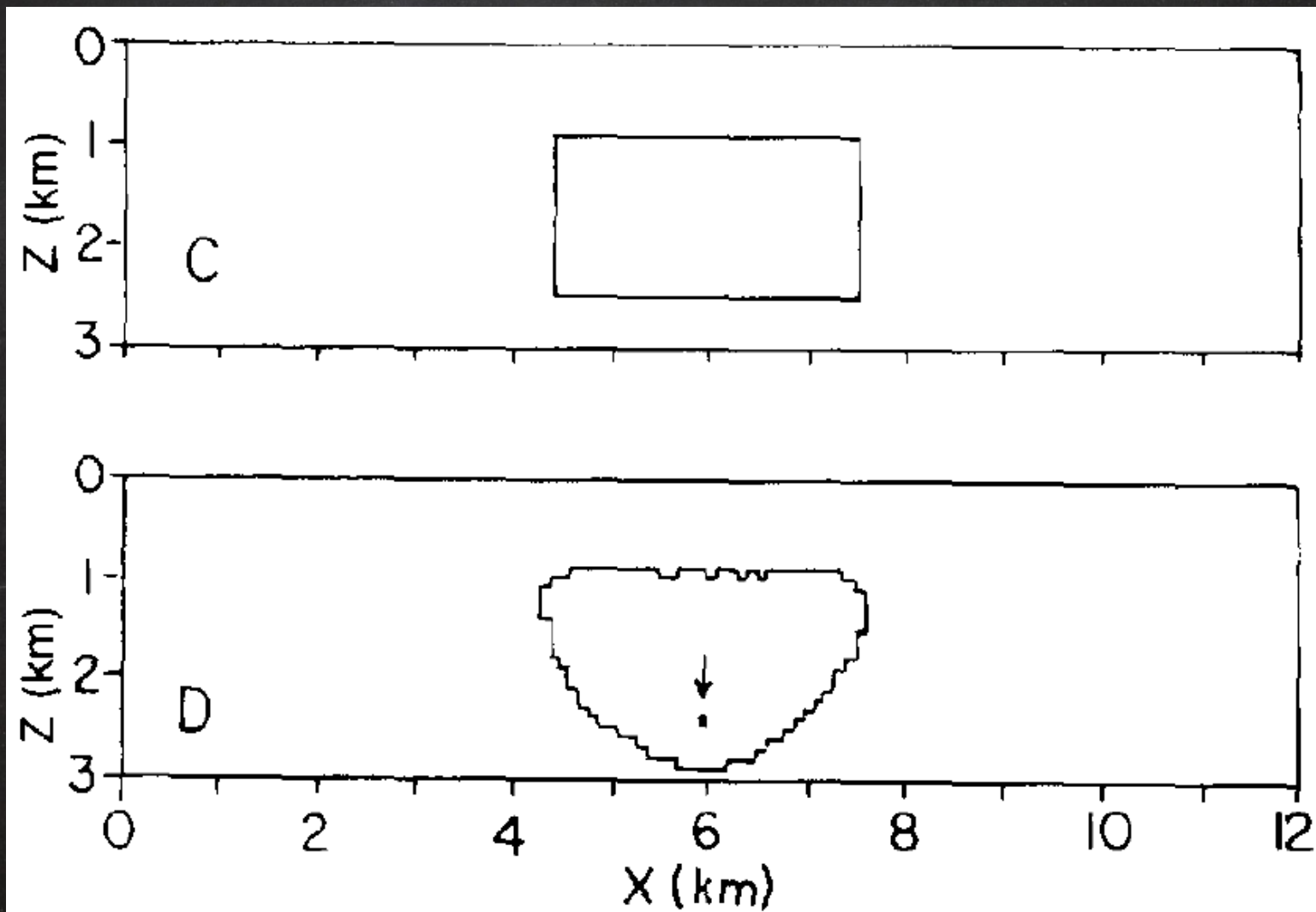
- ✓ Solução cresce entorno de "sementes"
- ✓ Busca restrita a "vizinhos"
- ✓ Solução compacta (limita vizinhos: "reject")



- ✗ Somente 1 contraste de densidade
- ✗ 2D

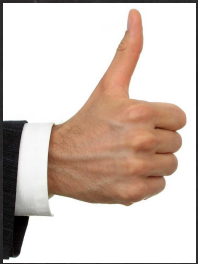
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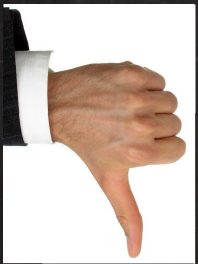


Modelagem inversa

Camacho *et al.* (2000): Growing bodies



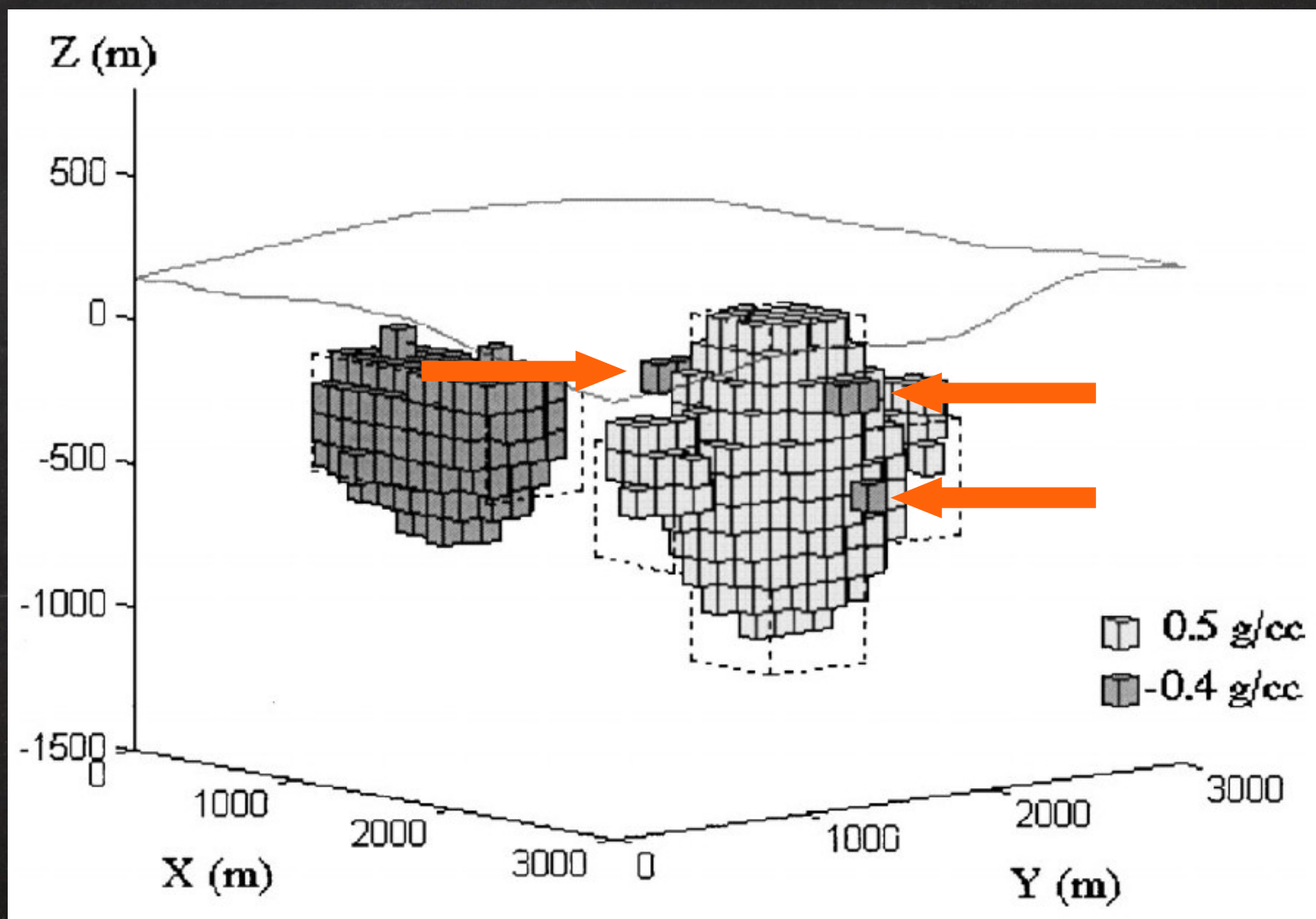
- ✓ 3D
- ✓ Não utiliza "sementes"
- ✓ Avalia todas células "vazias"



- ✗ Somente 2 contrastes de densidade
- ✗ Avalia todas células "vazias" = lento
- ✗ Não garante solução compacta

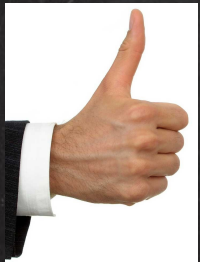
Modelagem inversa

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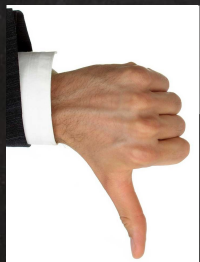


Modelagem inversa

Neste trabalho:



- ✓ 3D
- ✓ Utiliza "sementes"
- ✓ Contraste de densidade por "semente"
- ✓ Busca limitada a "vizinhos"
- ✓ Solução compacta (regularização)



- ✗ Fornecer sementes corretas
- ✓ Há métodos para isso (Beiki & Pedersen, 2010)

Modelagem inversa

Regularização:

$$\Gamma = \phi + \mu \theta$$

Função objetivo



$$\theta = \sum_{k=1}^M \frac{p_k}{\Delta \rho_{seed}} l_k^a$$

Regularizador

- ✓ l_k = distância do k-ésimo prisma a sua semente
- ✓ $\Delta \rho_{seed}$ = contraste de densidade da semente
- ✓ p_k = contraste de densidade do k-ésimo prisma
- ✓ a = potência

Modelagem inversa

Regularização:

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Regularizador

Minimizar θ impõe compacidade

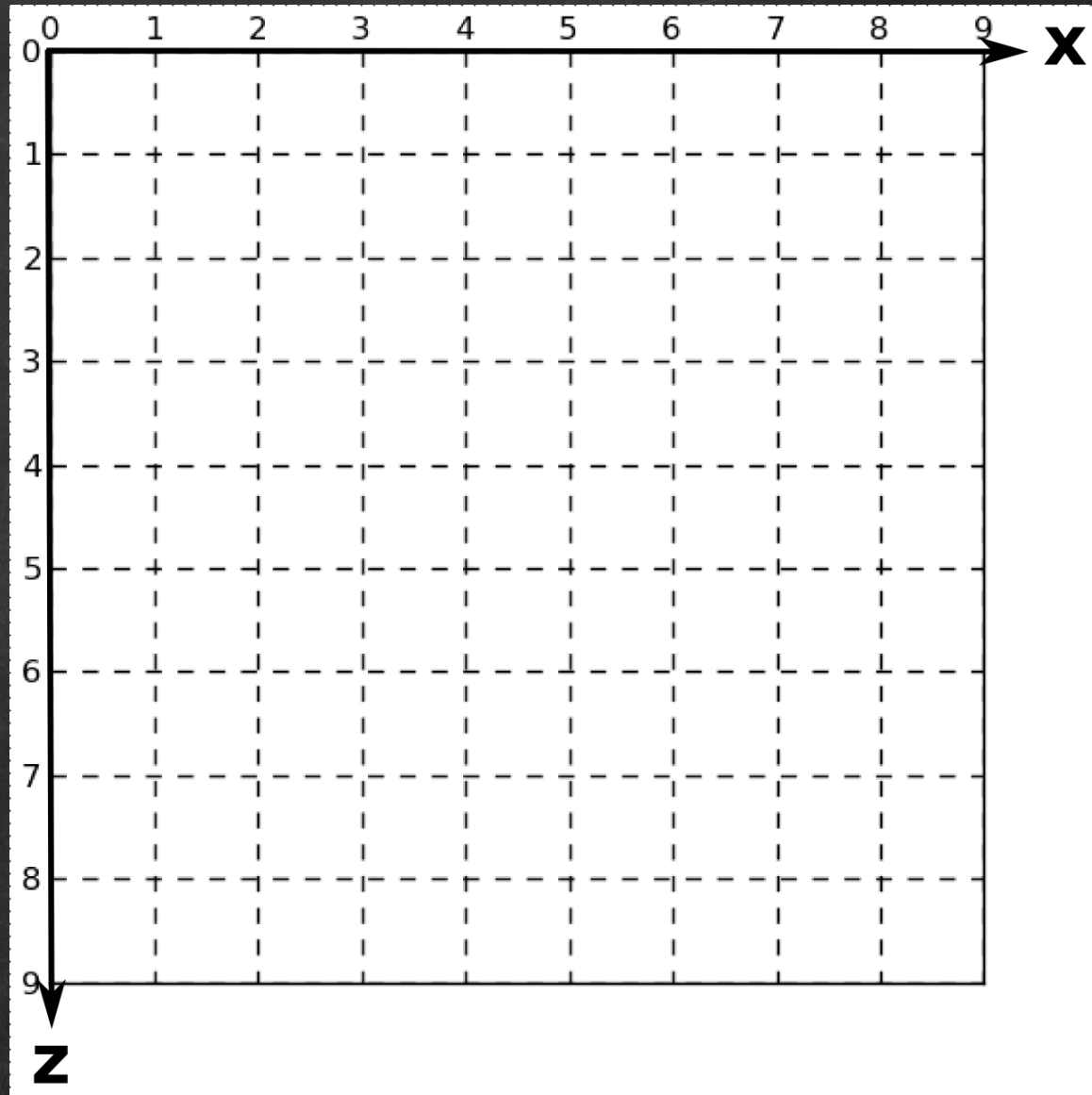
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Algoritmo


```

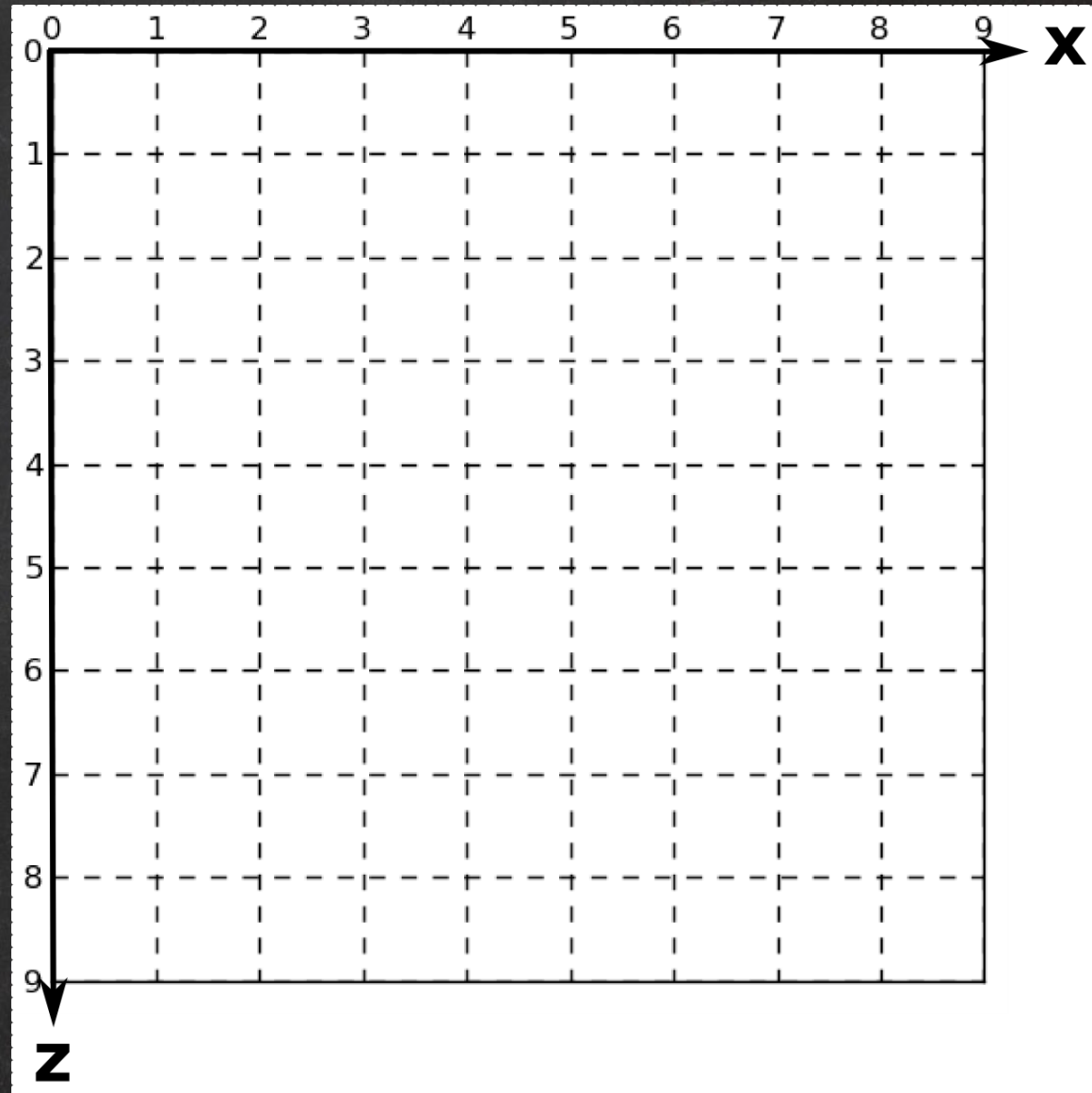
r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

```



$r = d$

```
for s in seeds:
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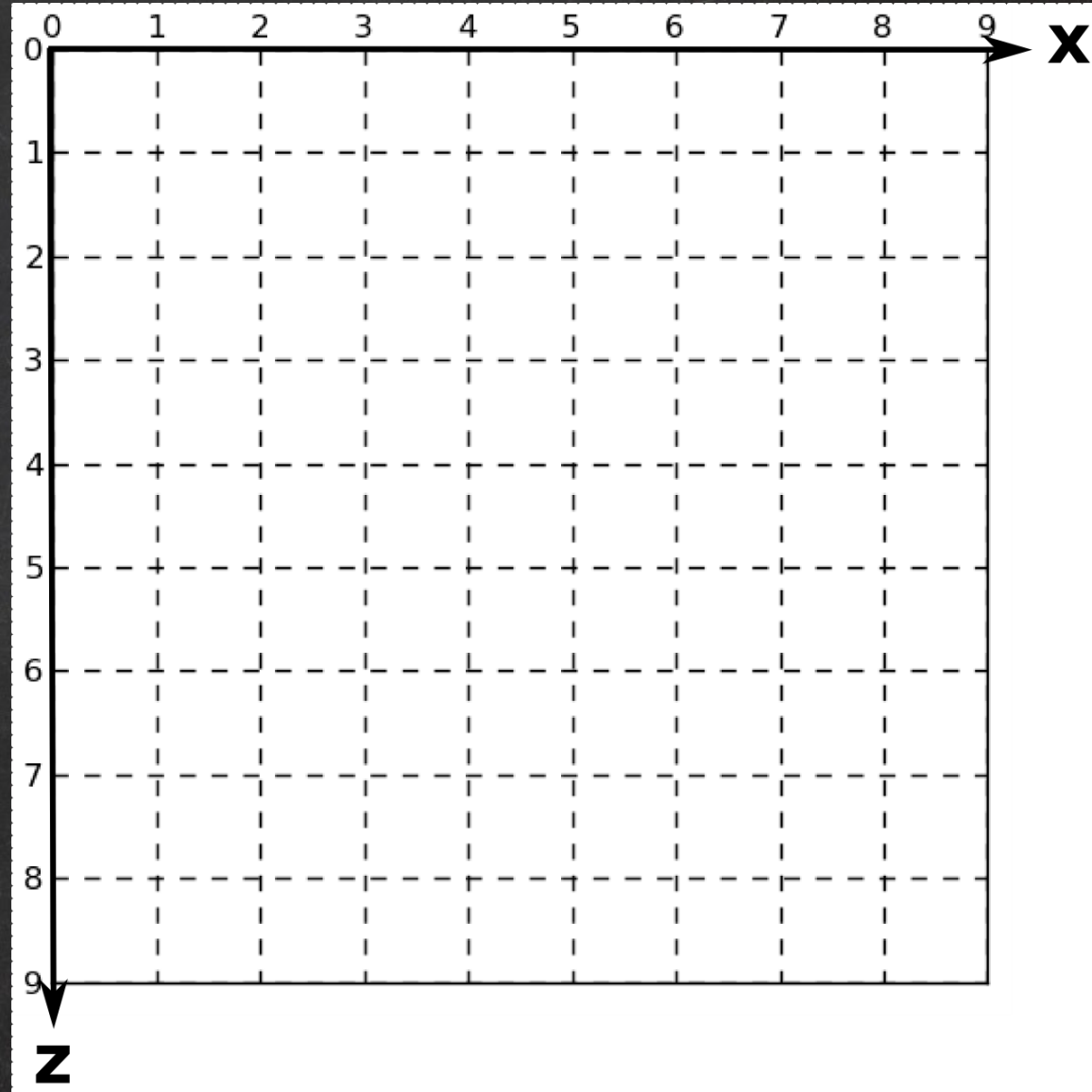
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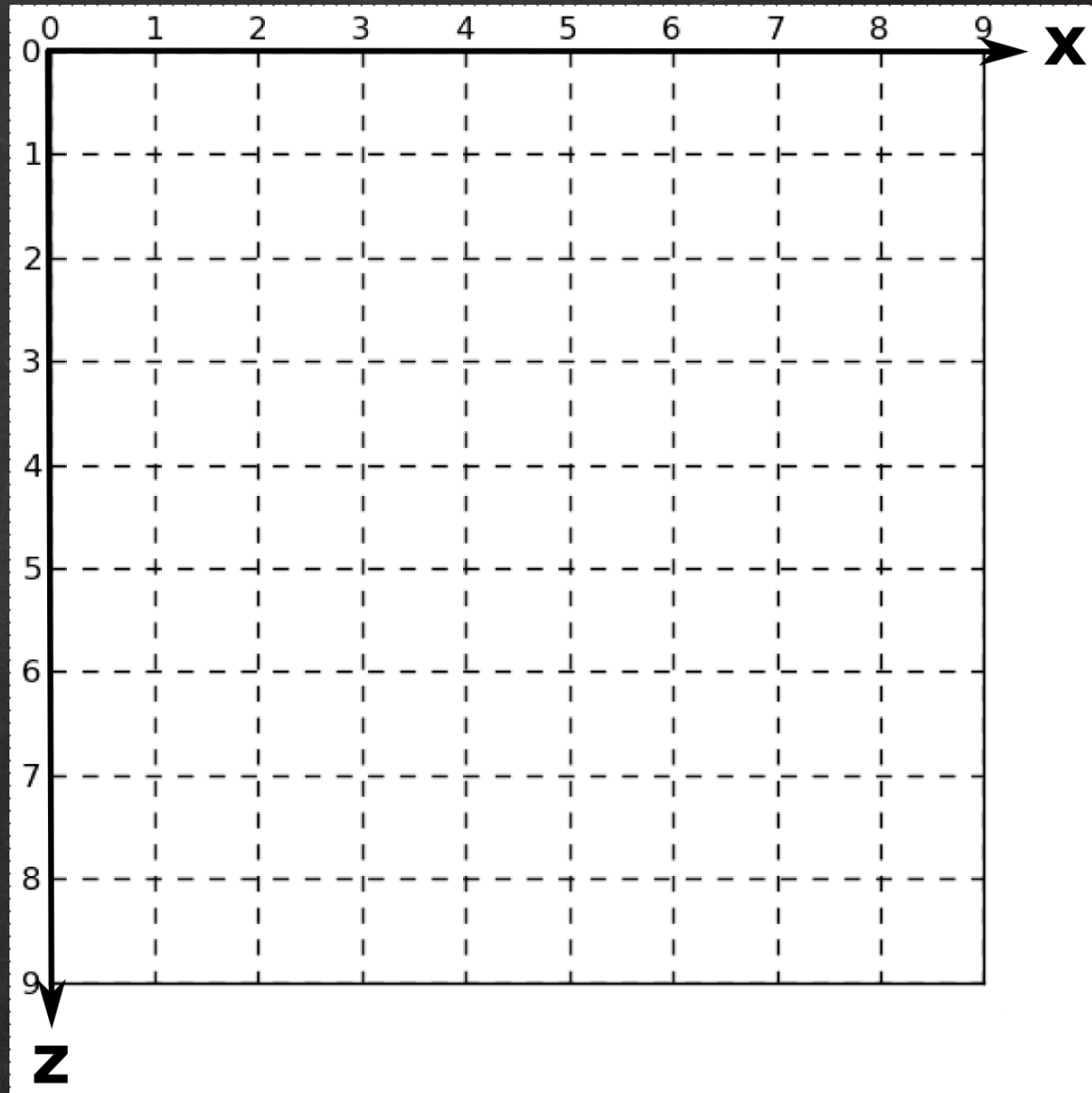
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            if misfit + reg < best:
```

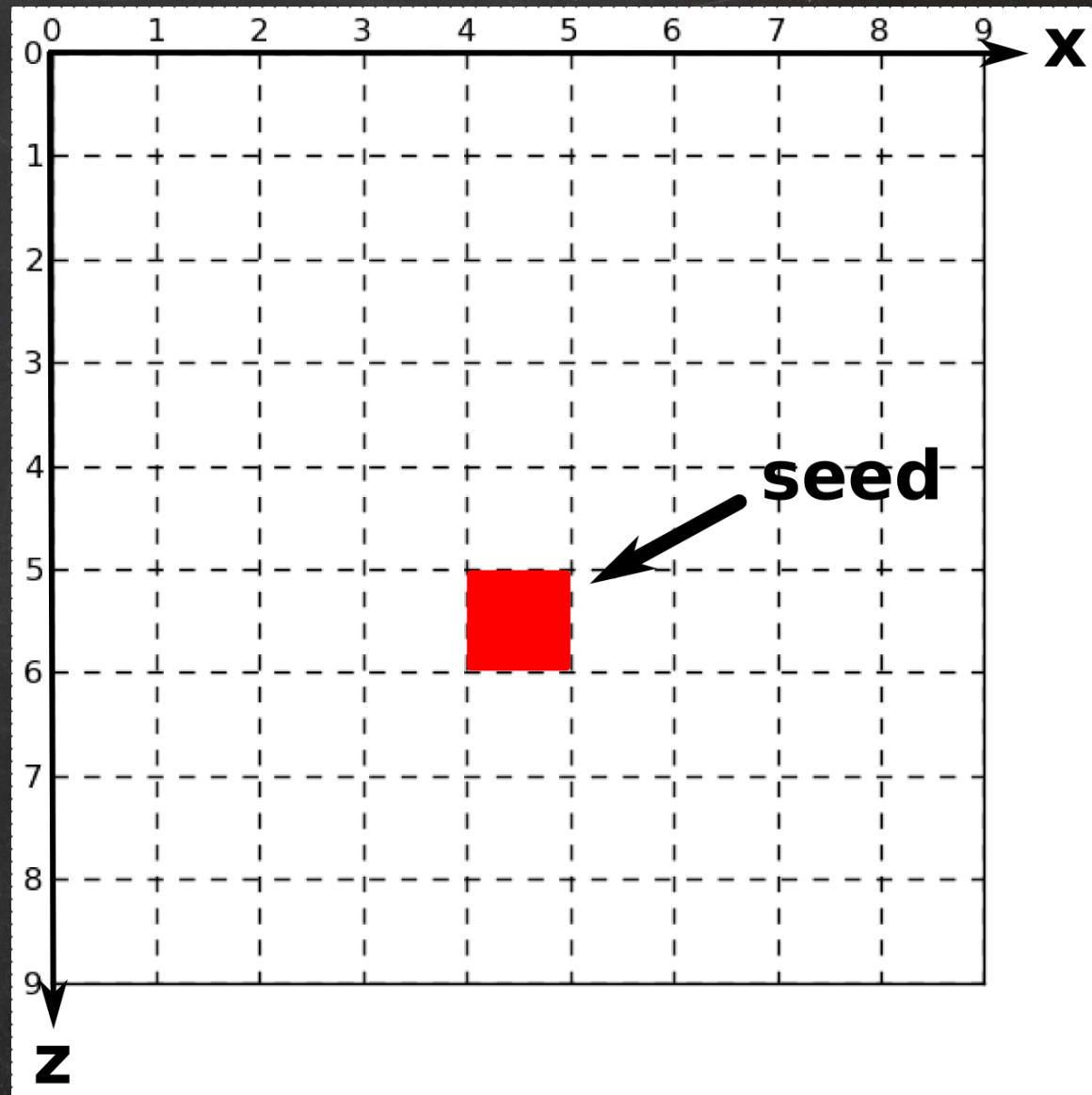
```
                best_n = n
```

```
update_p_r(best_n)
```

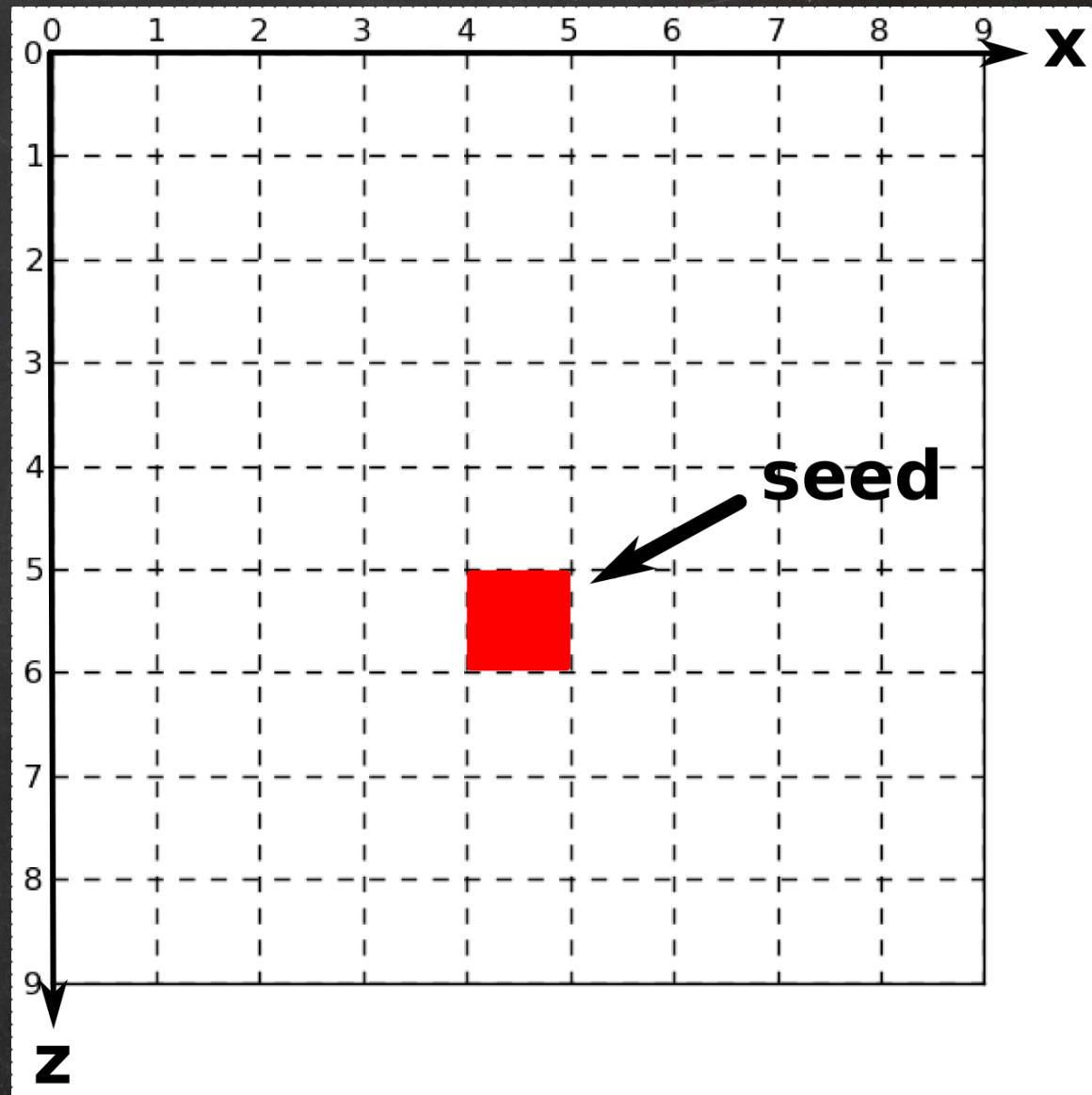
```
append_neighbors(best_n)
```



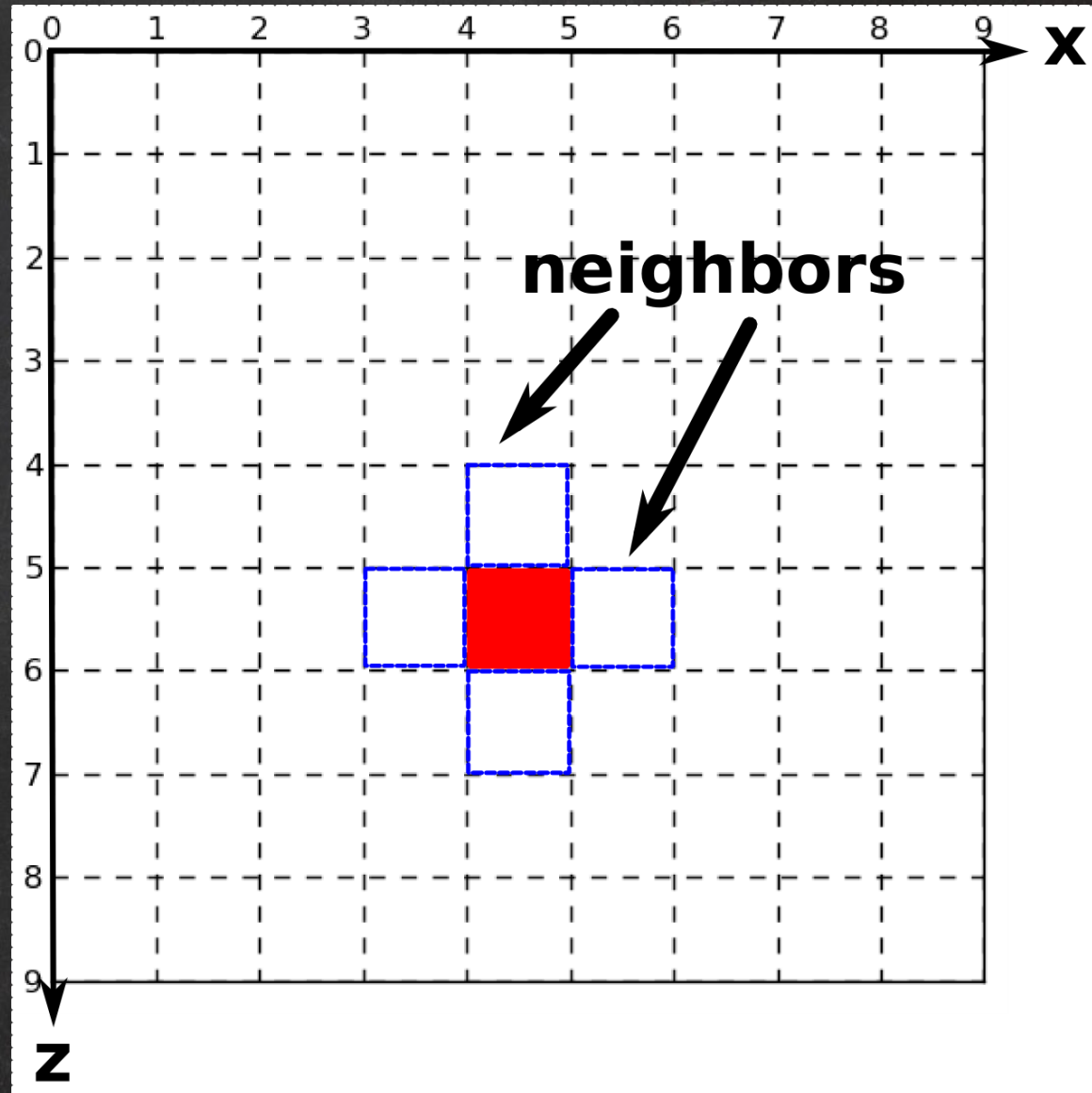

```
r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)
```




```
r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)
```



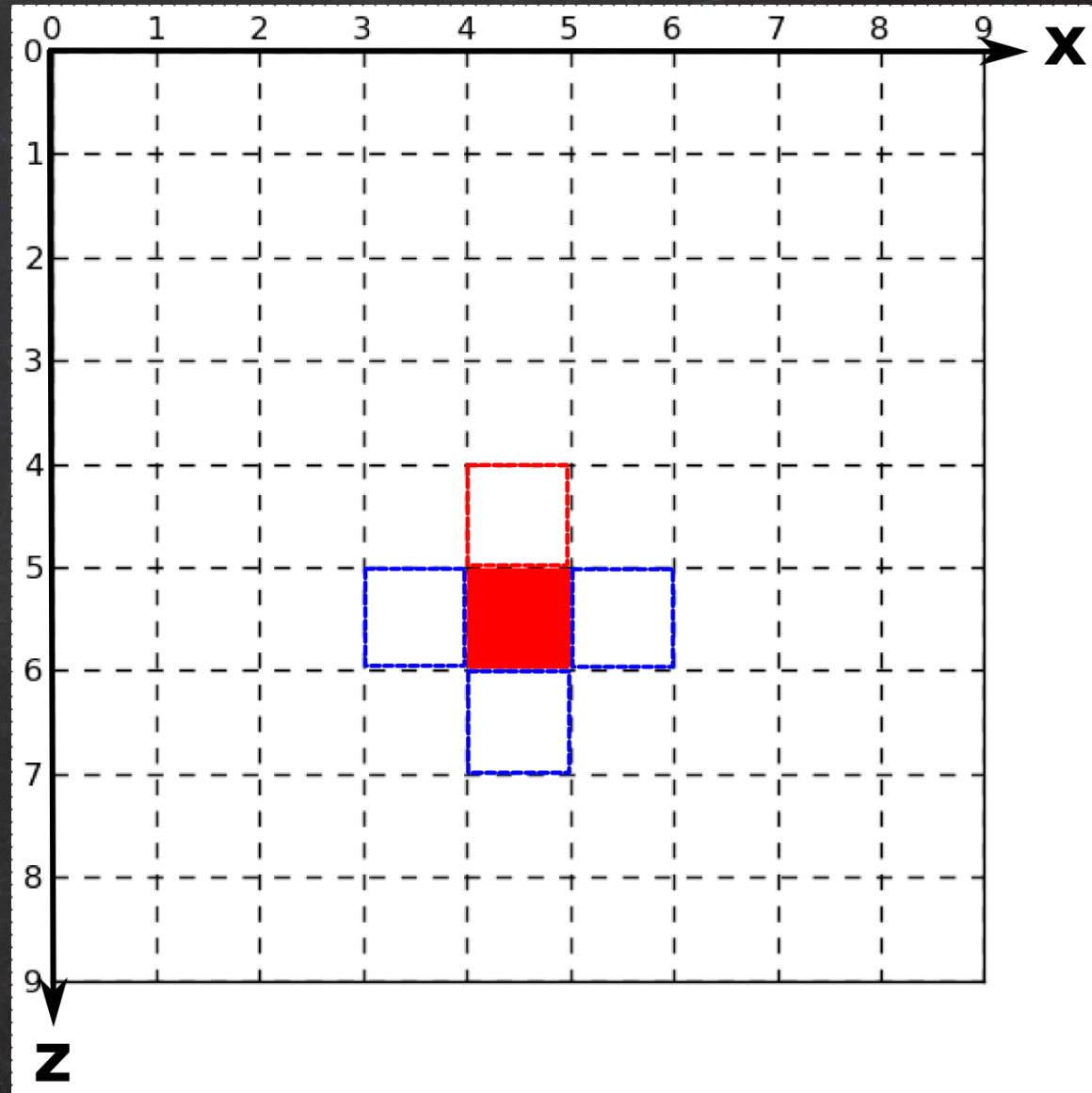

```
r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
        update_p_r(best_n)
    append_neighbors(best_n)
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

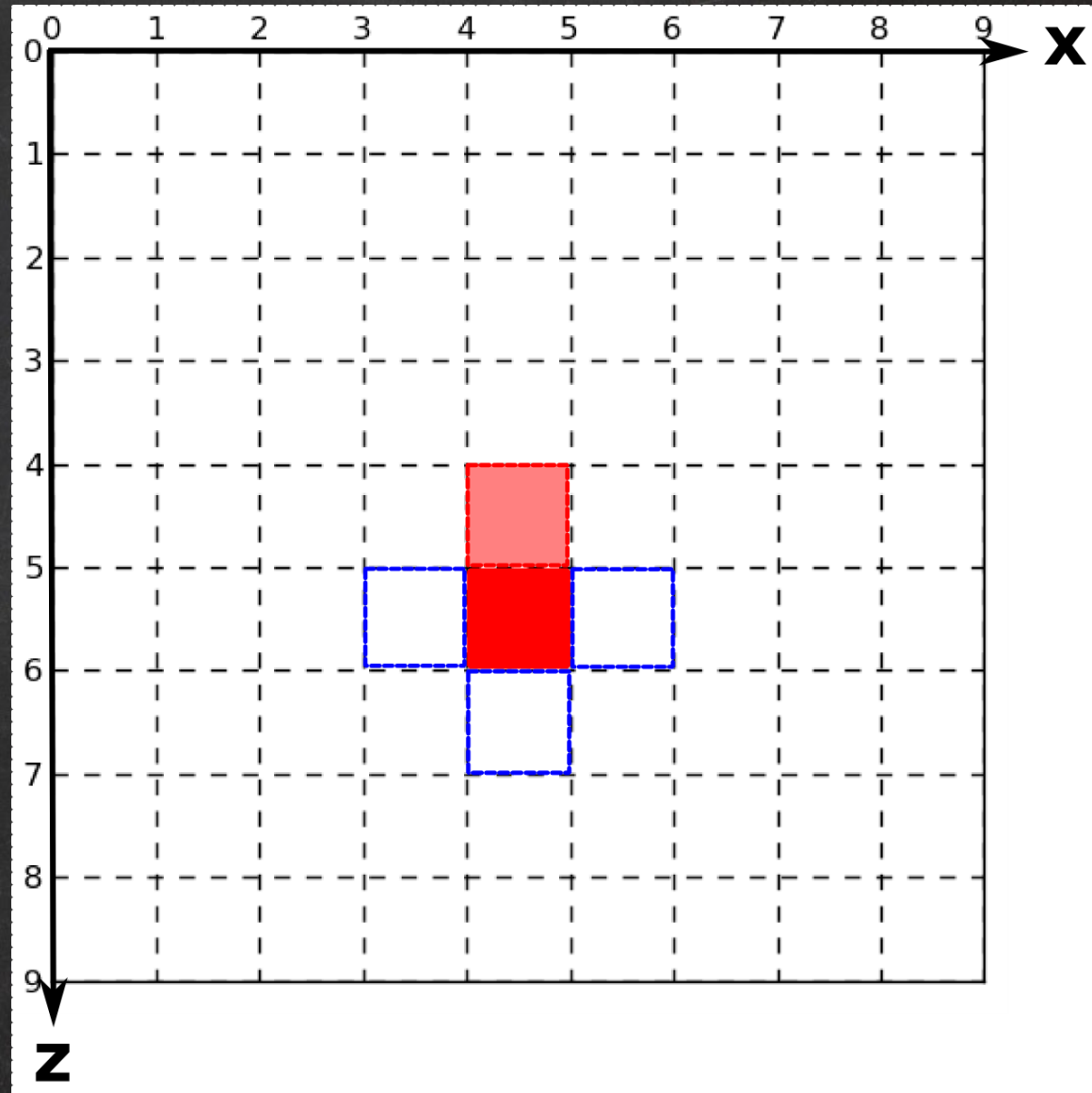
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

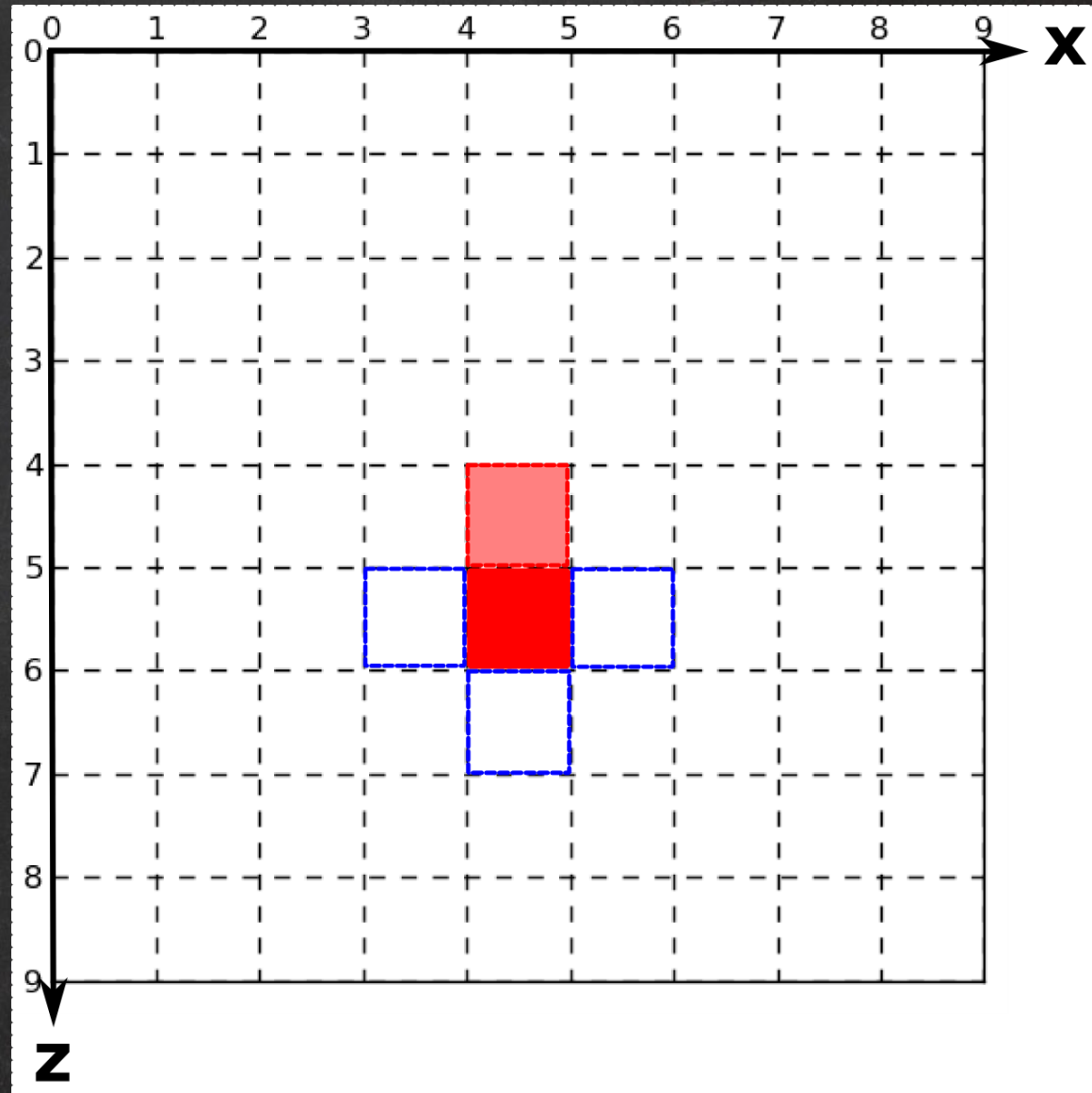
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

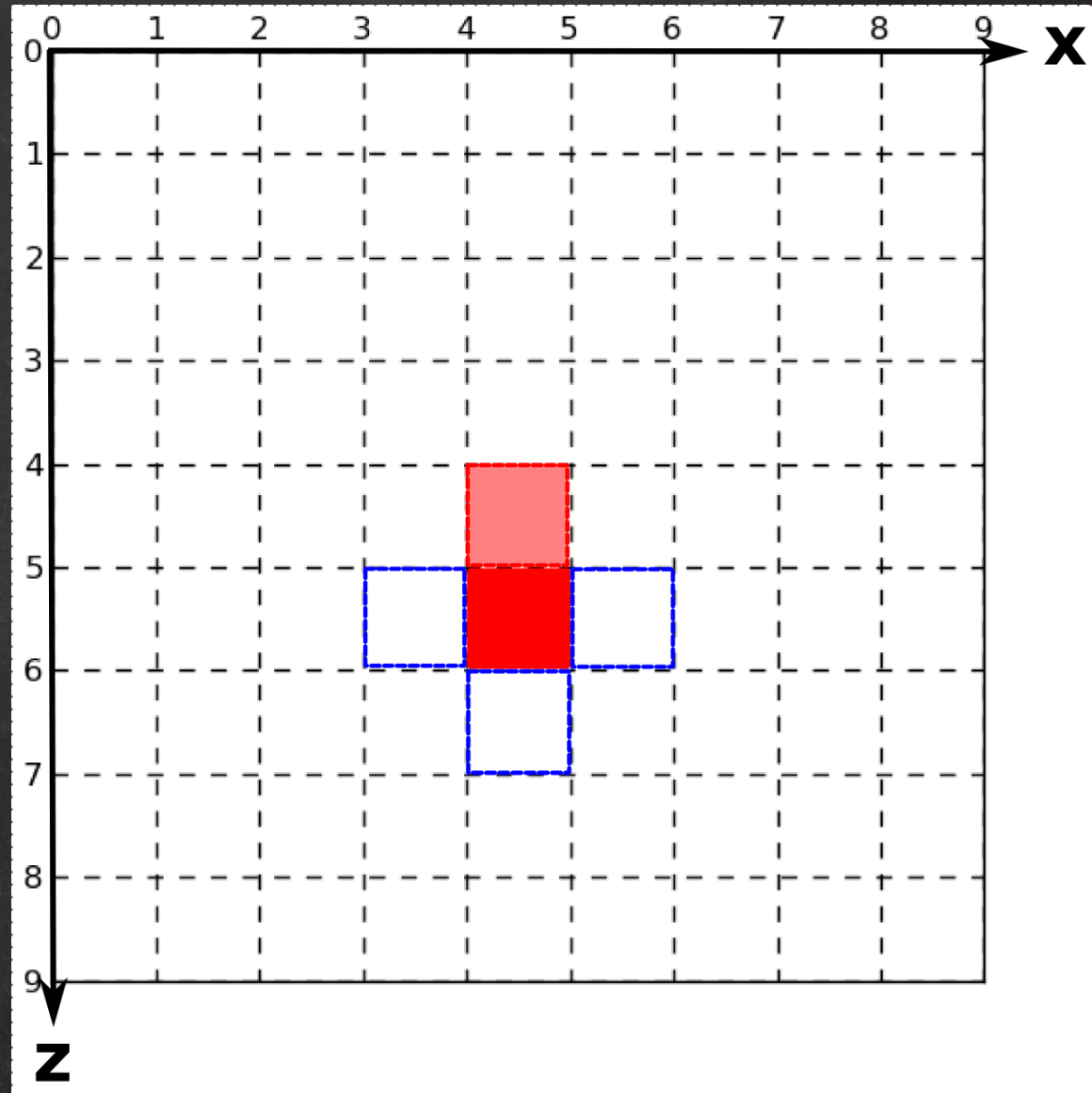
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

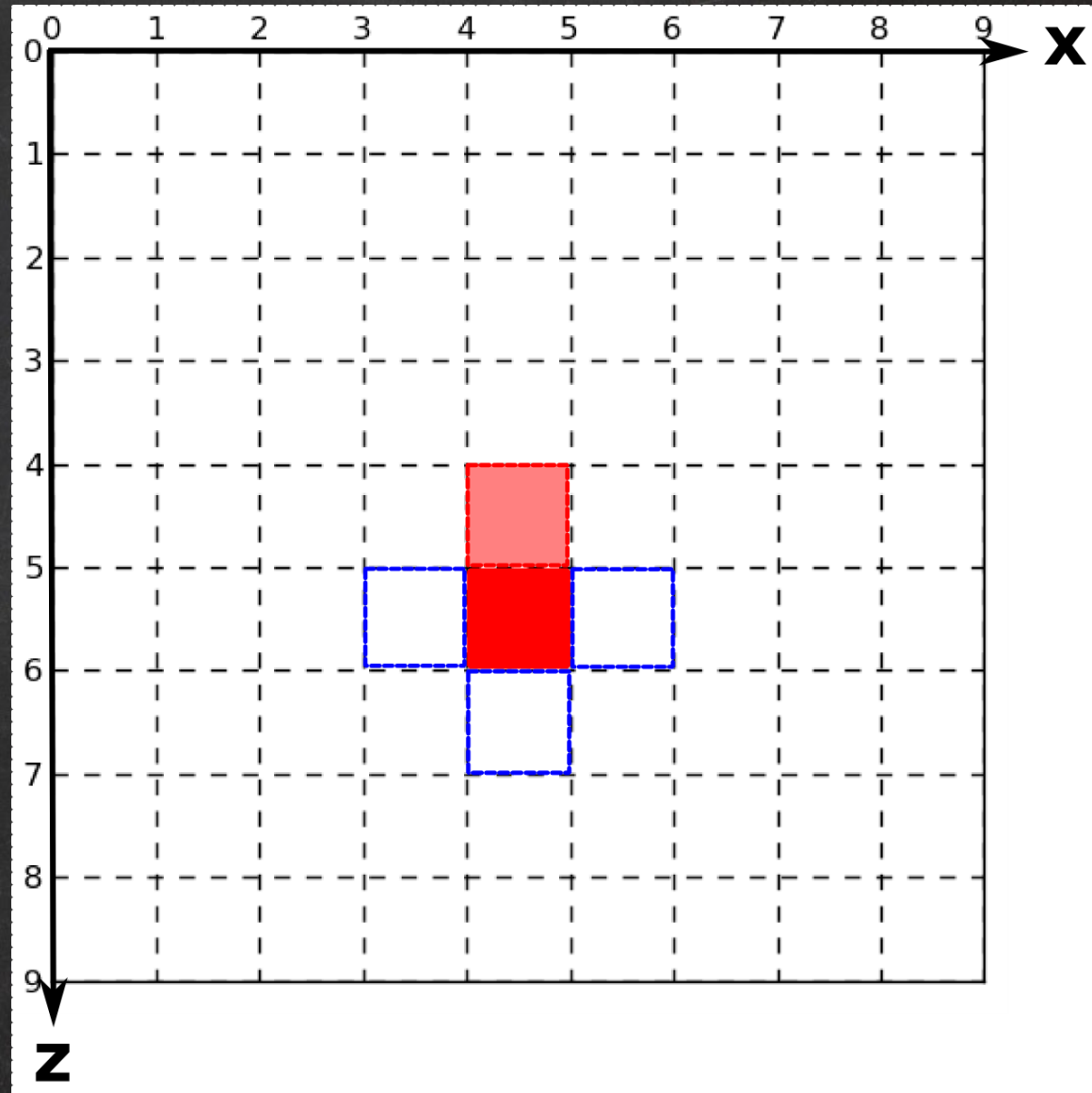
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

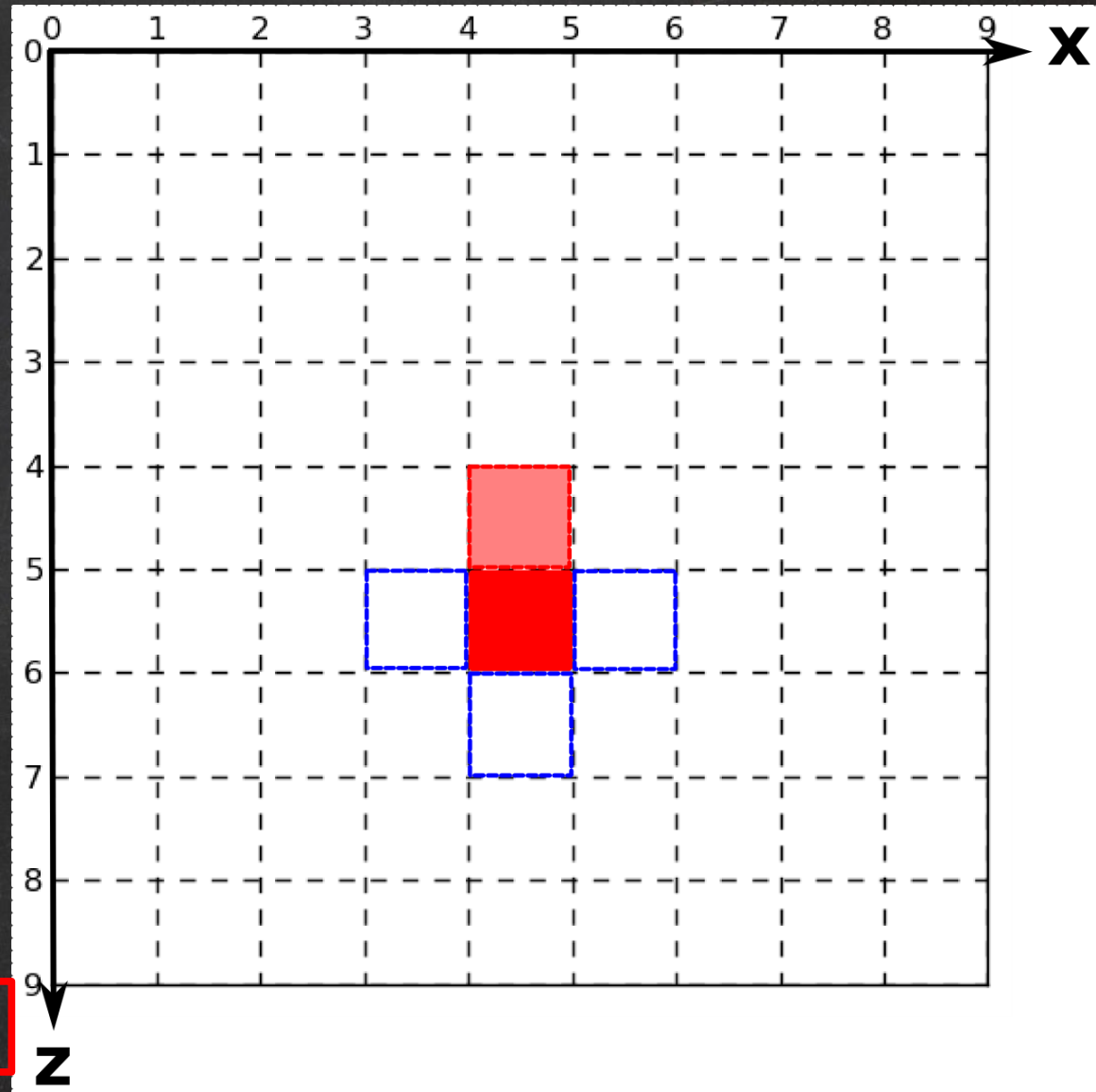
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

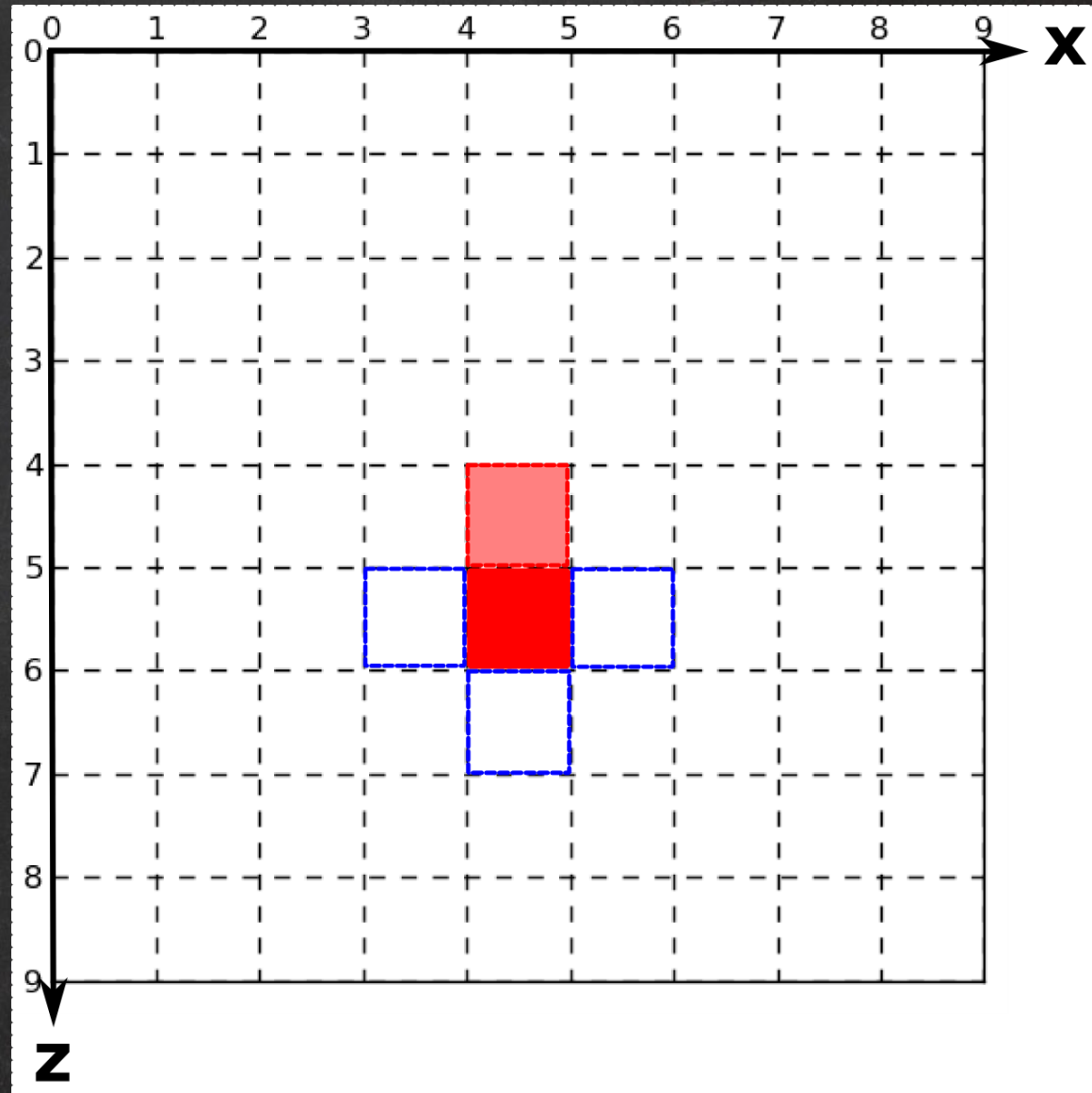
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

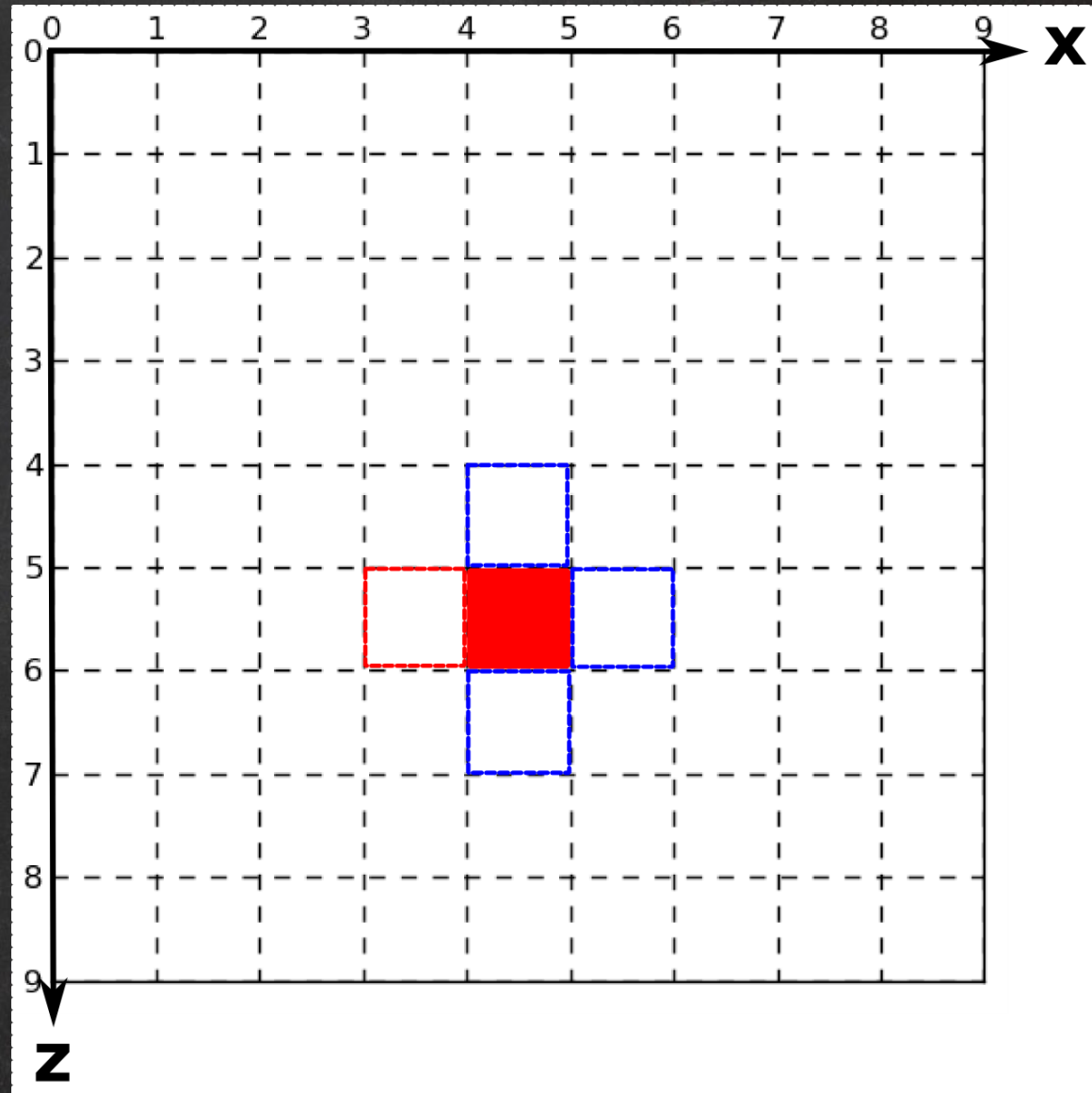
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

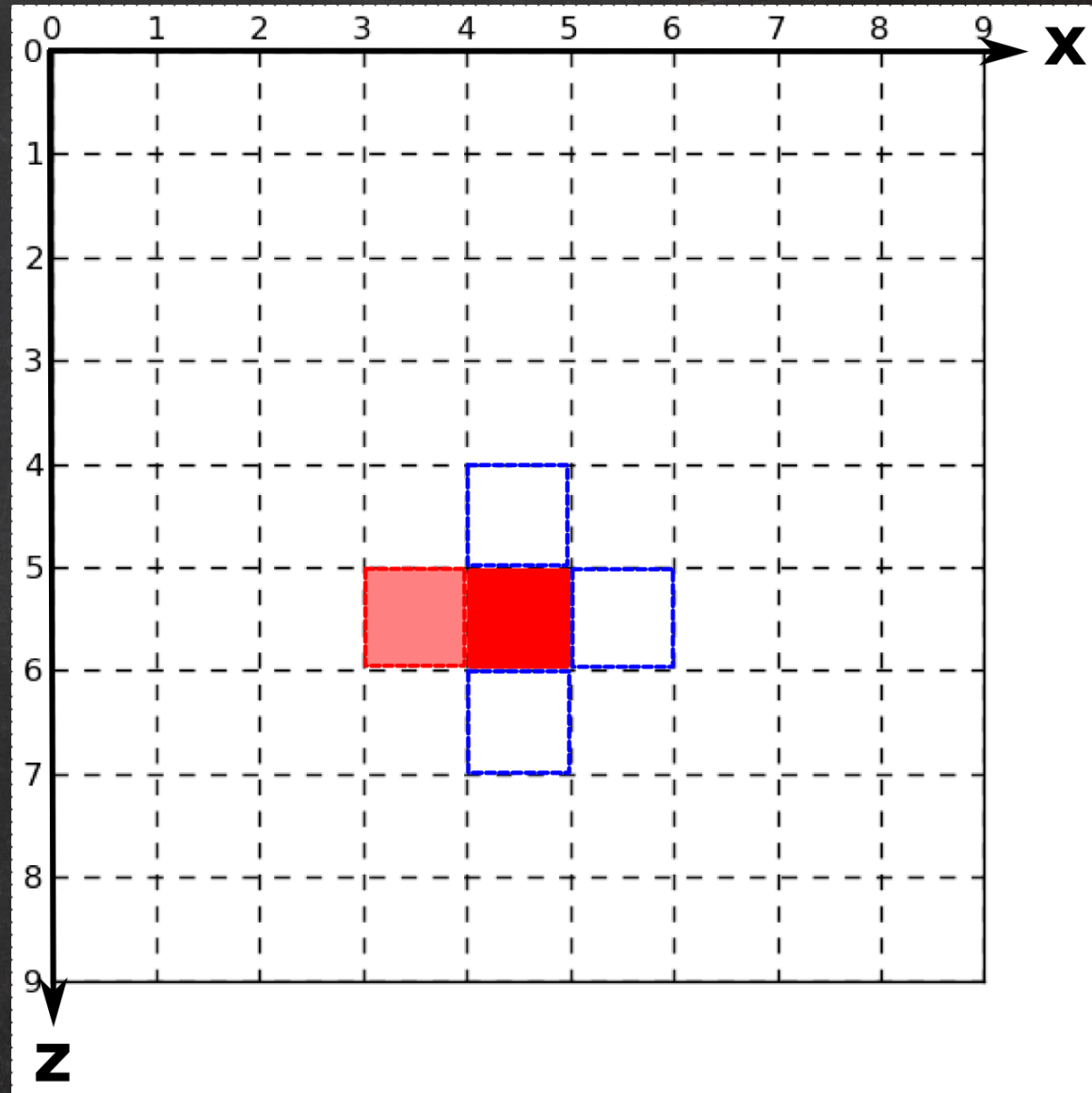
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

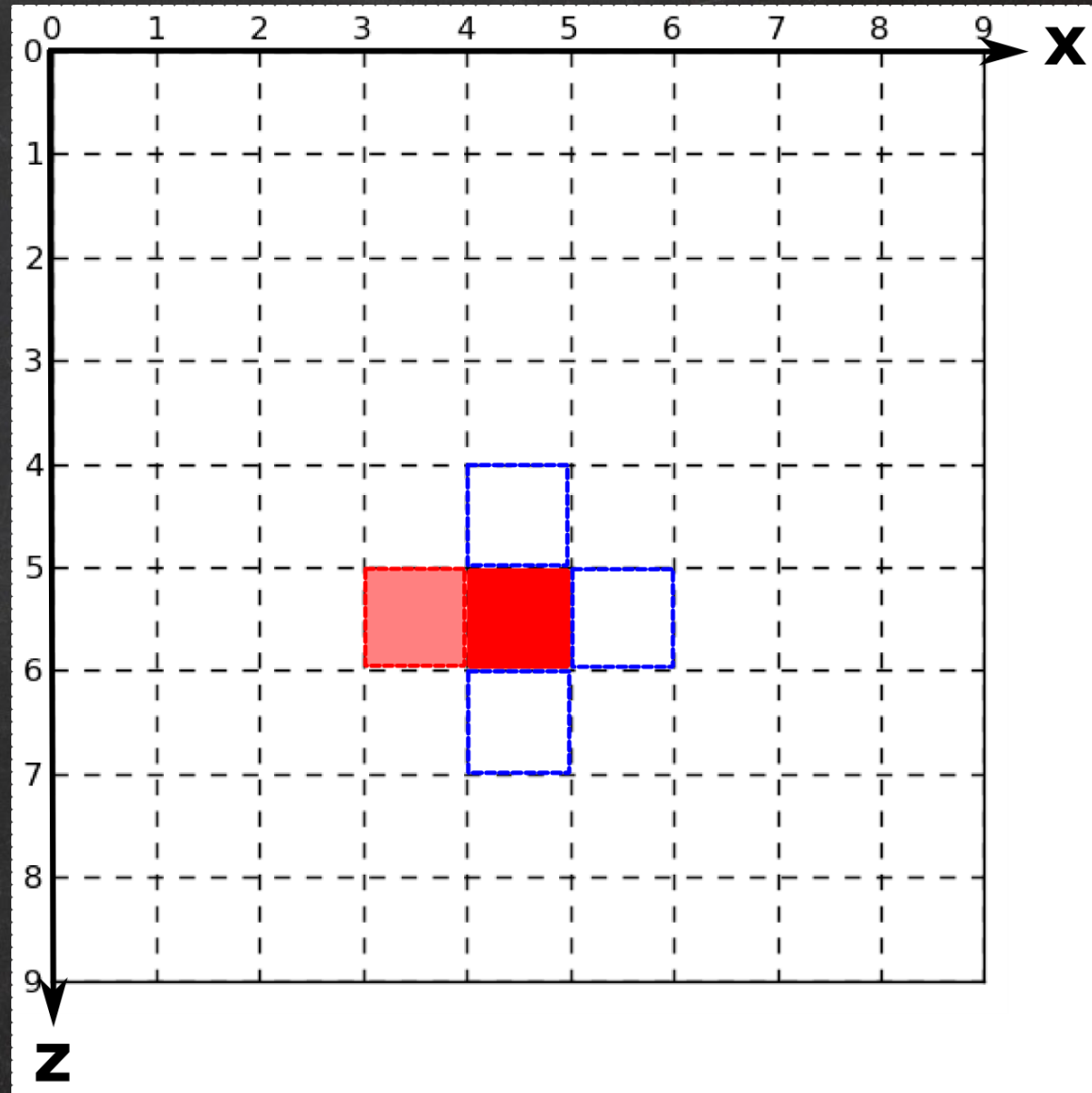
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

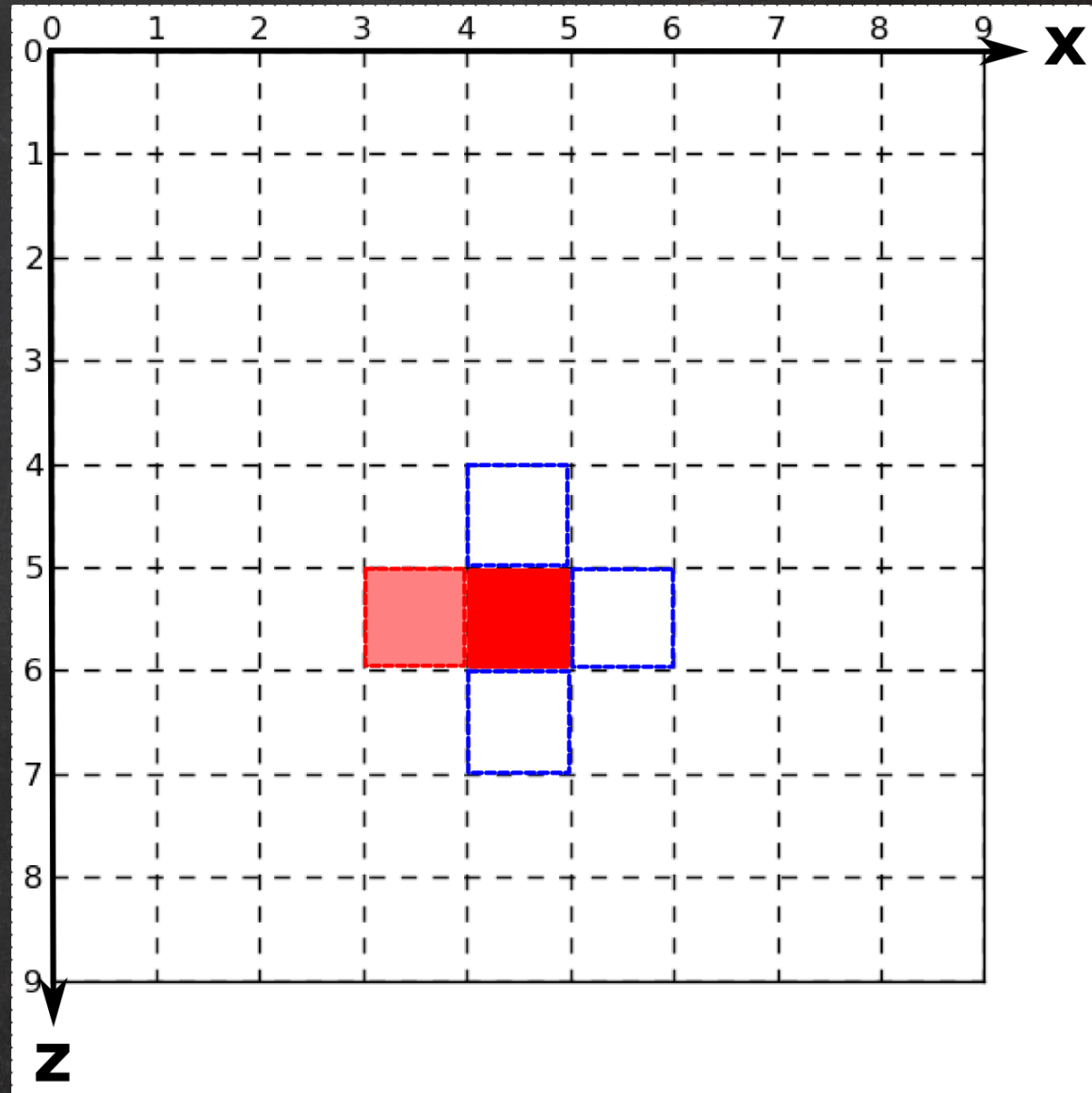
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

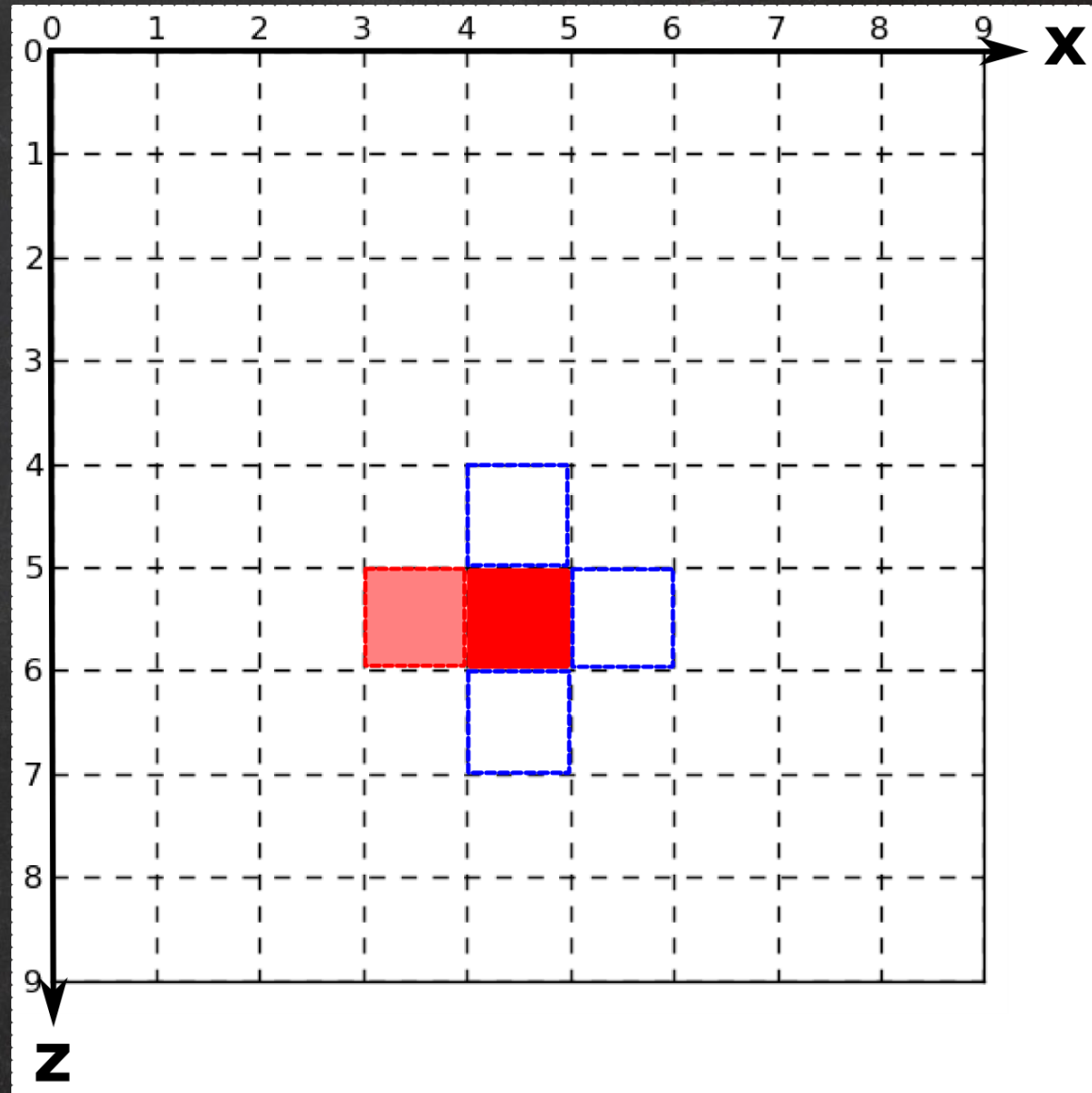
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

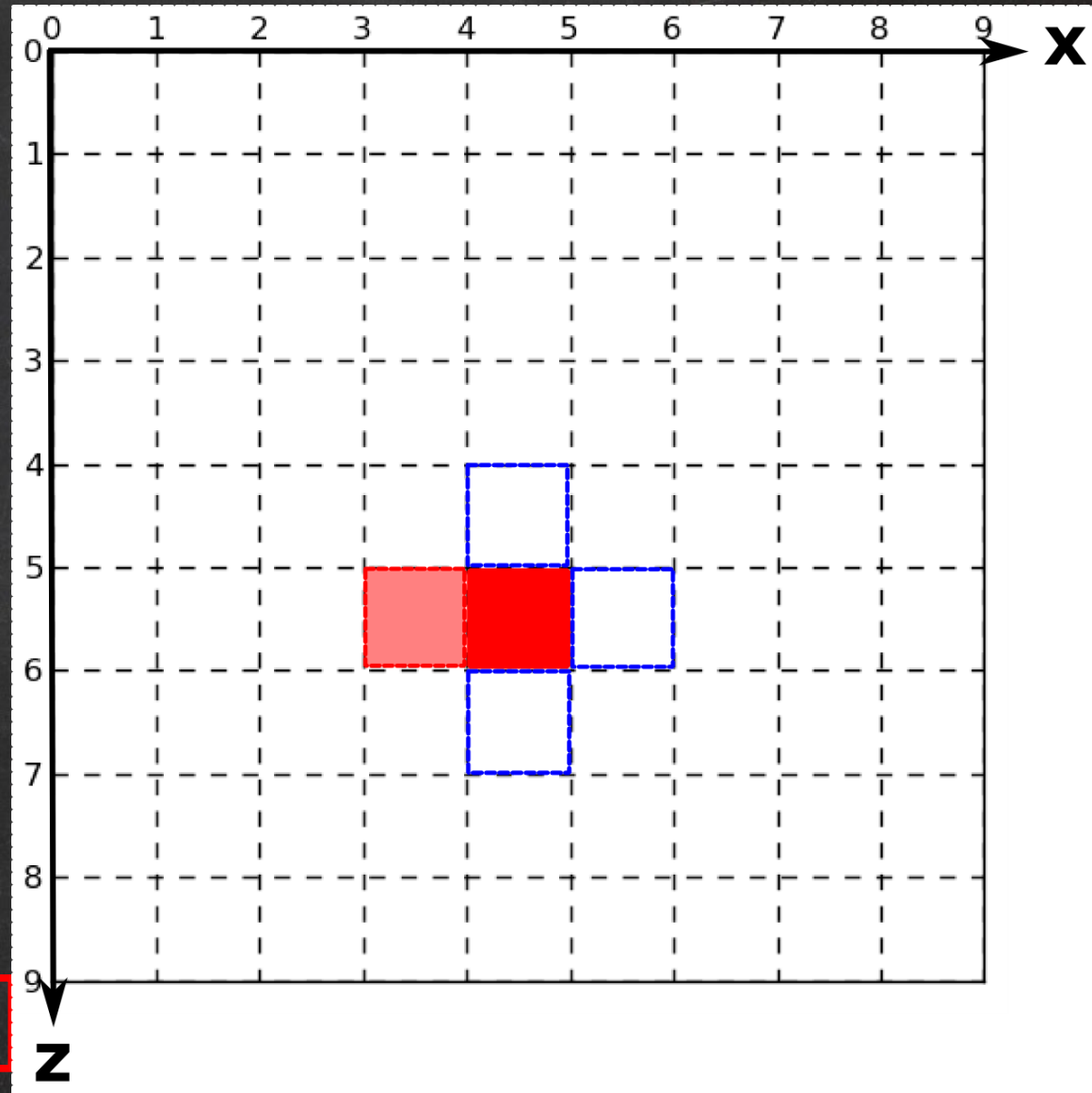
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

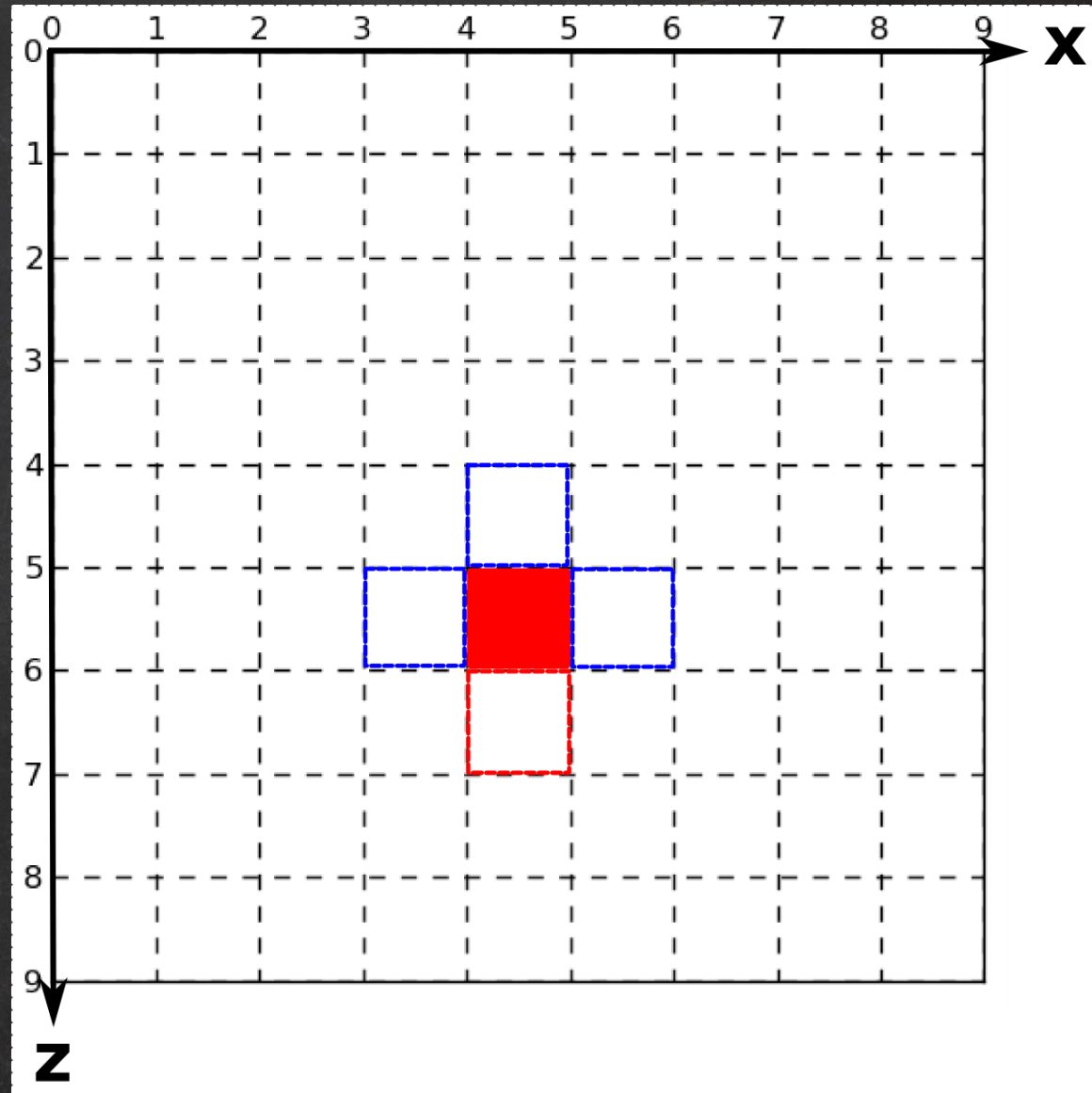
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

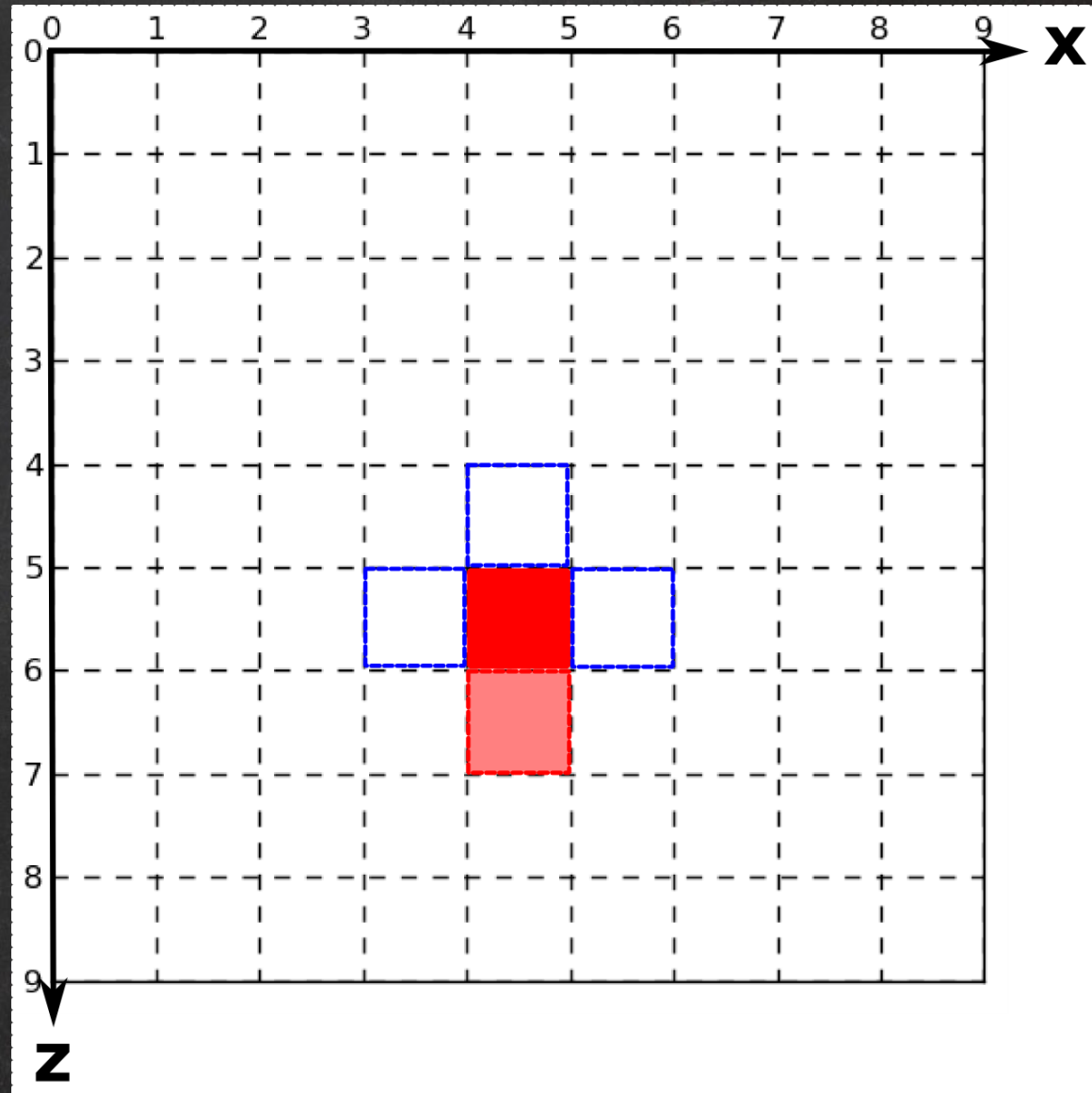
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

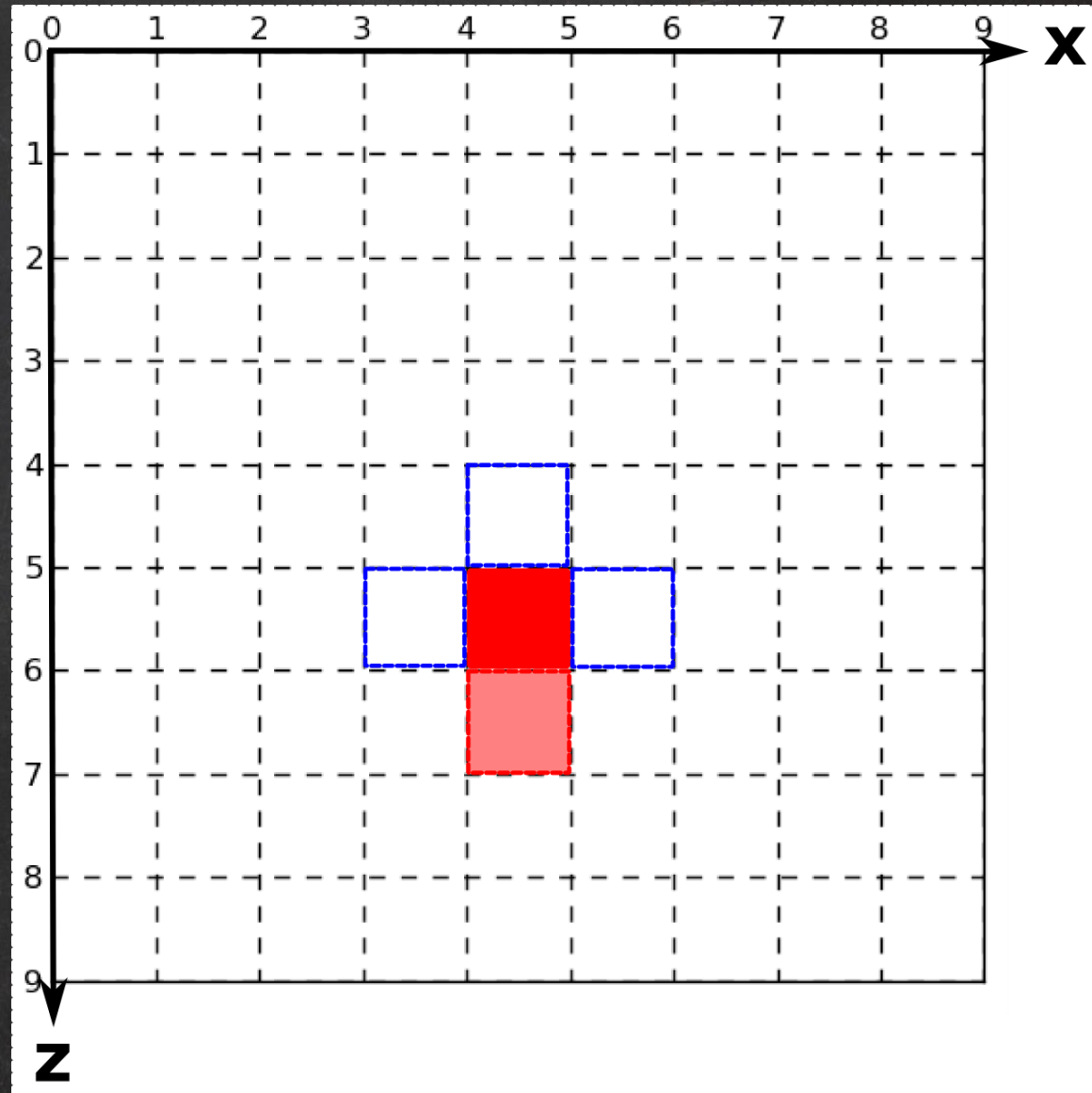
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

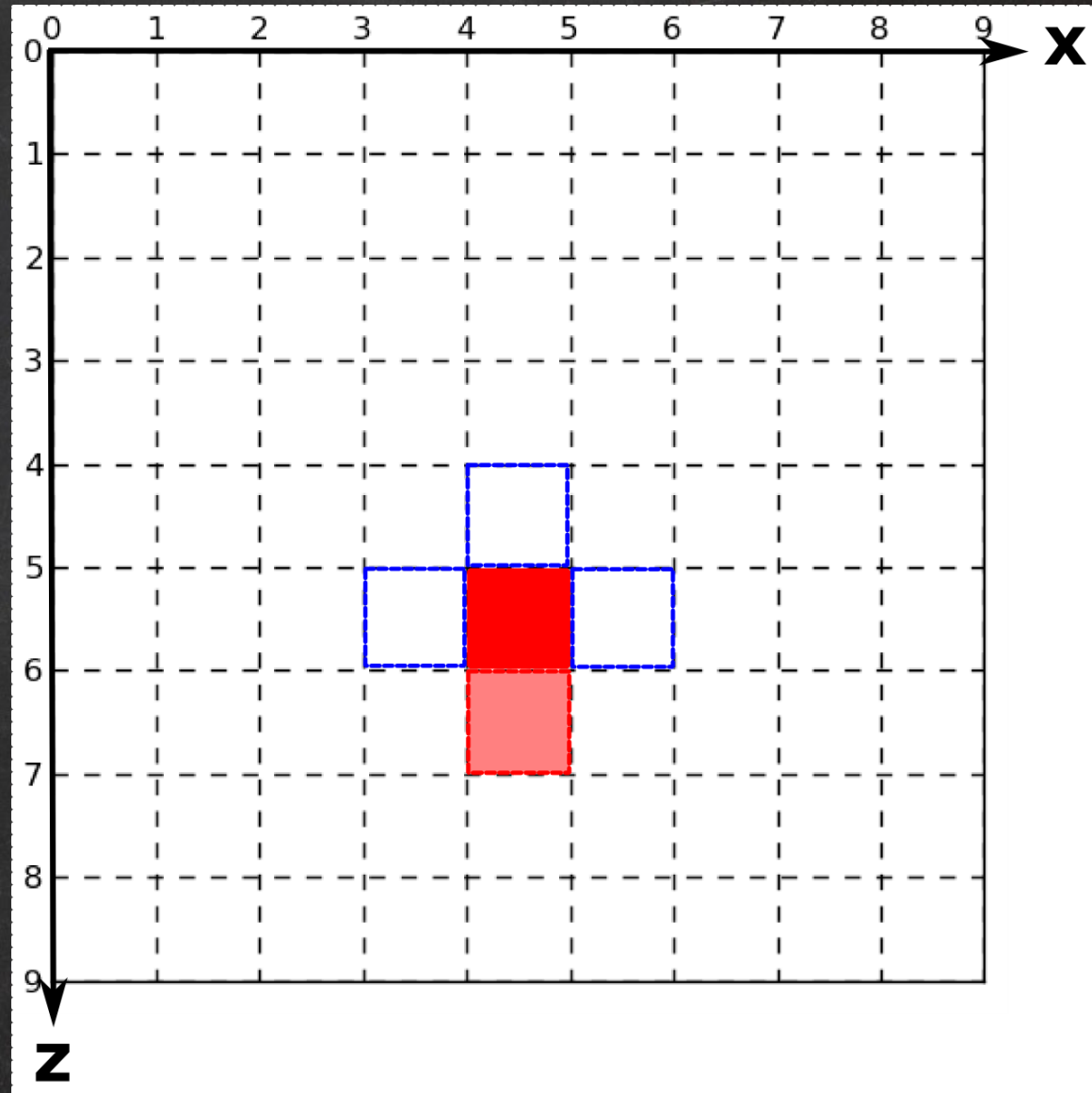
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
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for i in maxit:
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            reg = regularizer(p)
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    append_neighbors(best_n)

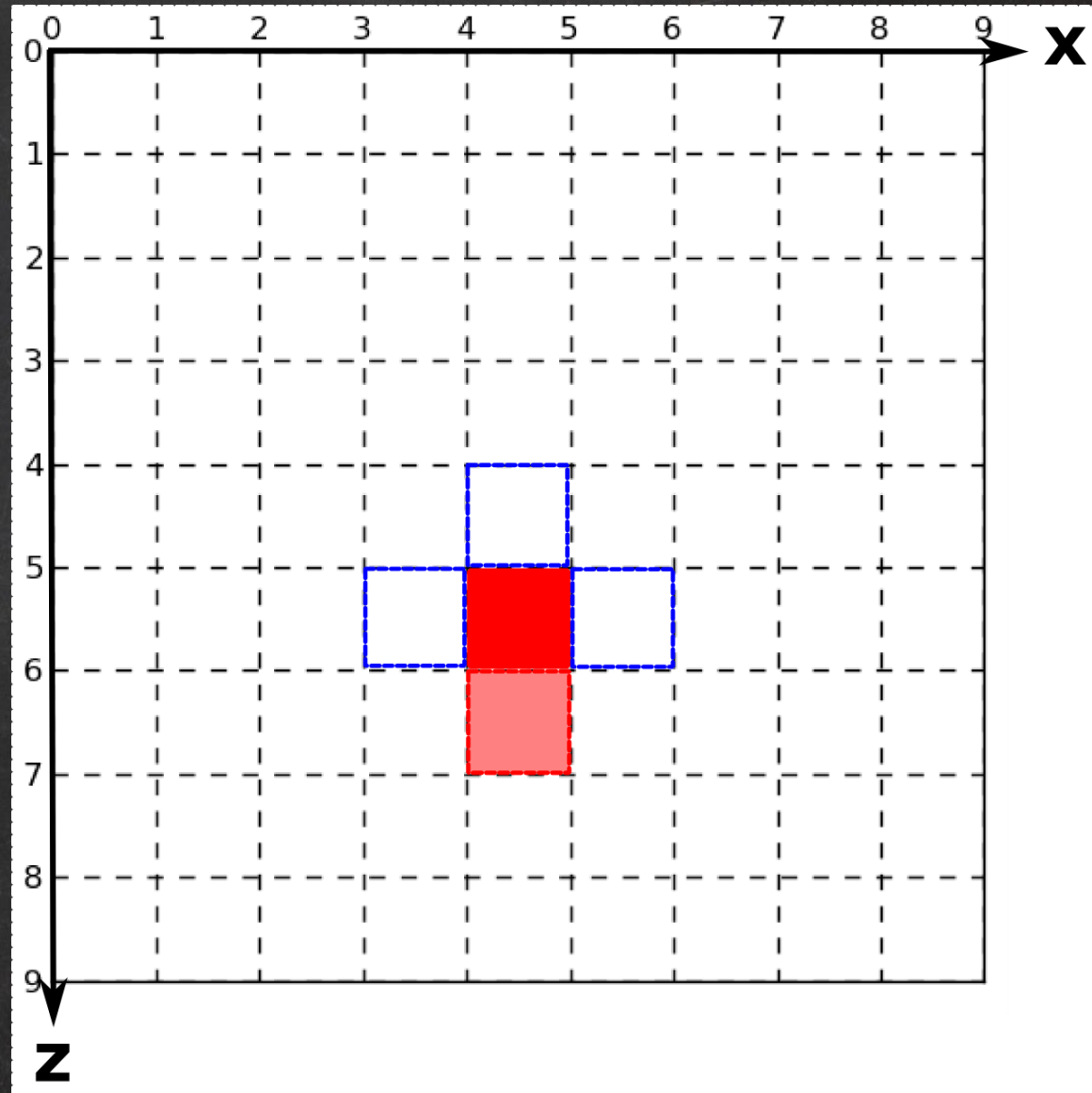
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

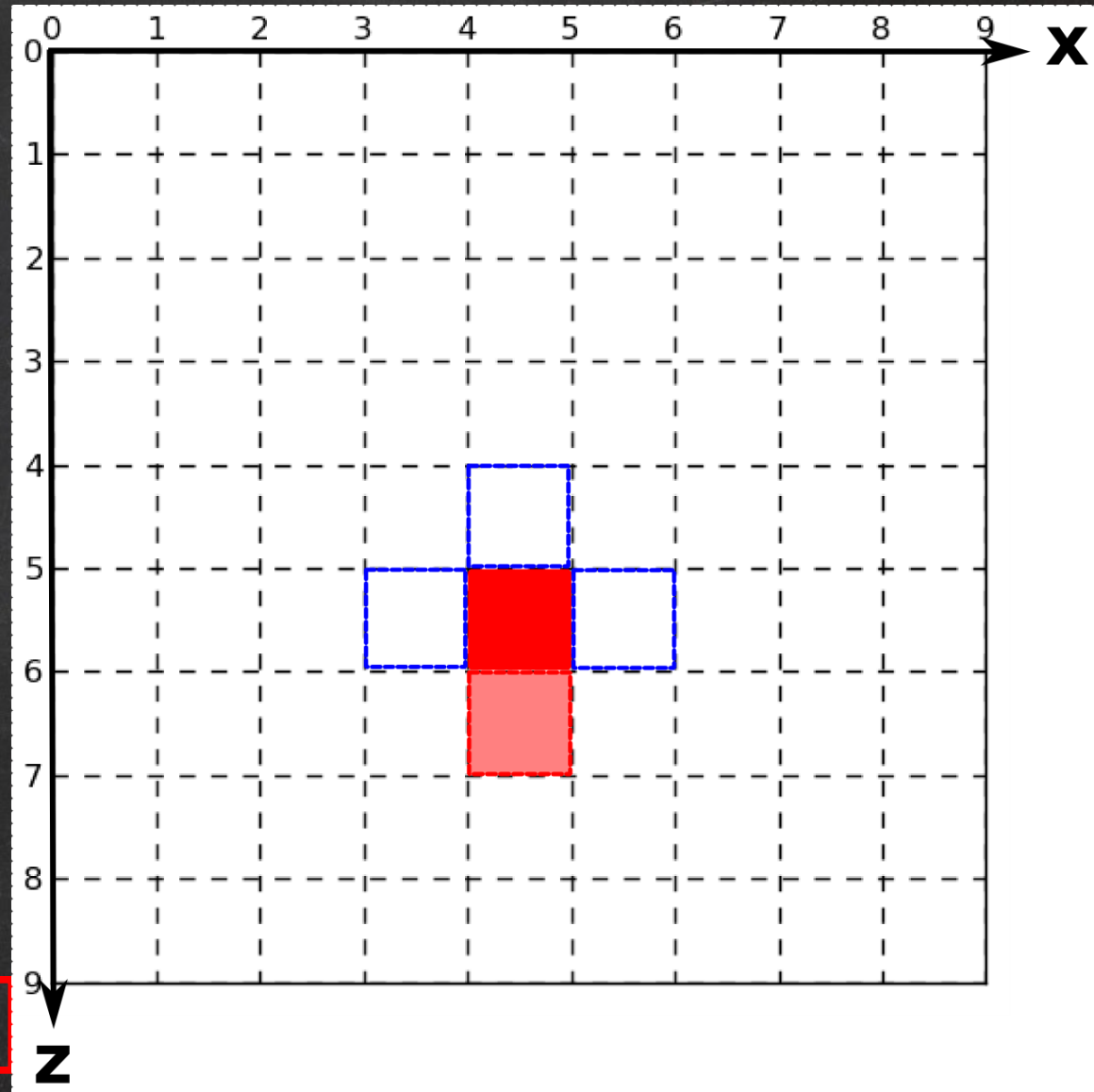
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
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    update_p_r(best_n)
    append_neighbors(best_n)

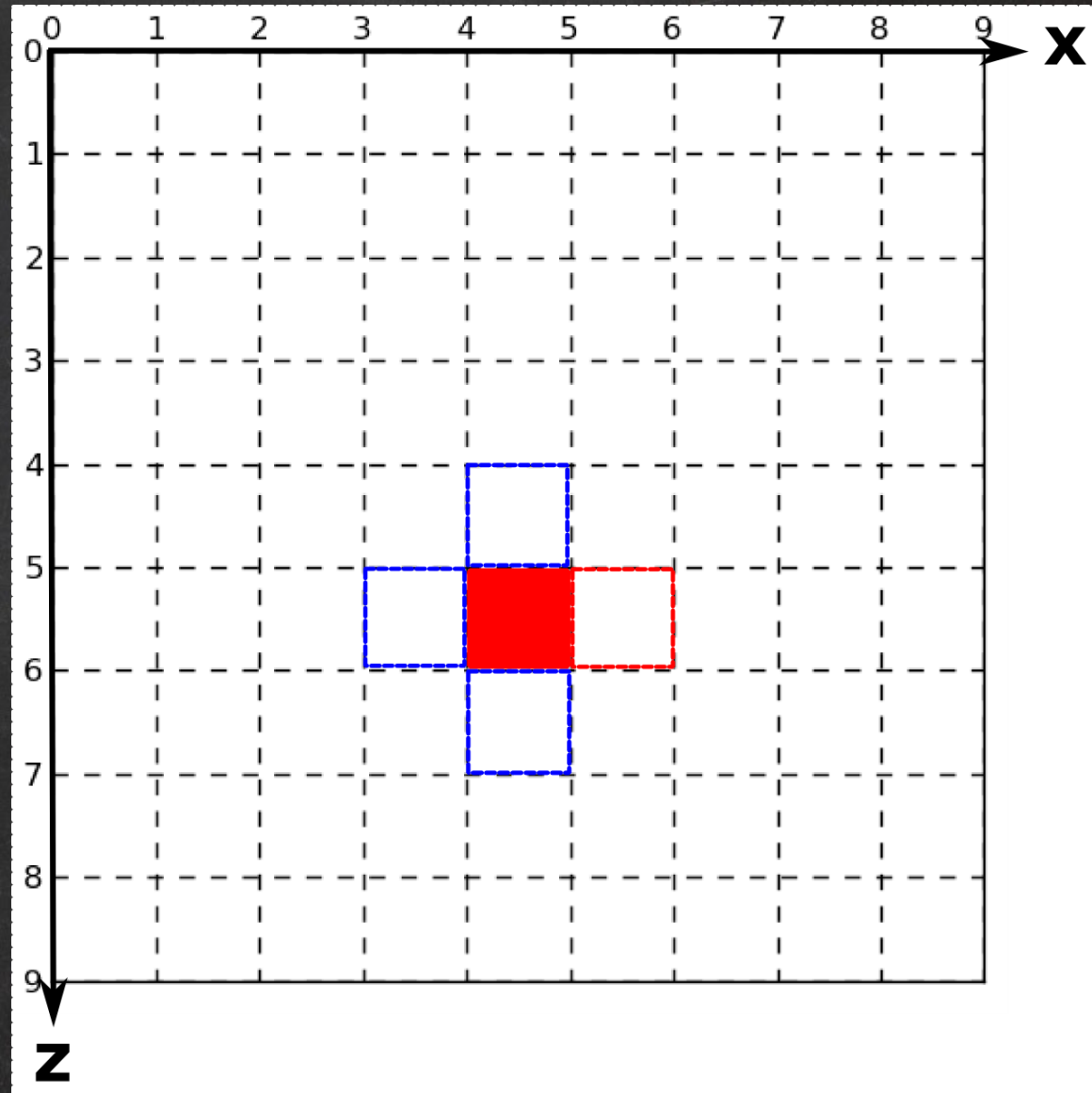
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

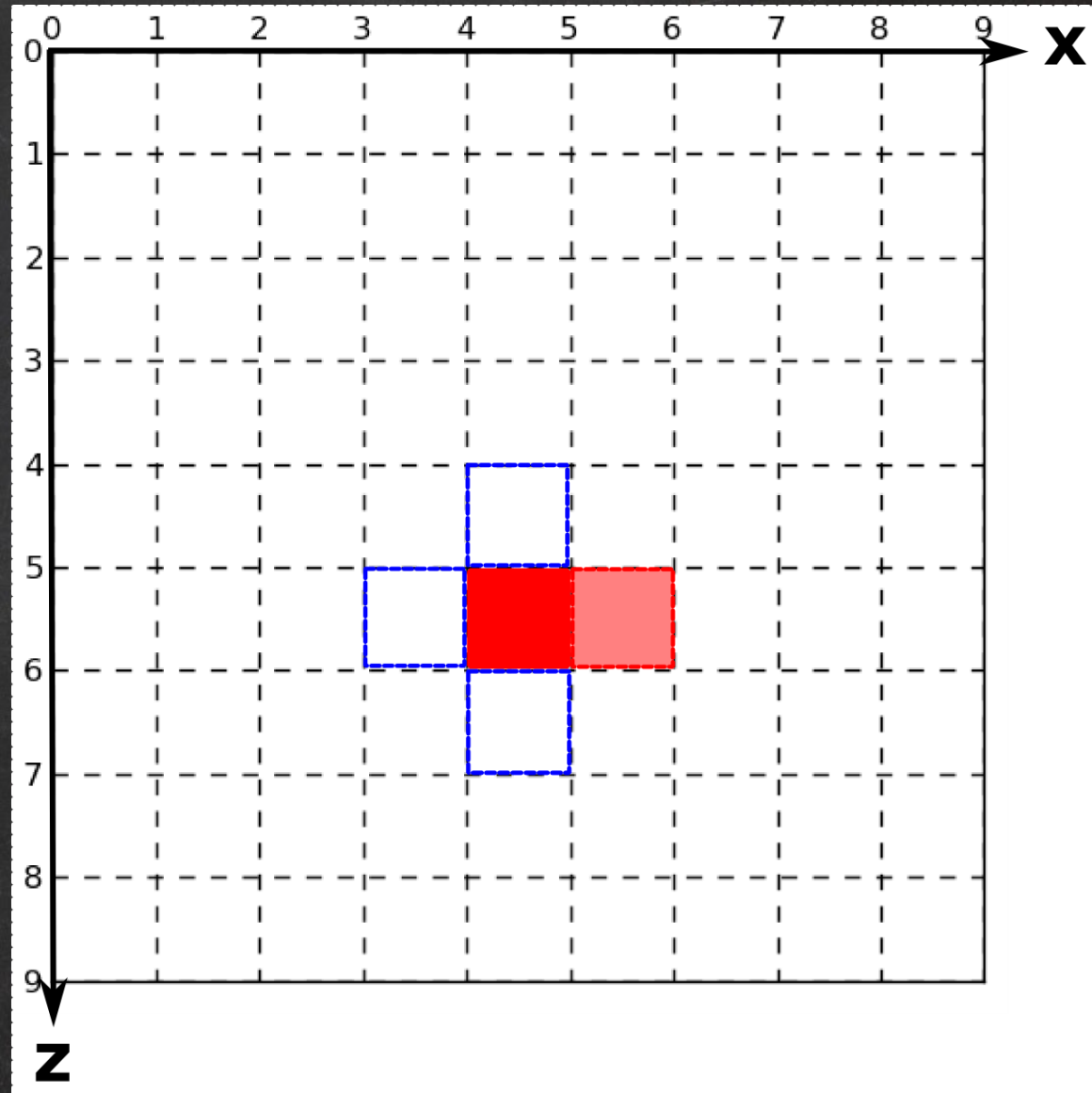
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

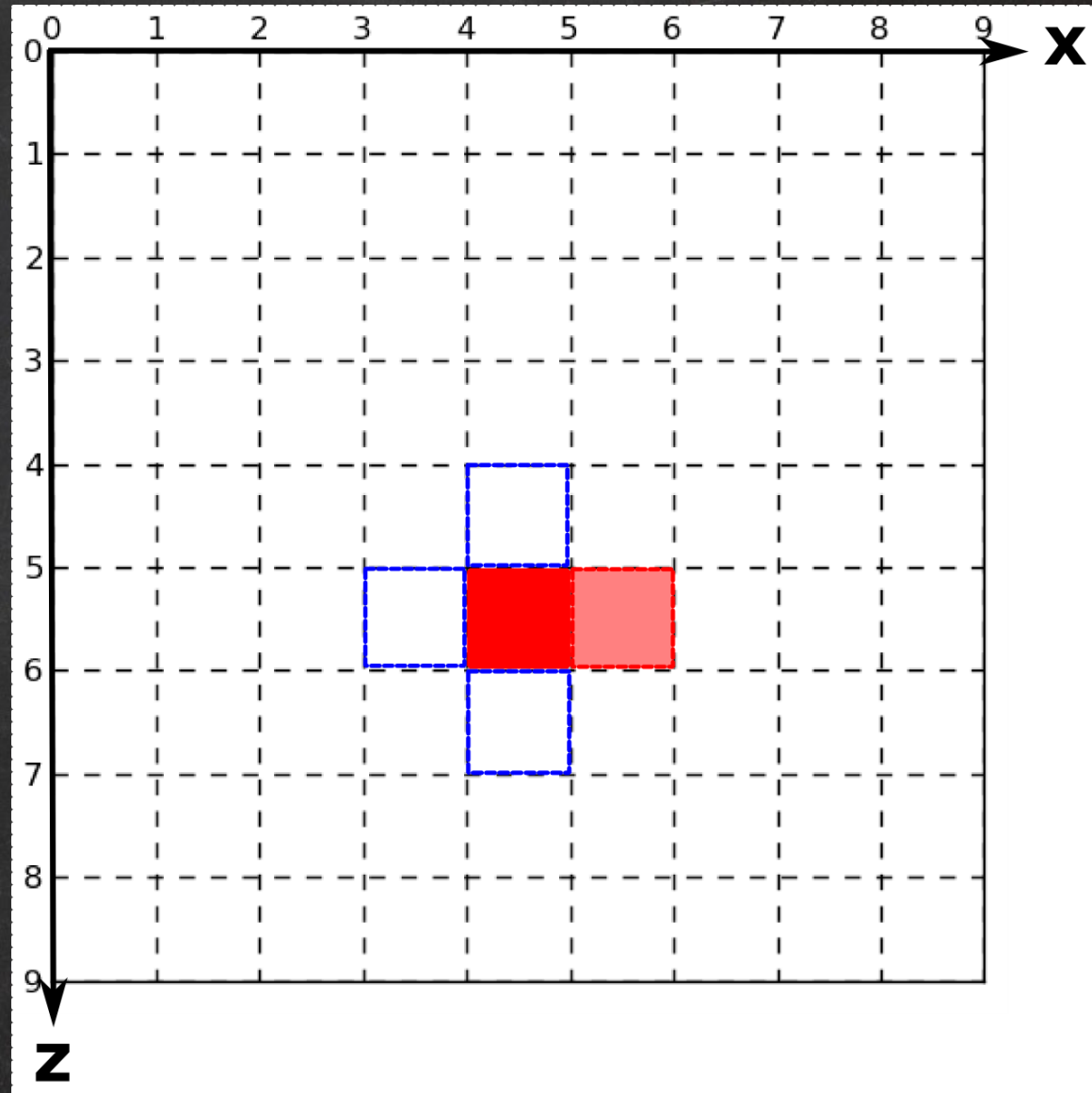
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

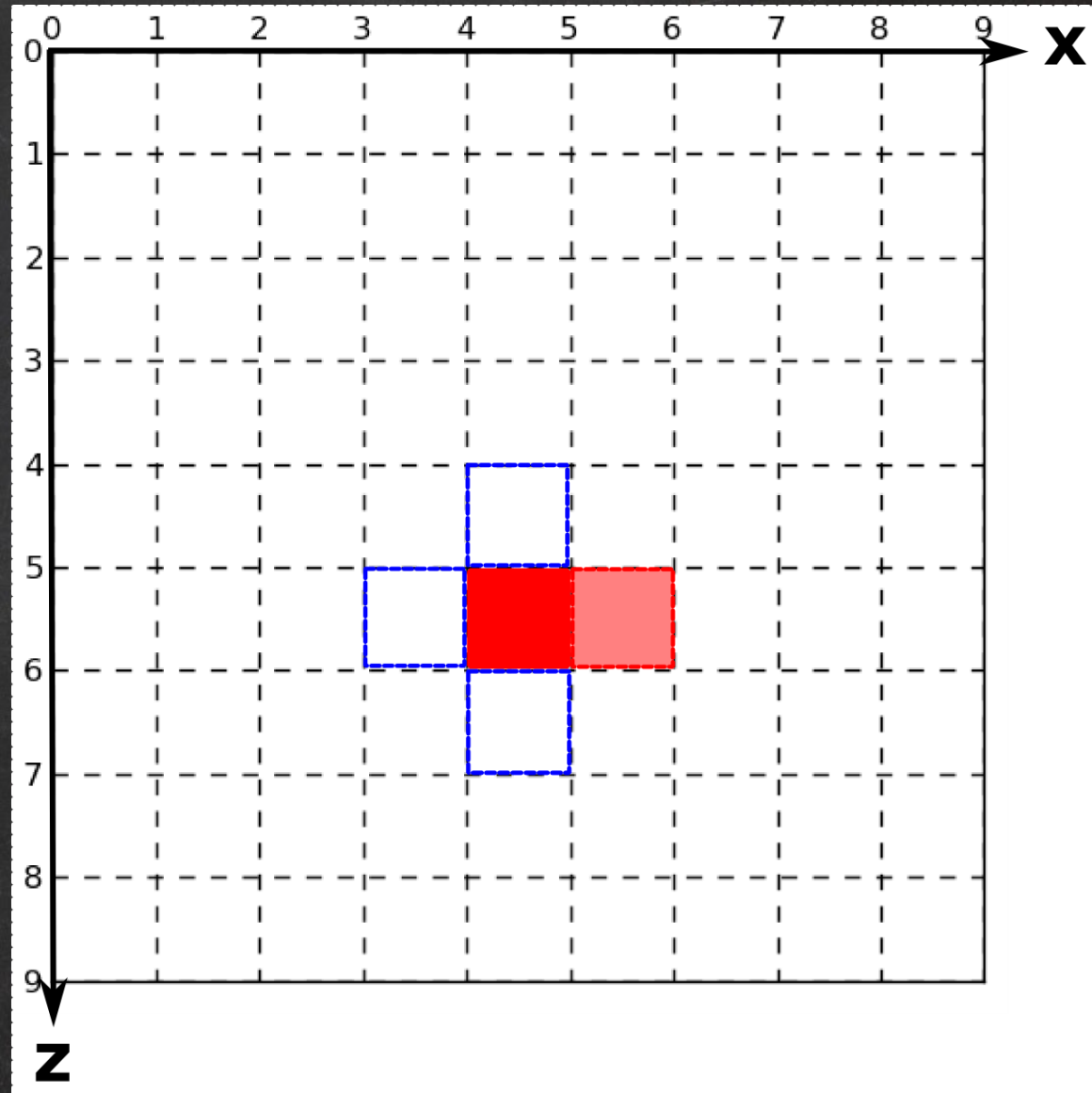
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

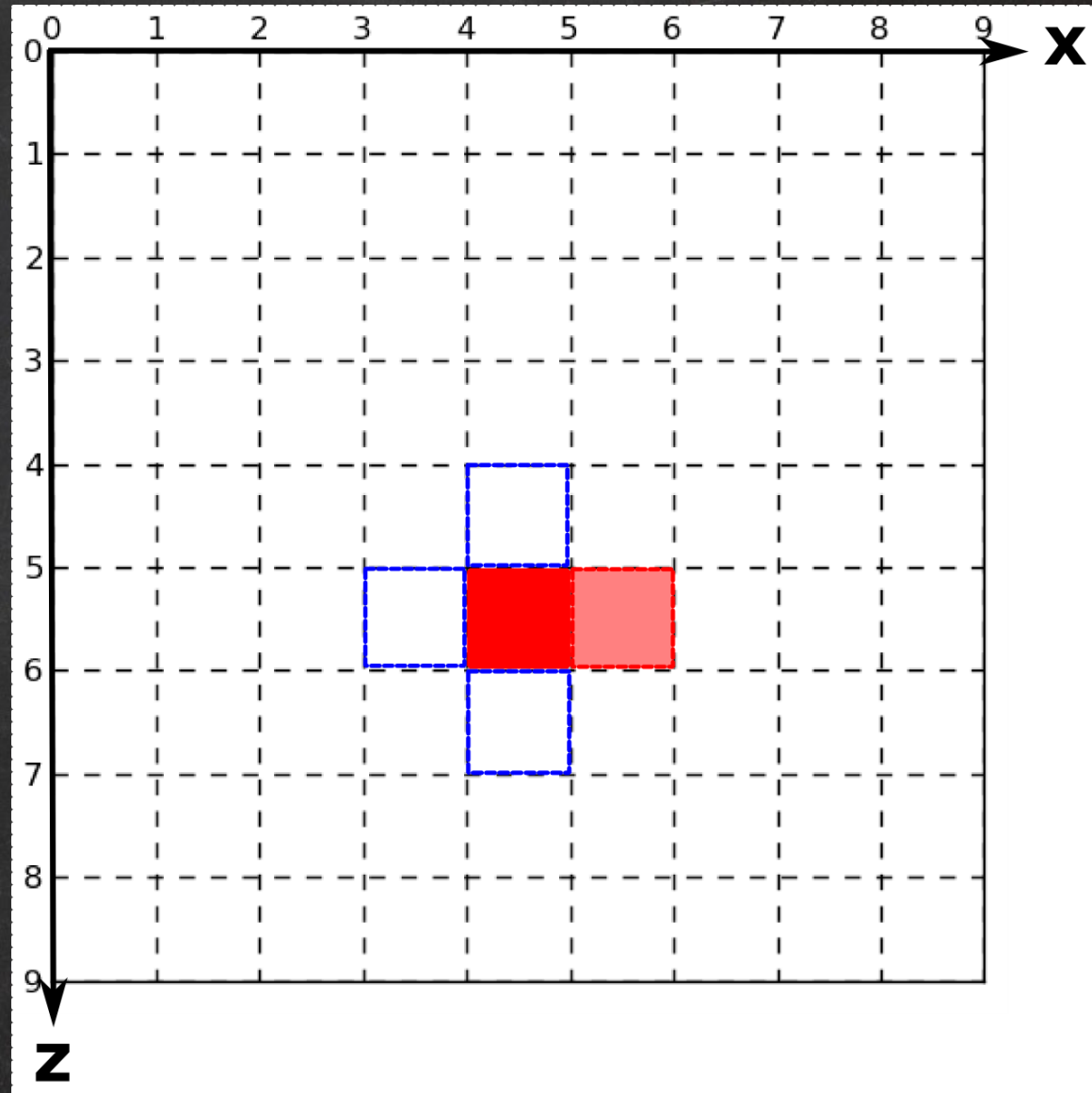
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

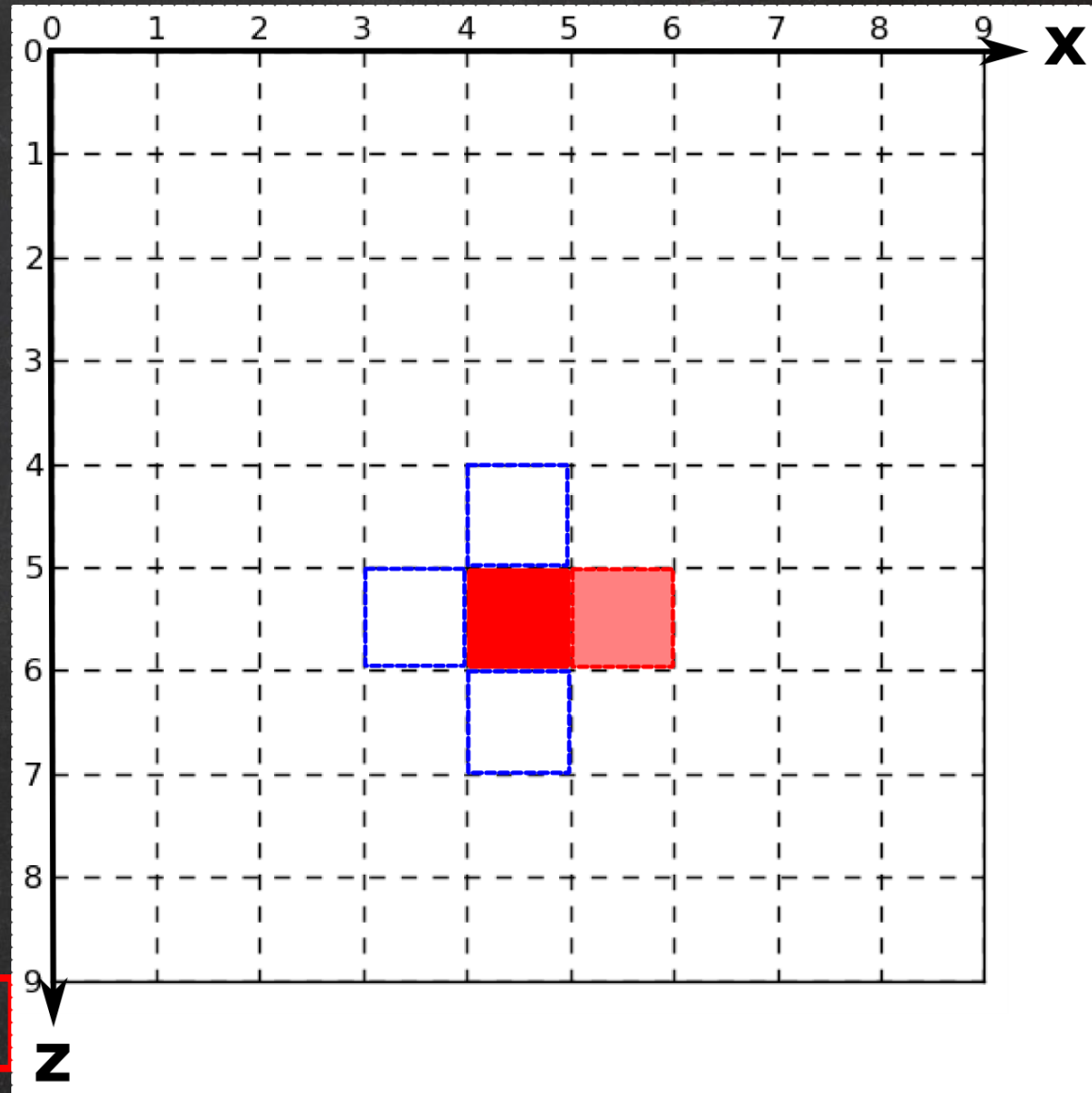
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

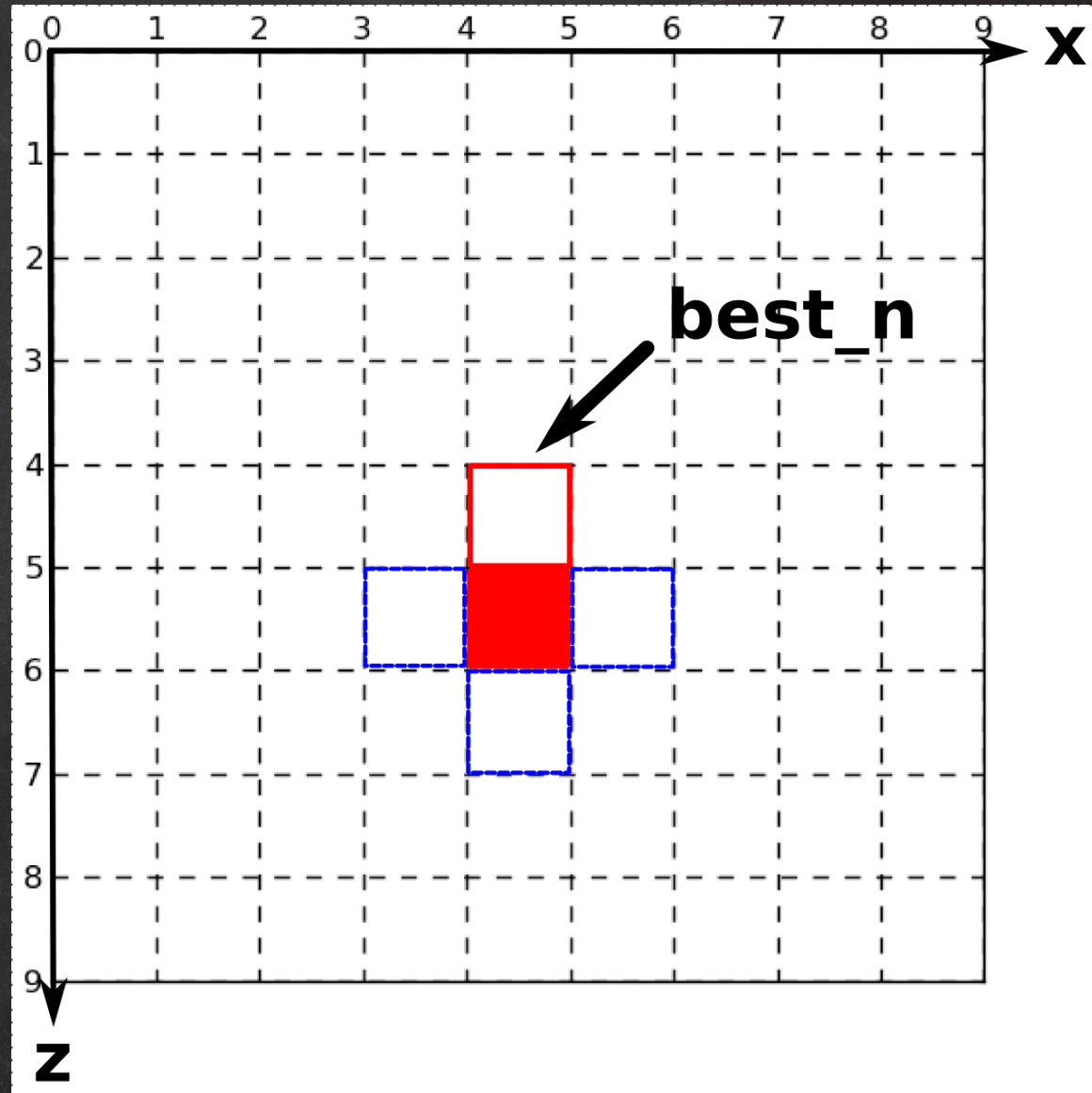
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

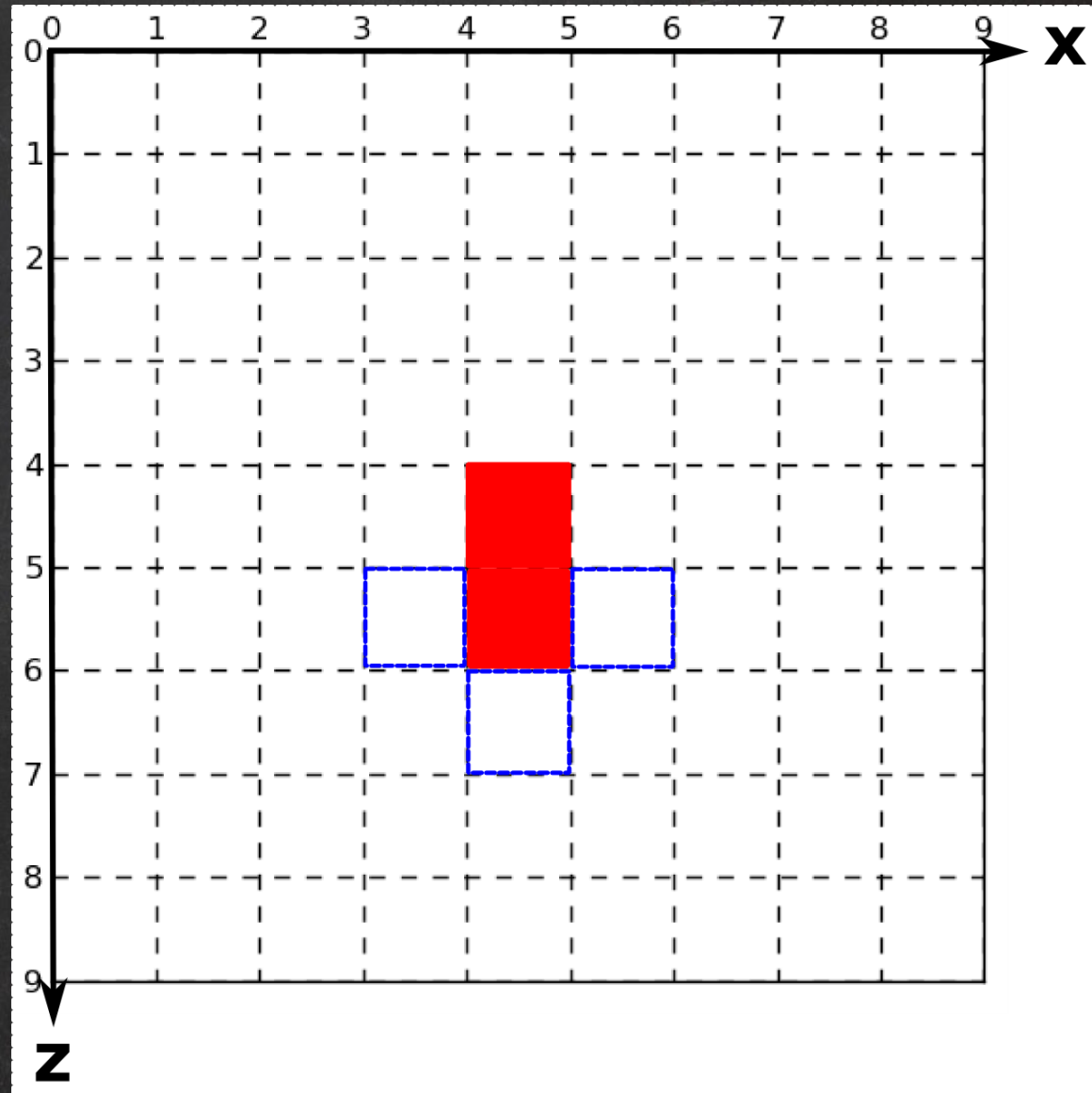
```




```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
            update_p_r(best_n)
        append_neighbors(best_n)

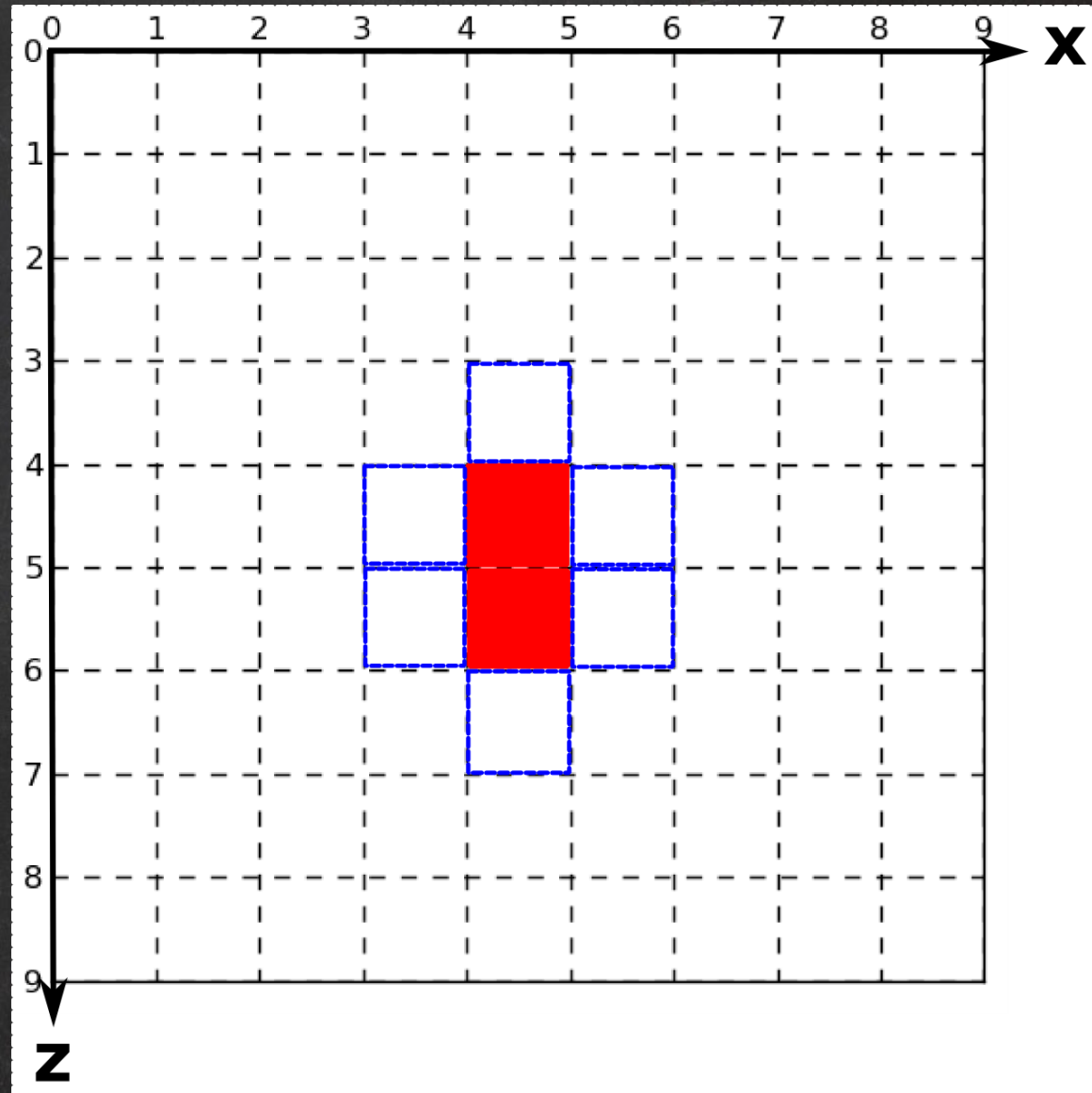
```



```

r = d
for s in seeds:
    r -= dens[s]*Gtrans(s)
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans(n)
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)

```



Otimizações


```
r = d
for s in seeds:
    r -= dens[s]*Gtrans[s]
    p[s] = dens[s]
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans[n]
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
    update_p_r(best_n)
    append_neighbors(best_n)
```



```
r = d
```

```
for s in seeds:
```

```
    r -= dens[s]*Gtrans[s]
```

```
    p[s] = dens[s]
```

```
for i in maxit:
```

```
    for s in seeds:
```

```
        for n in neighbors[s]:
```

```
            p[n] = dens[s]
```

```
            newr -= p[n]*Gtrans[n]
```

```
            misfit = norm(newr)
```

```
            reg = regularizer(p)
```

```
            if misfit + reg < best:
```

```
                best_n = n
```

```
            update_p_r(best_n)
```

```
            append_neighbors(best_n)
```



```
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans[n]
            misfit = norm(newr)
            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
        update_p_r(best_n)
        append_neighbors(best_n)
```



```
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    for s in seeds:
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            reg = regularizer(p)
            if misfit + reg < best:
                best_n = n
            update_p_r(best_n)
            append_neighbors(best_n)
```

✓ Crescer ↓ misfit

✓ Crescer ↑ reg

2 casos:

✓ misfit >> reg

✓ Crescer ↓ func. obj.

✓ Misfit << reg

✓ Crescer ↑ func. obj.

✓ Não consegue crescer

✓ Não ajusta os dados


```
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
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            newr -= p[n]*Gtrans[n]
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            if misfit + reg < best:
                best_n = n
        update_p_r(best_n)
        append_neighbors(best_n)
```

Para garantir o ajuste:

- ✓ Obrigatório ↓ misfit
- ✓ Escolhe o que produz menor f. obj.


```
for i in maxit:
    for s in seeds:
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            newr -= p[n]*Gtrans[n]
            misfit = norm(newr)
            reg = regularizer(p)
            goal = misfit + reg
            if misfit < last_misfit:
                if goal < best_goal:
                    best_n = n
        update_p_r(best_n)
    append_neighbors(best_n)
```

Para garantir o ajuste:

- ✓ Obrigatório ↓ misfit
- ✓ Escolhe o que produz menor f. obj.
- ✓ Continua compacto
- ✓ ... e ajusta o dado


```
for i in maxit:
    for s in seeds:
        for n in neighbors[s]:
            p[n] = dens[s]
            newr -= p[n]*Gtrans[n]
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            goal = misfit + reg
            if misfit < last_misfit:
                if goal < best_goal:
                    best_n = n
        update_p_r(best_n)
        append_neighbors(best_n)
```

Só usa colunas
dos vizinhos


```
for i in maxit:
    for s in seeds:
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            p[n] = dens[s]
            newr -= p[n]*Gtrans[n]
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                    best_n = n
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```

... nunca mais usa
a coluna best_n


```
for i in maxit:
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            goal = misfit + reg
            if misfit < last_misfit:
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        update_p_r(best_n)
        append_neighbors(best_n)
```

✓ Não precisa calcular
Jacobiana inteira


```
for i in maxit:
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            misfit = norm(newr)
            reg = regularizer(p)
            goal = misfit + reg
            if misfit < last_misfit:
                if goal < best_goal:
                    best_n = n
        update_p_r(best_n)
        append_neighbors(best_n)
```

- ✓ Não precisa calcular Jacobiana inteira
- ✓ Só quando necessário (Lazy evaluation)


```
for i in maxit:
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```

- ✓ Não precisa calcular Jacobiana inteira
- ✓ Só quando necessário (Lazy evaluation)
- ✓ Apaga coluna best_n


```
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                    best_n = n
        update_p_r(best_n)
        append_neighbors(best_n)
```

- ✓ Não precisa calcular Jacobiana inteira
- ✓ Só quando necessário (Lazy evaluation)
- ✓ Apaga coluna best_n
- ✓ Economiza RAM e processamento

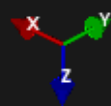
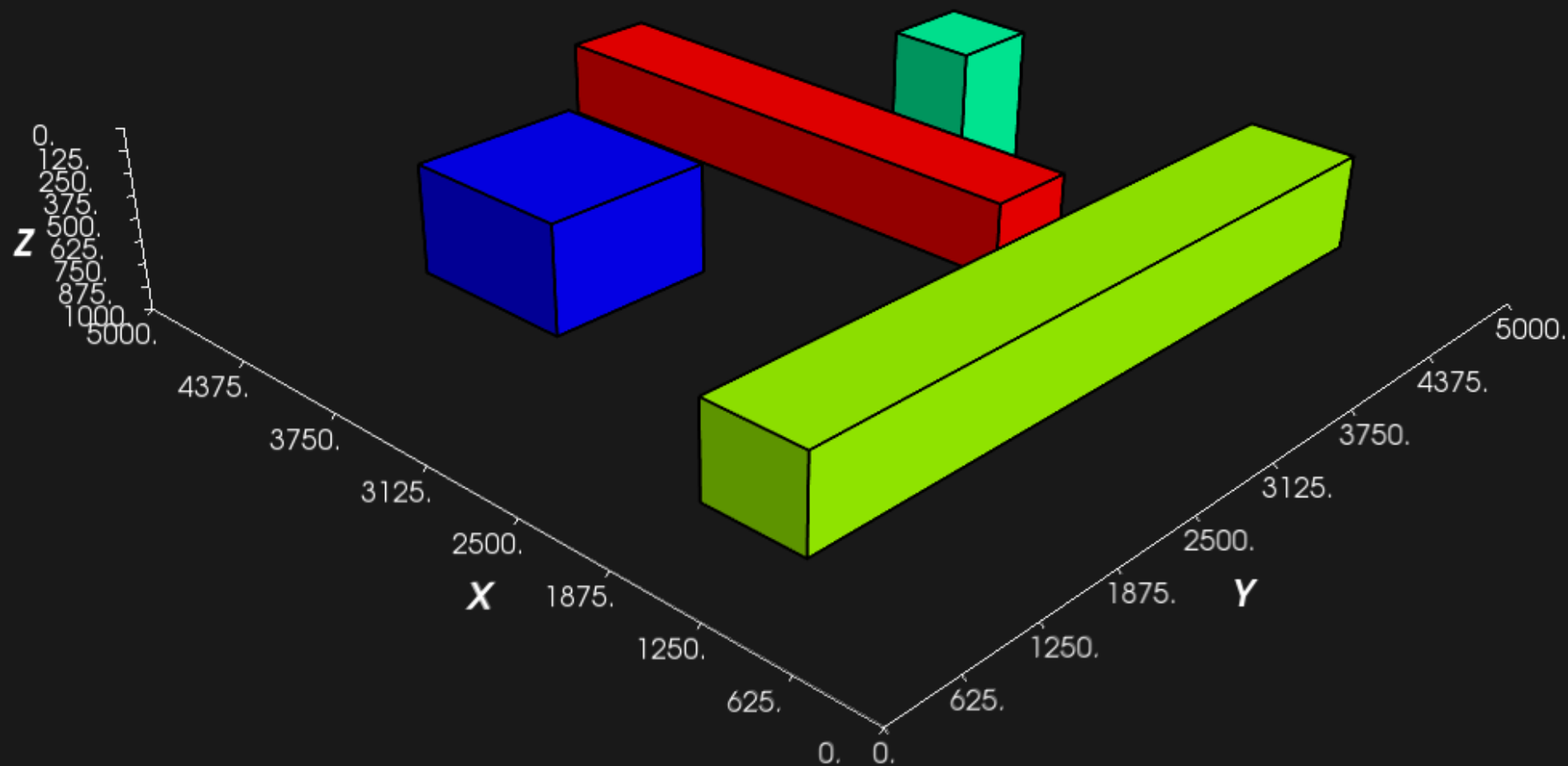

```
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            goal = misfit + reg
            if misfit < last_misfit:
                if goal < best_goal:
                    best_n = n
            update_p_r(best_n)
            append_neighbors(best_n)
```

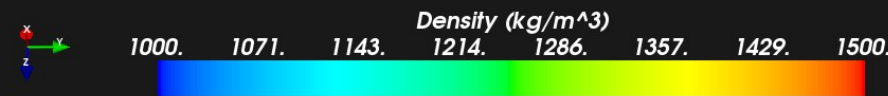
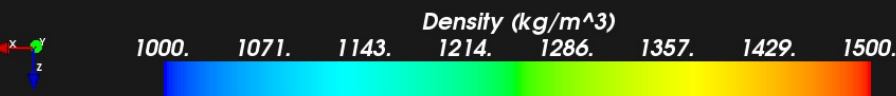
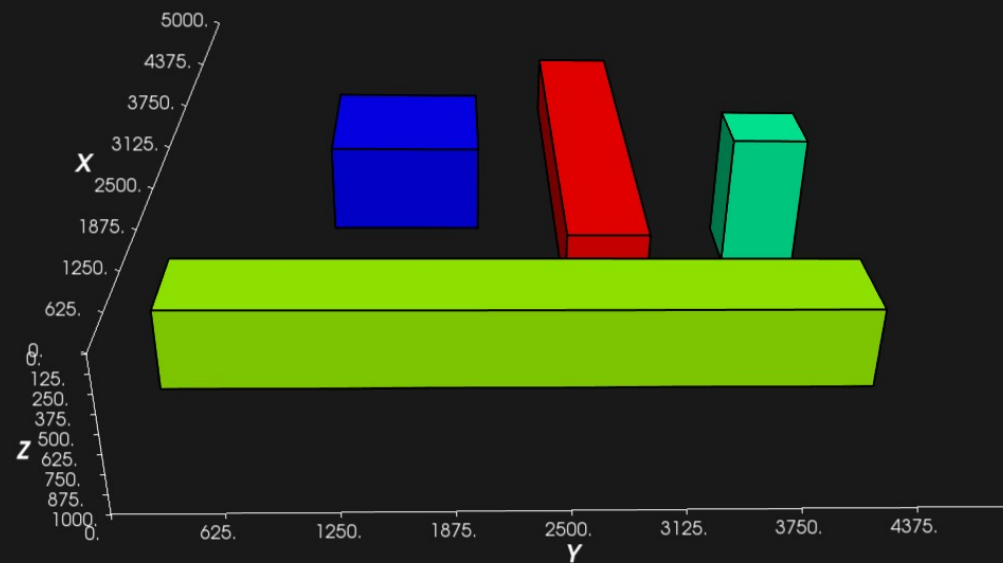
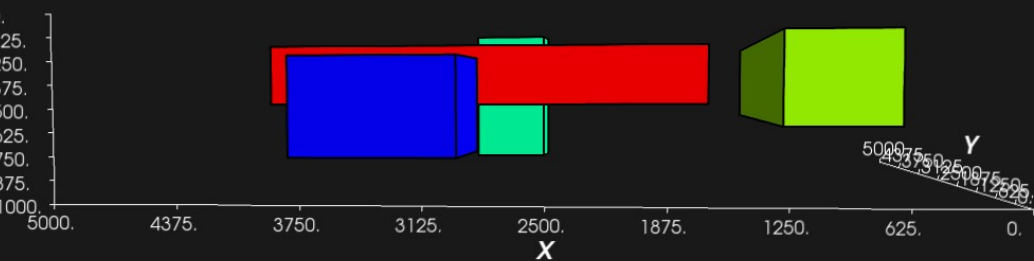
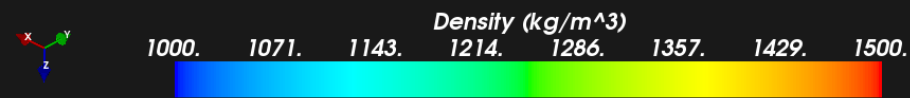
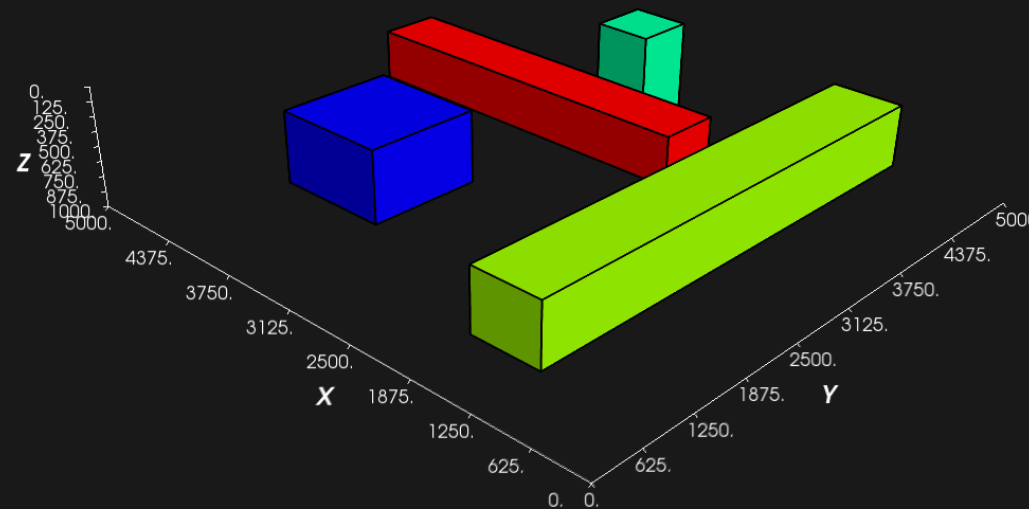
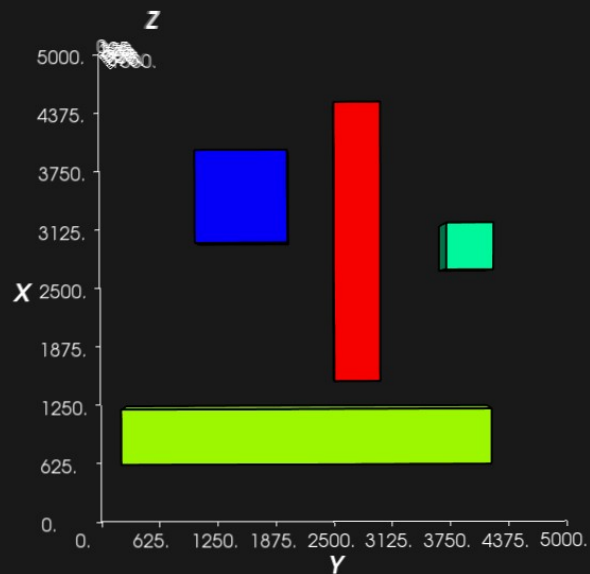
- ✓ Não precisa calcular Jacobiana inteira
- ✓ Só quando necessário (Lazy evaluation)
- ✓ Apaga coluna best_n
- ✓ Economiza RAM e processamento
- ✓ Inverter muitos dados


```
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```

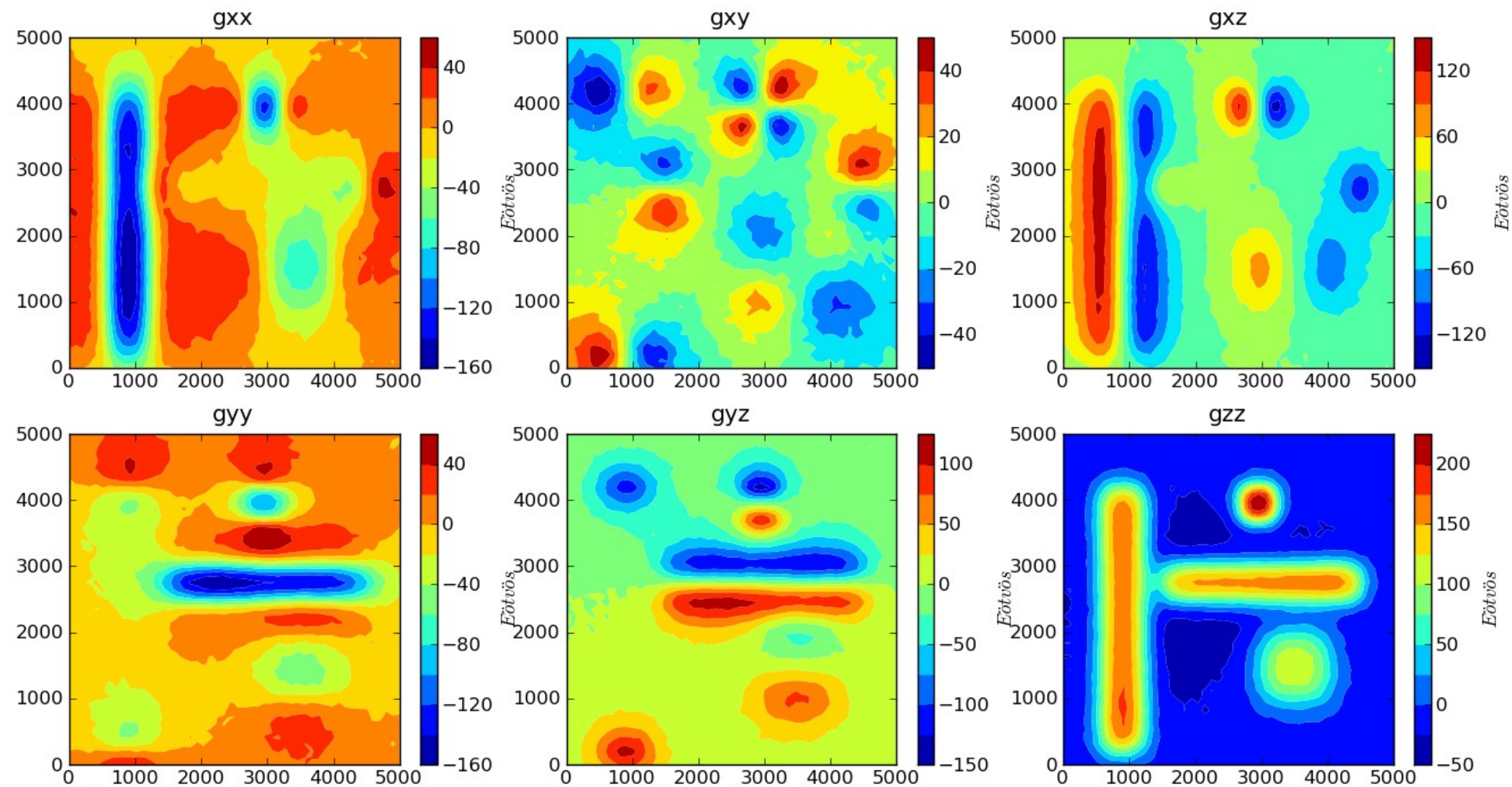
- ✓ Não precisa calcular Jacobiana inteira
- ✓ Só quando necessário (Lazy evaluation)
- ✓ Apaga coluna best_n
- ✓ Economiza RAM e processamento
- ✓ Inverter muitos dados
- ✓ ... e com malhas finas

Dados sintéticos

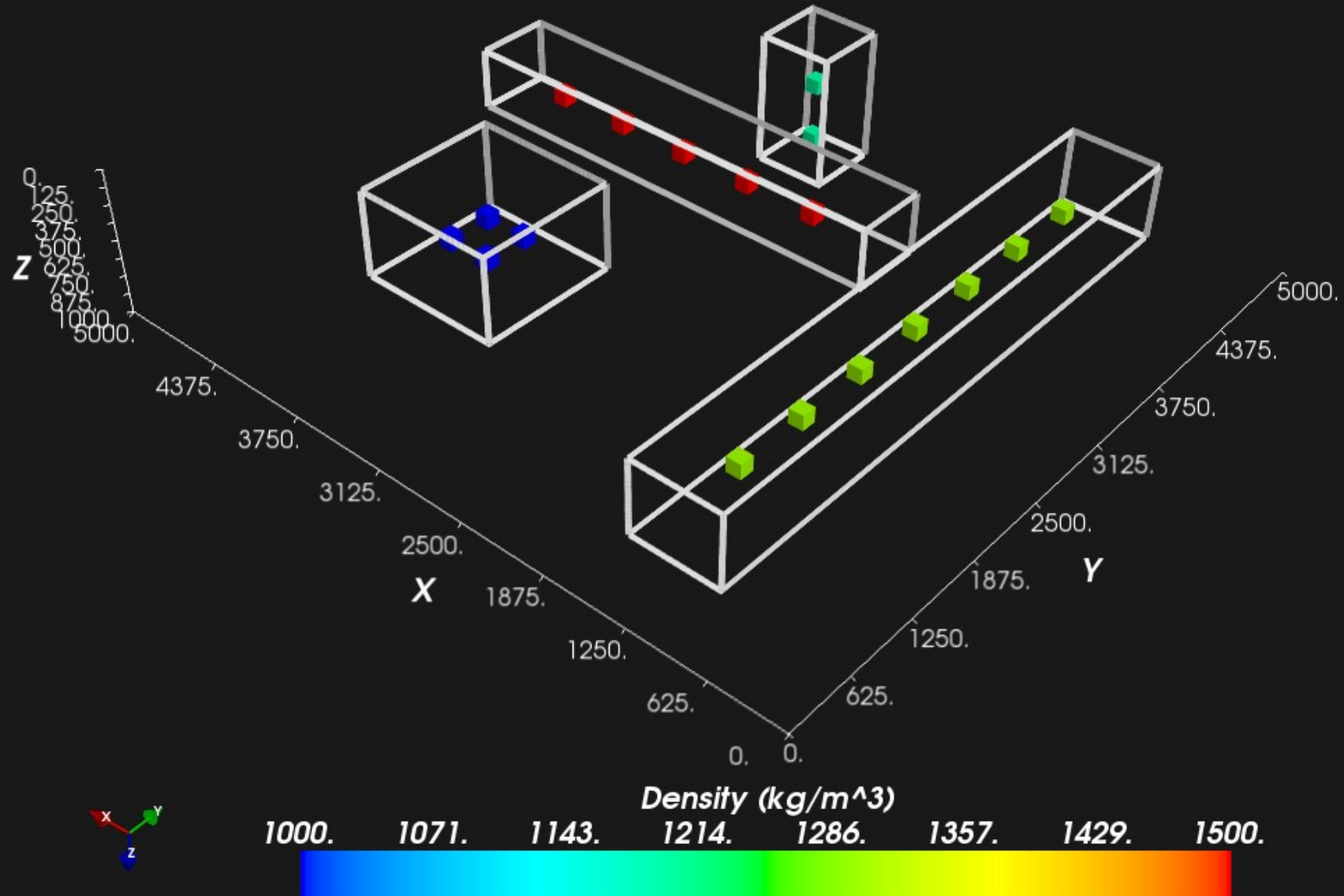




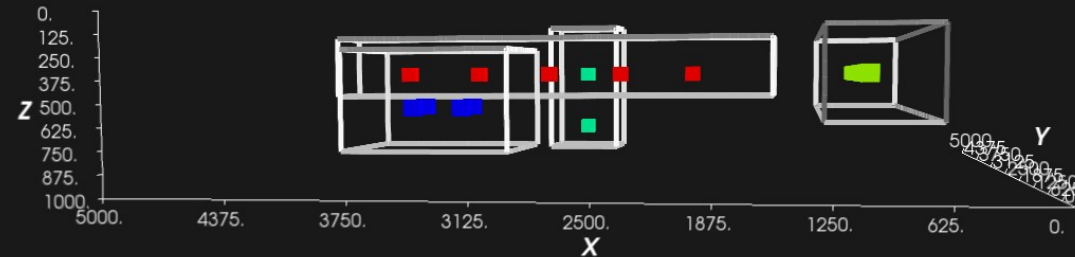
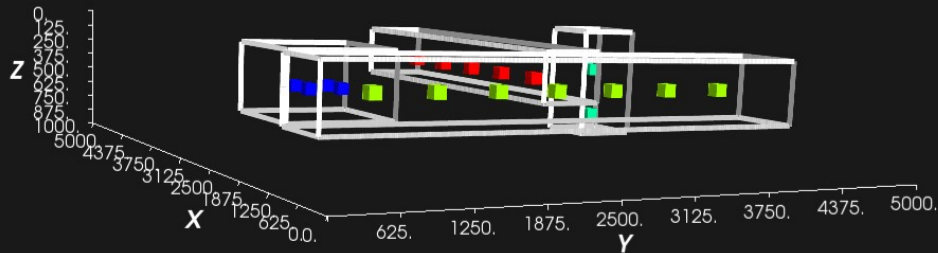
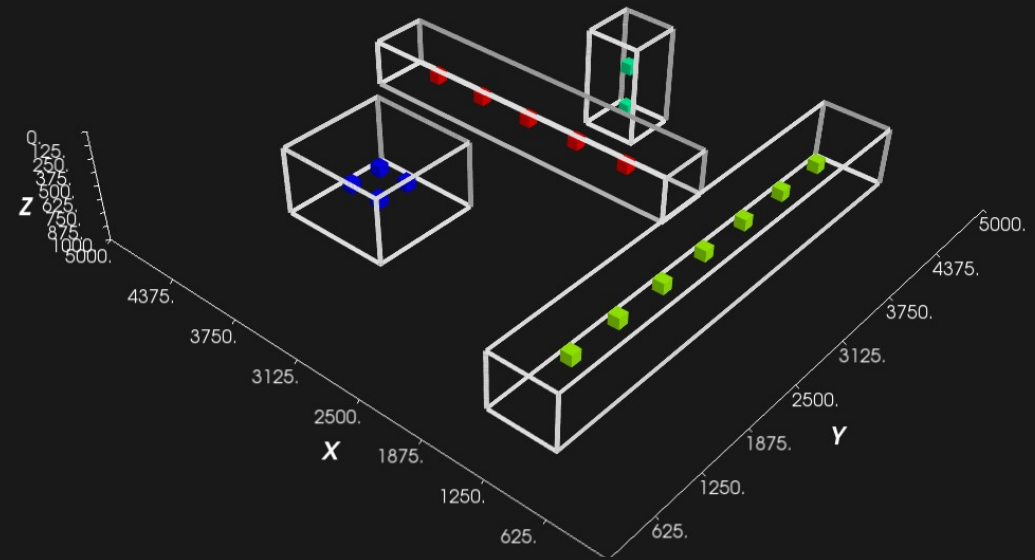
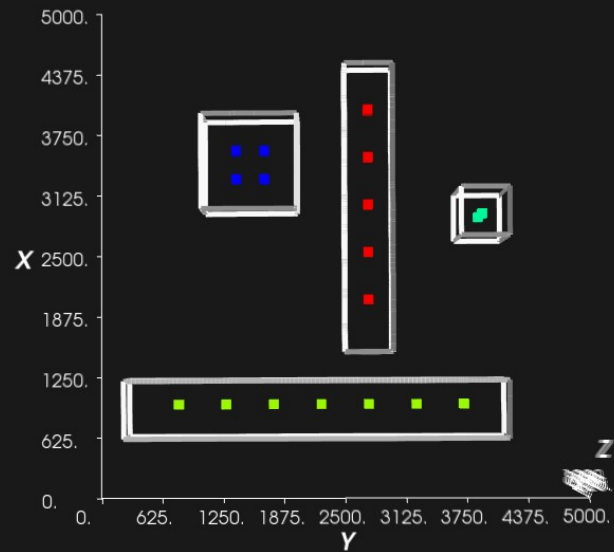
Synthetic FTG data with 2 *Eötvös* noise



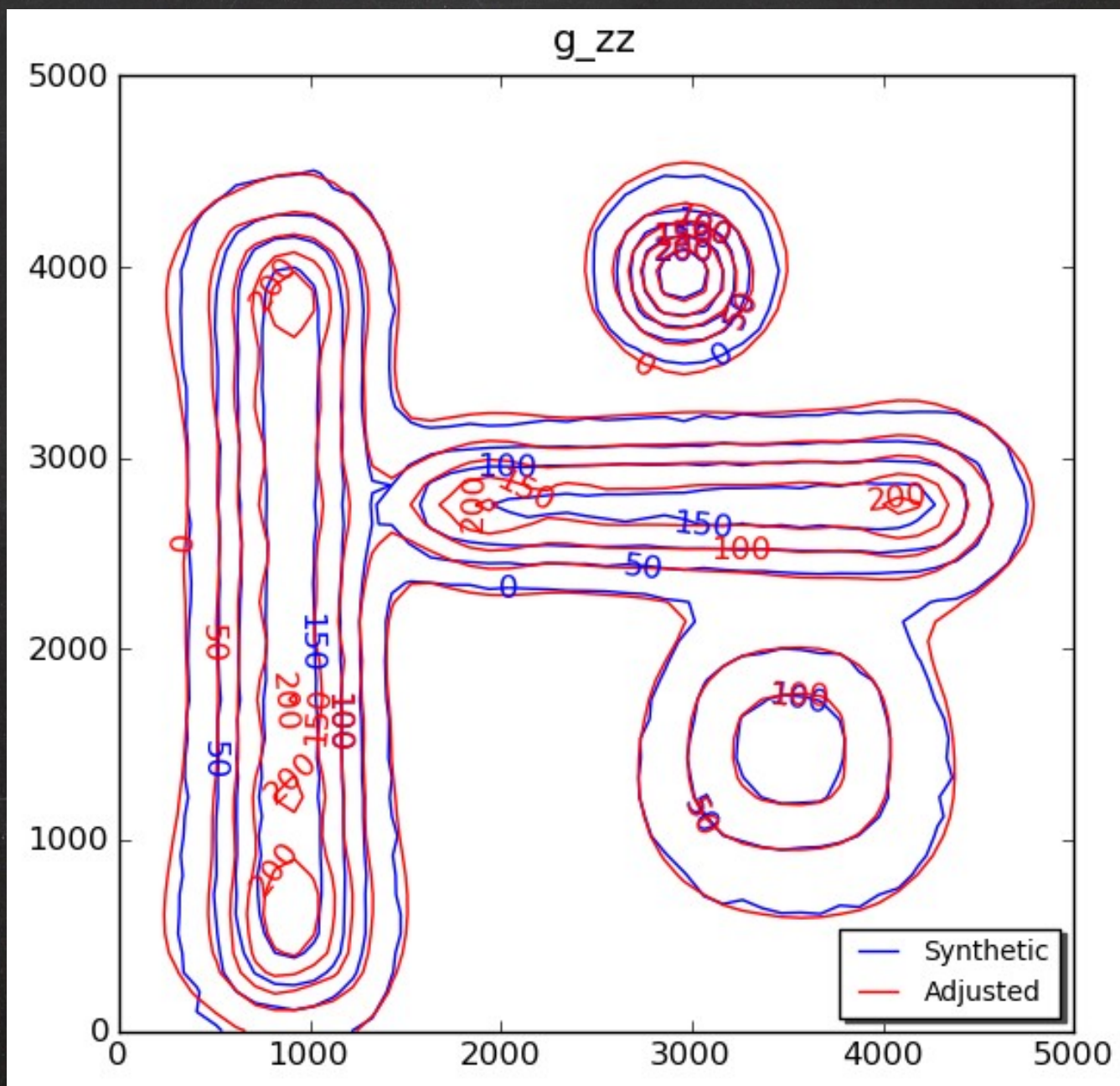
Sementes



Sementes

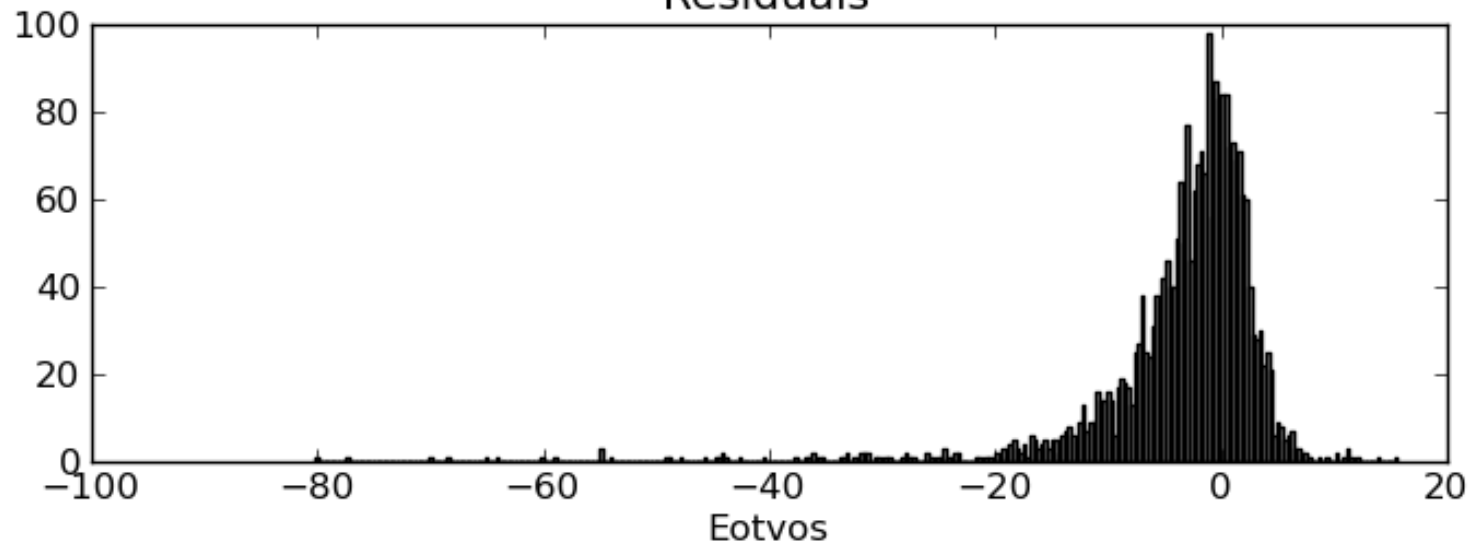


Resultados

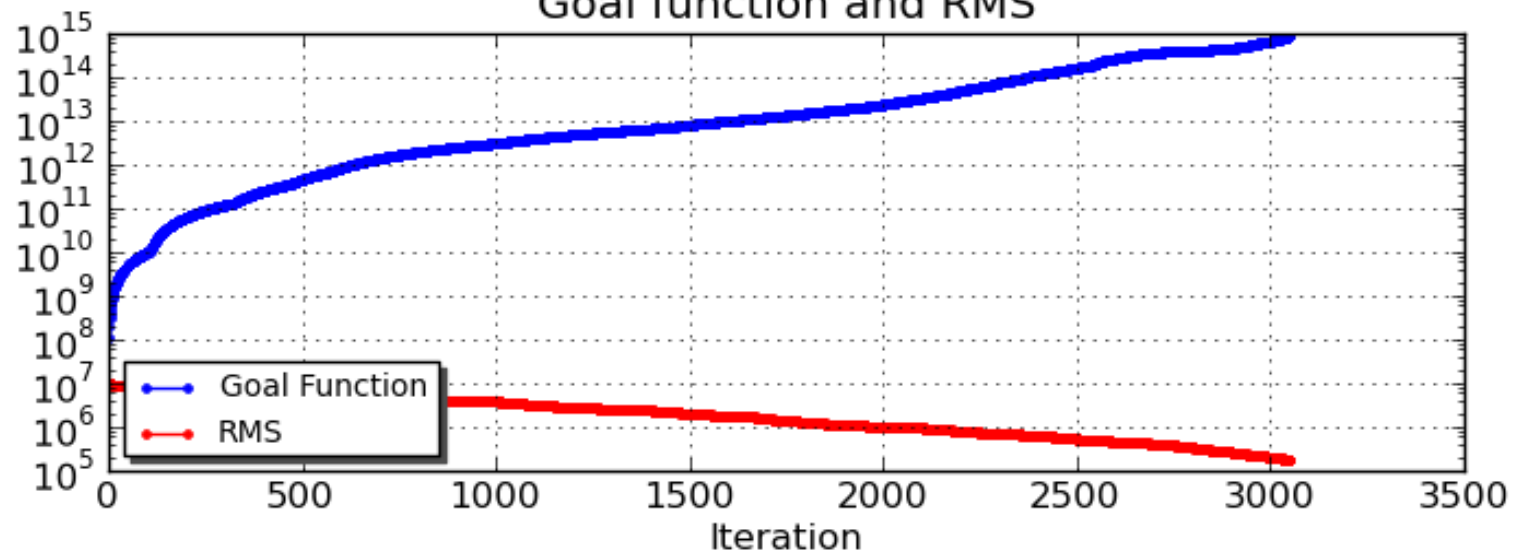


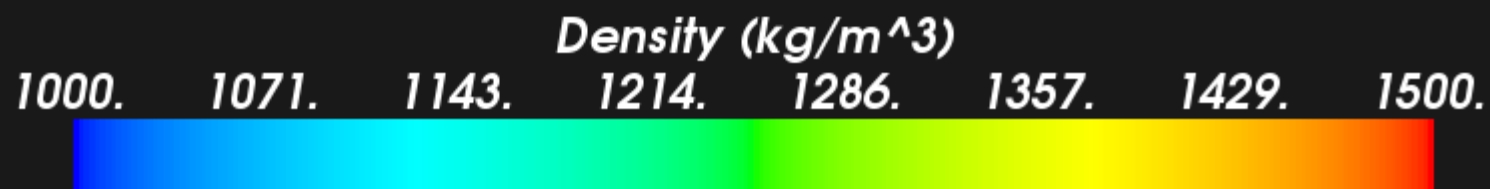
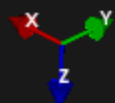
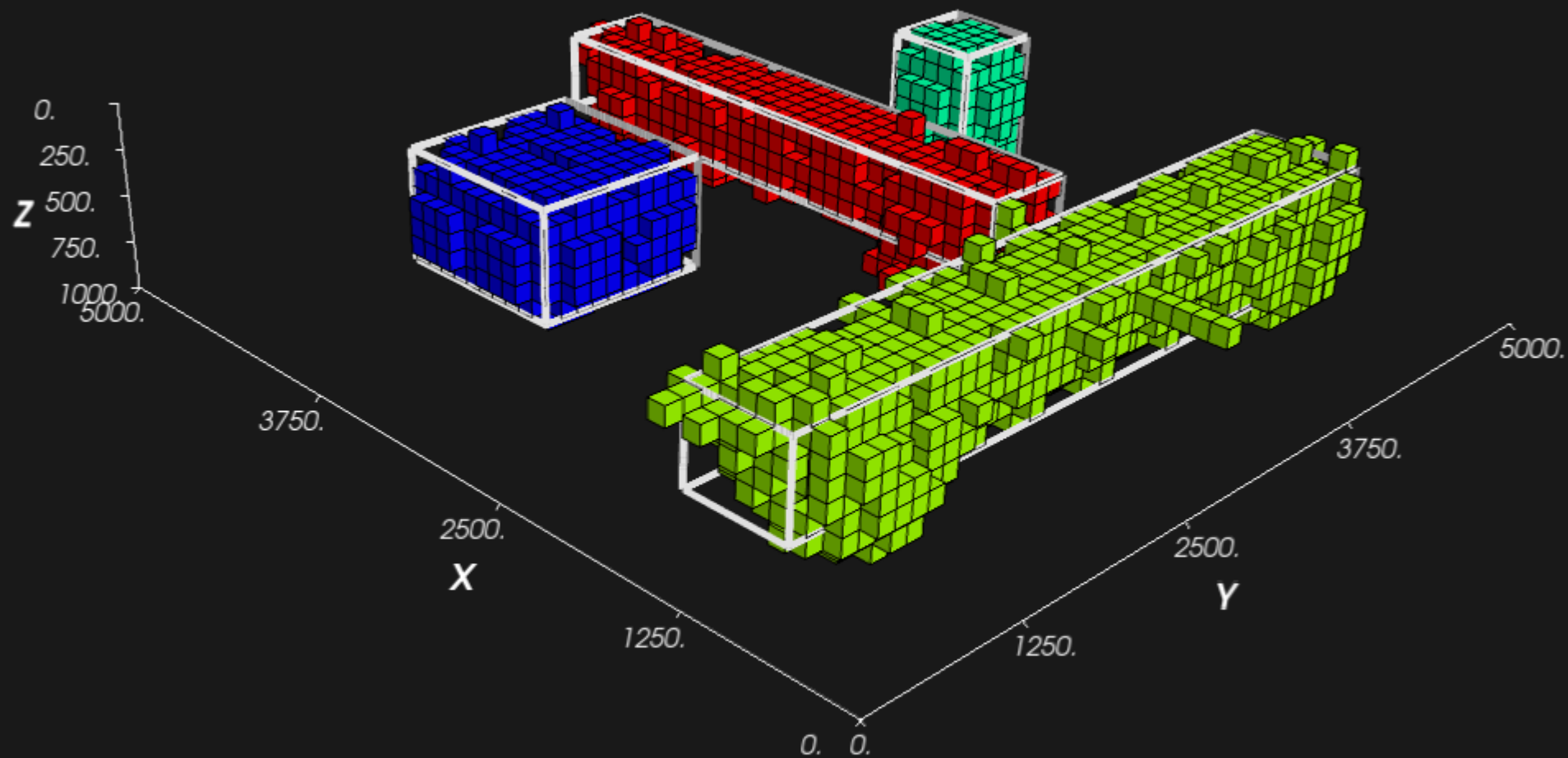
Resultados

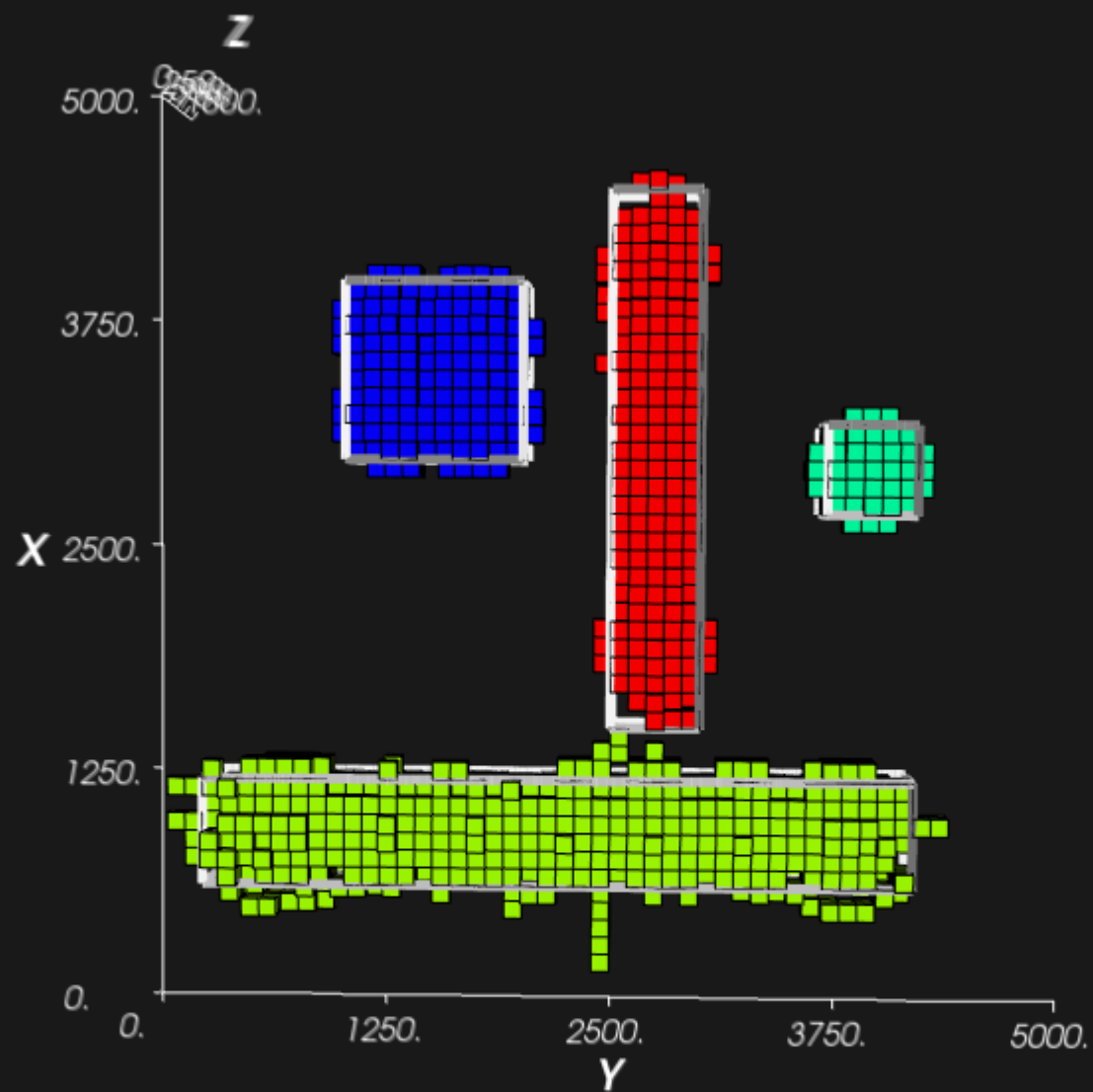
Inversion results:
Residuals



Goal function and RMS



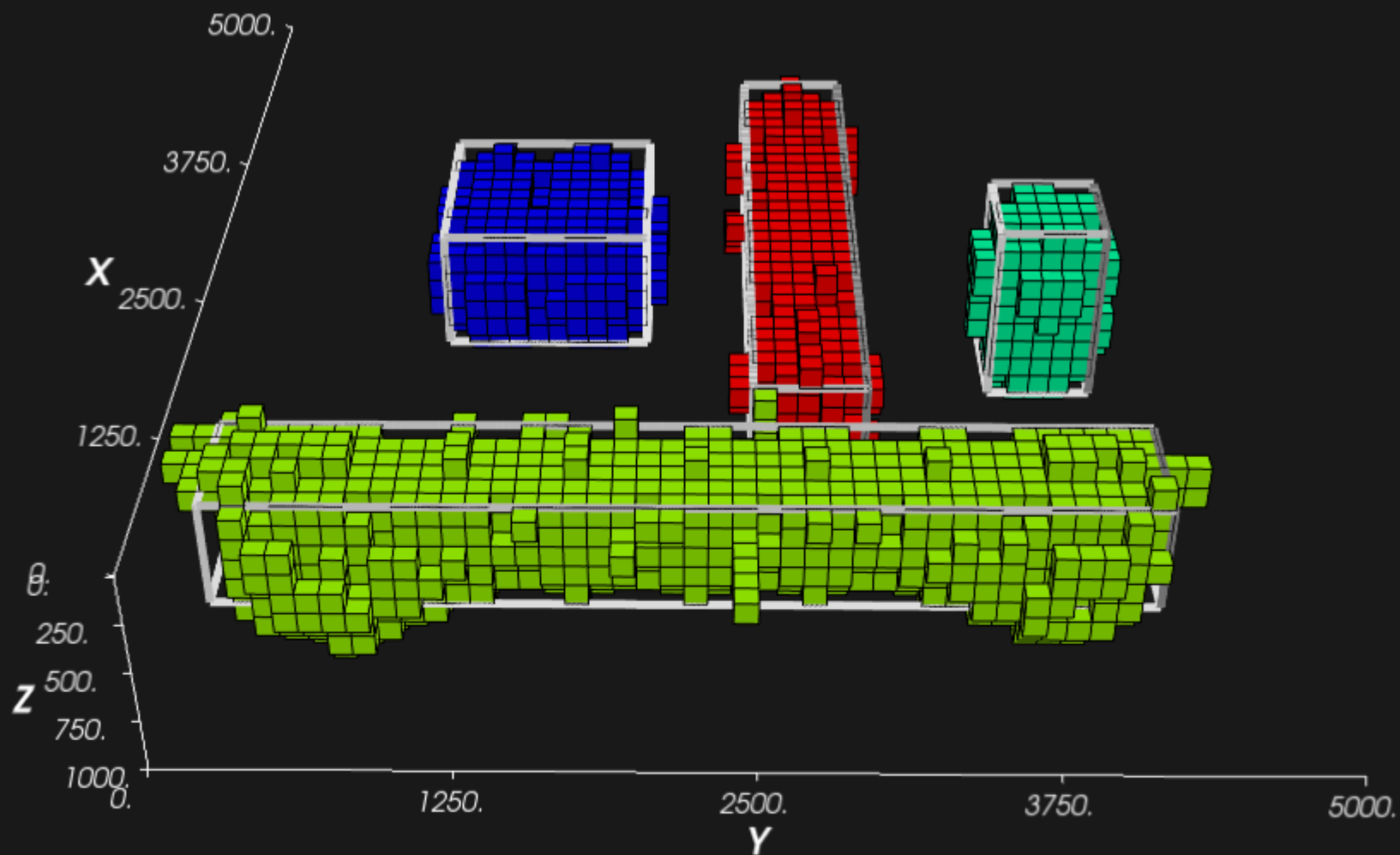




Density (kg/m^3)

Density (kg/m^3)
1000.
1071.
1143.
1214.
1286.
1357.
1429.
1500.

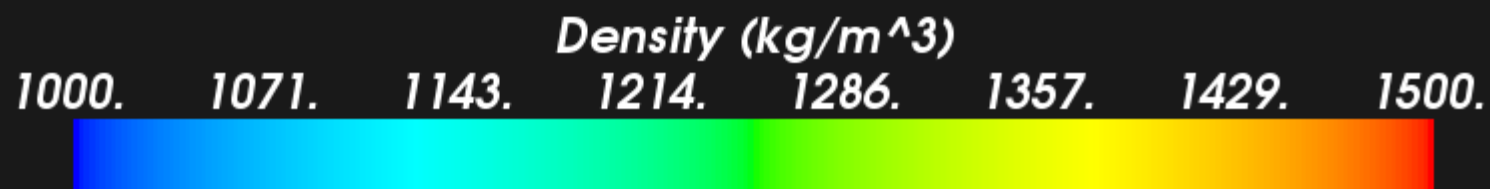
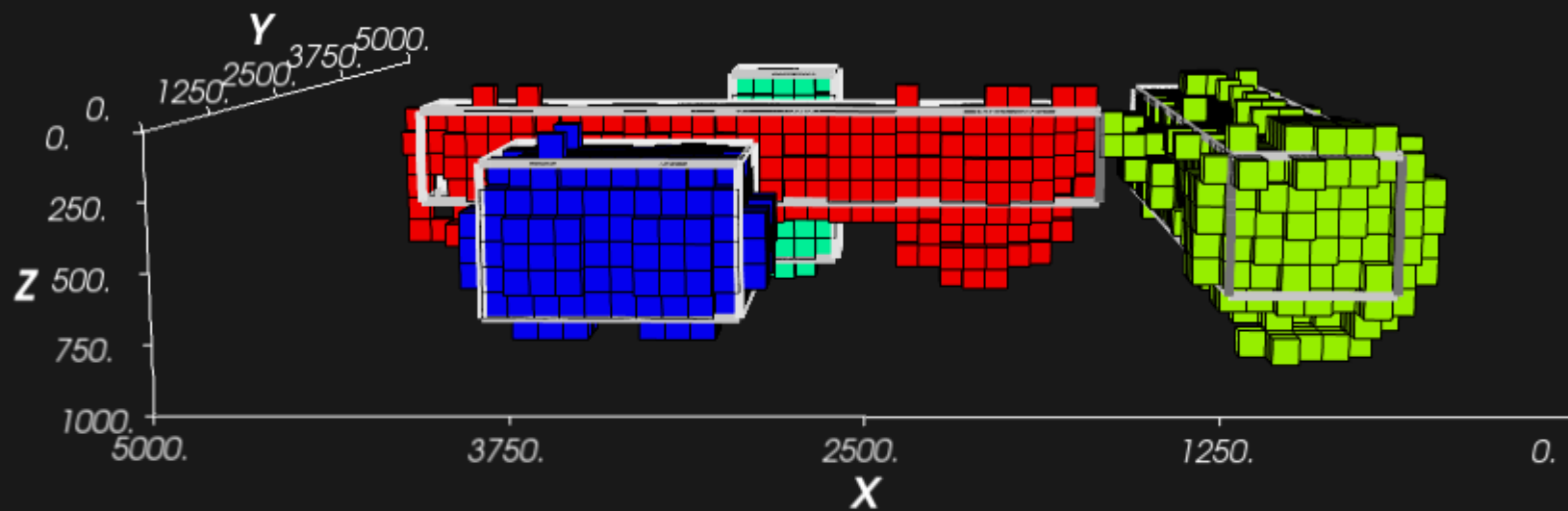


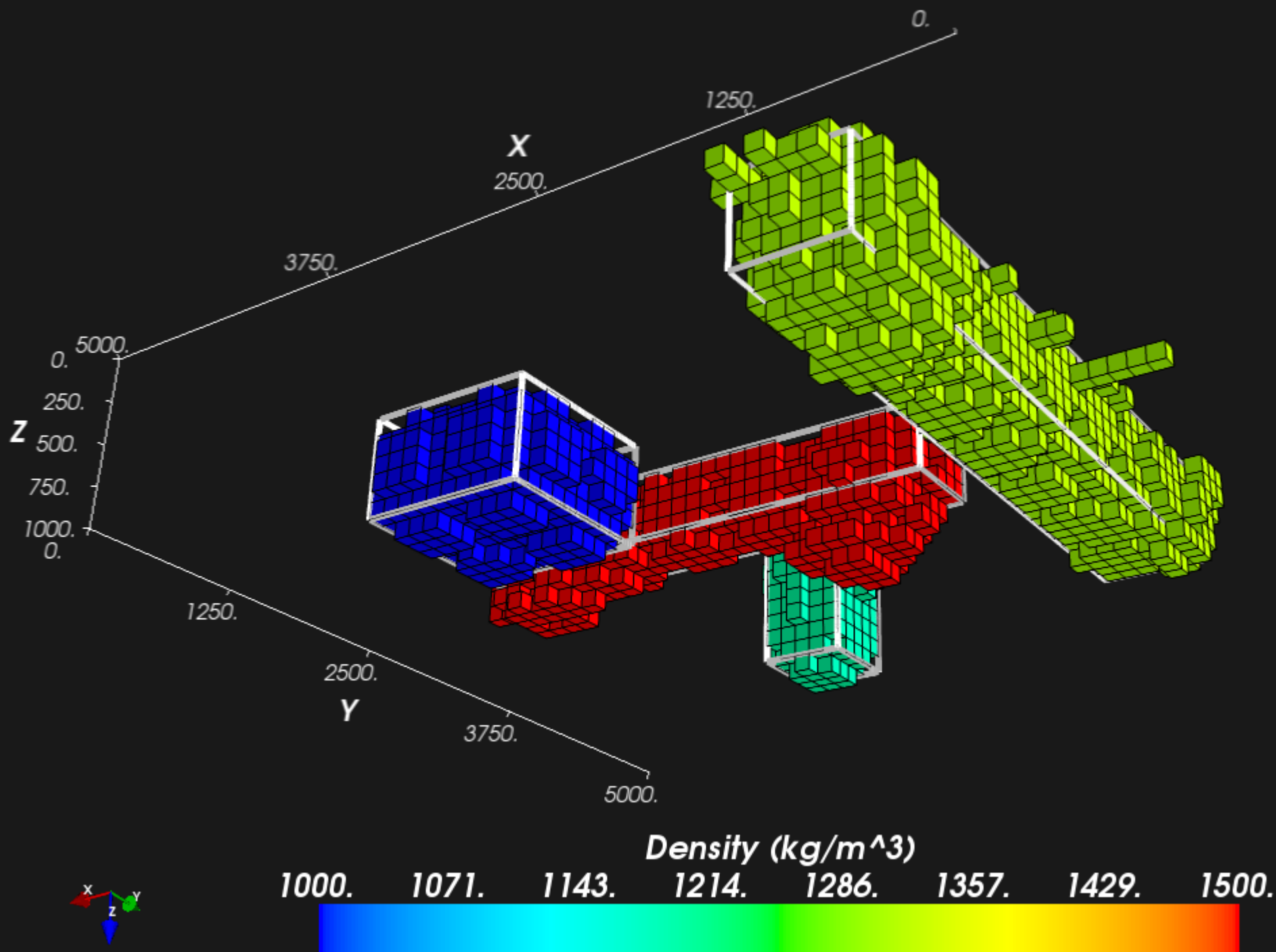


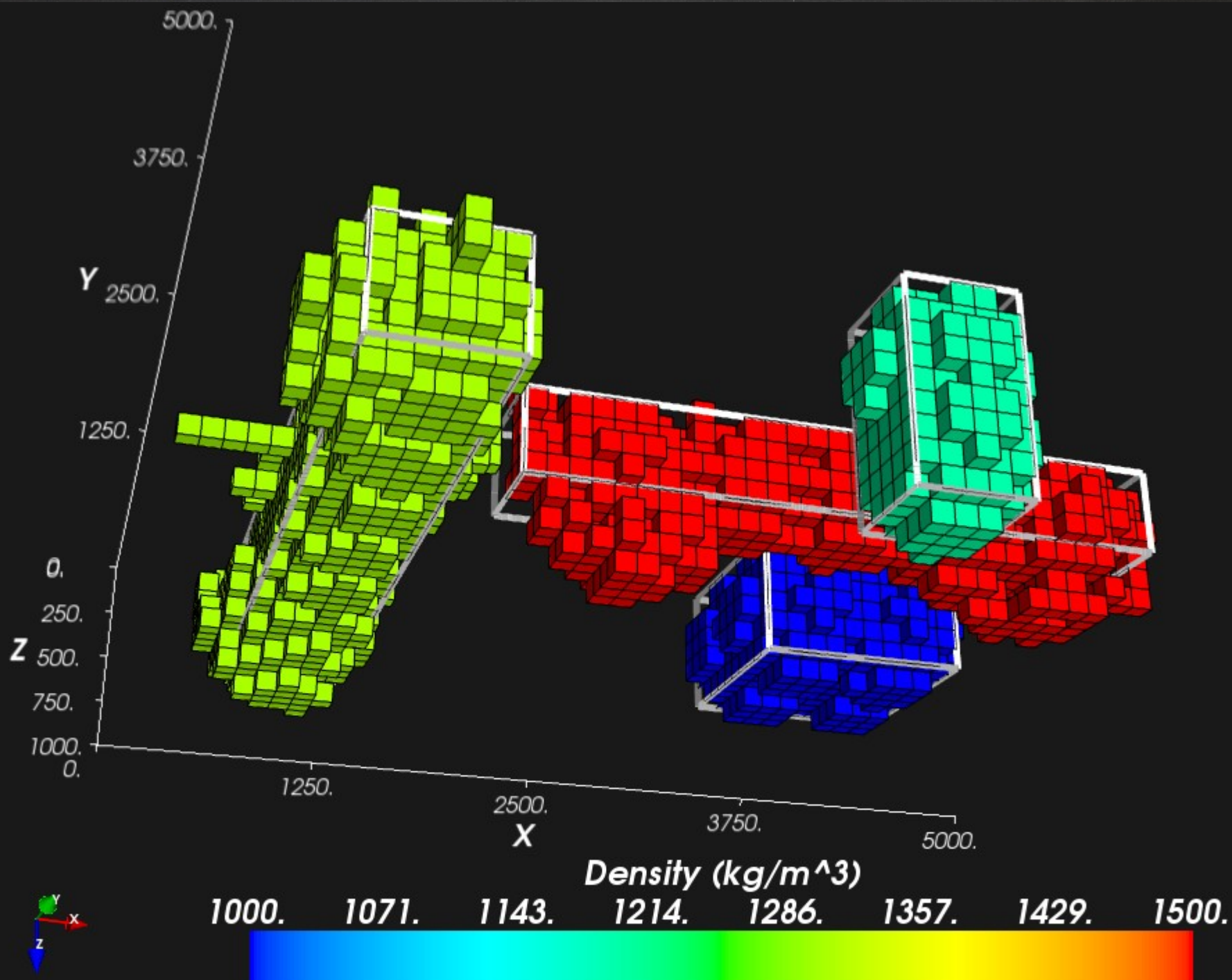
Density (kg/m^3)

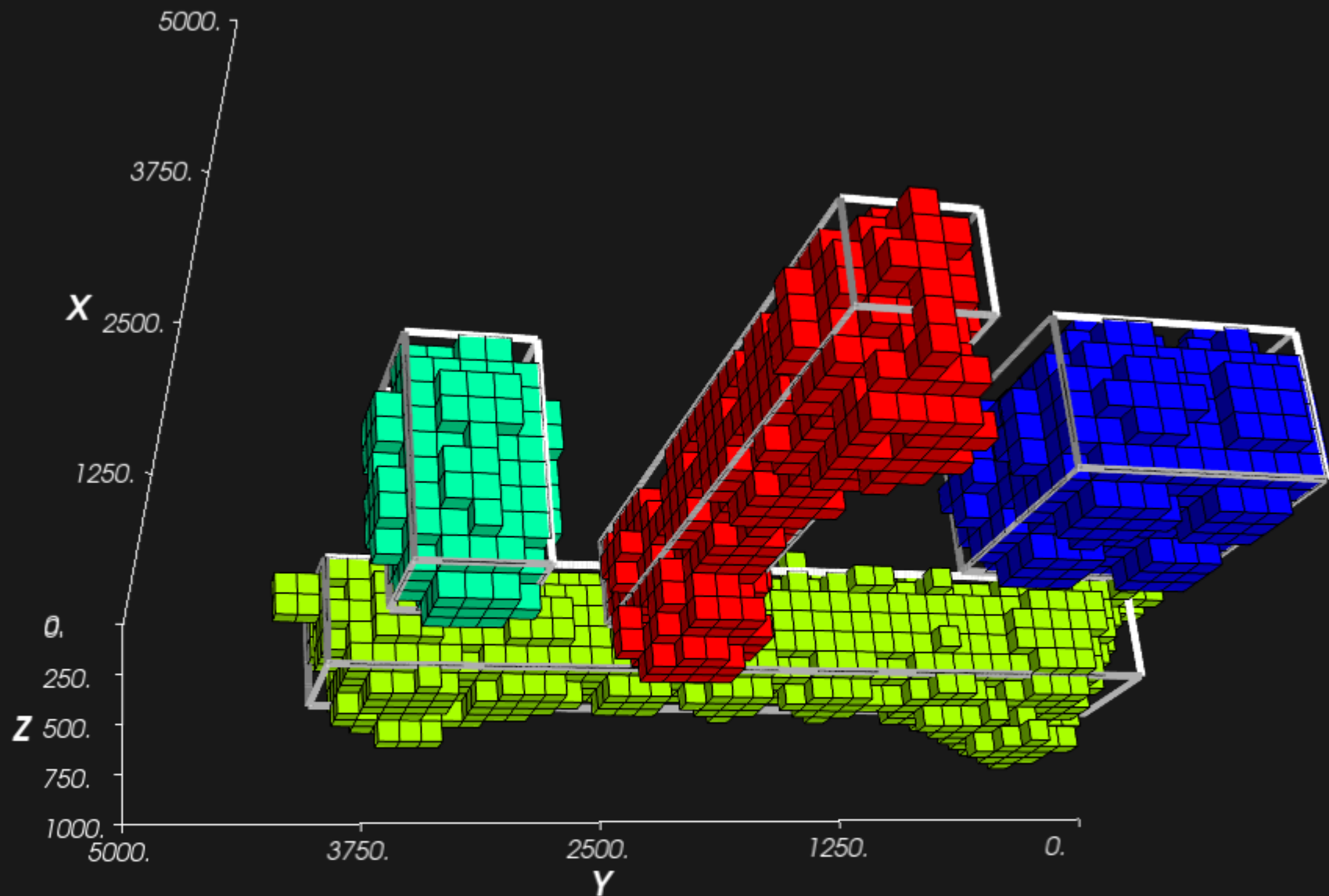
1000. 1071. 1143. 1214. 1286. 1357. 1429. 1500.











Density (kg/m^3)

1000. 1071. 1143. 1214. 1286. 1357. 1429. 1500.

