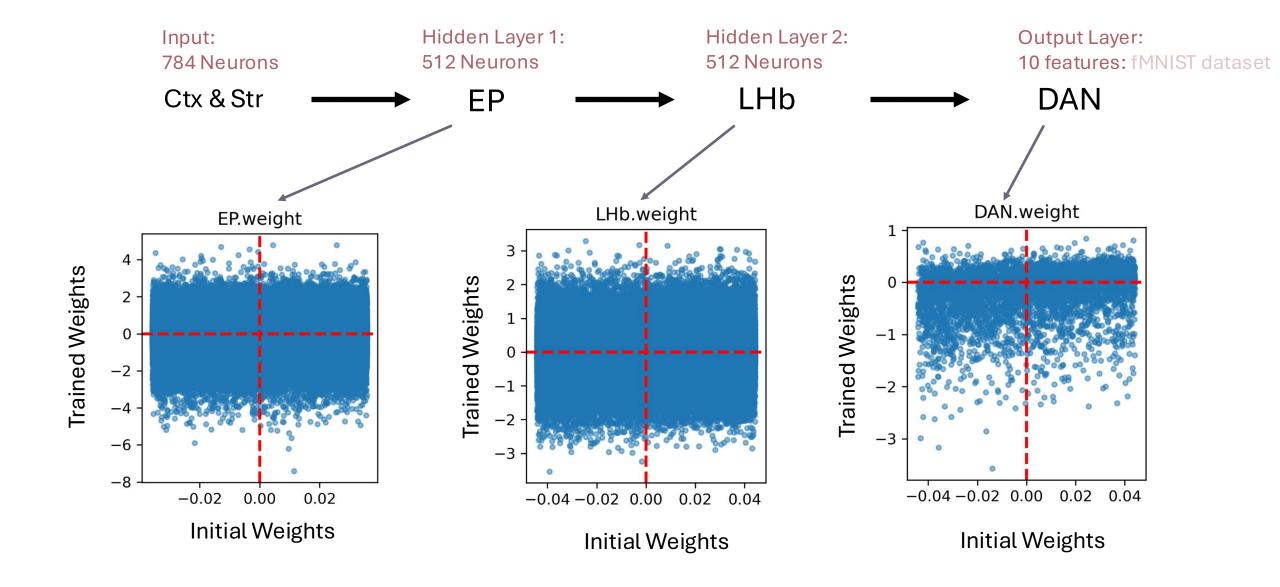
Is there a functional advantage for co-releasing in learning?

Elliot Jerng Sabatini Lab Meeting

Standard MLP: Control



Standard MLP Code

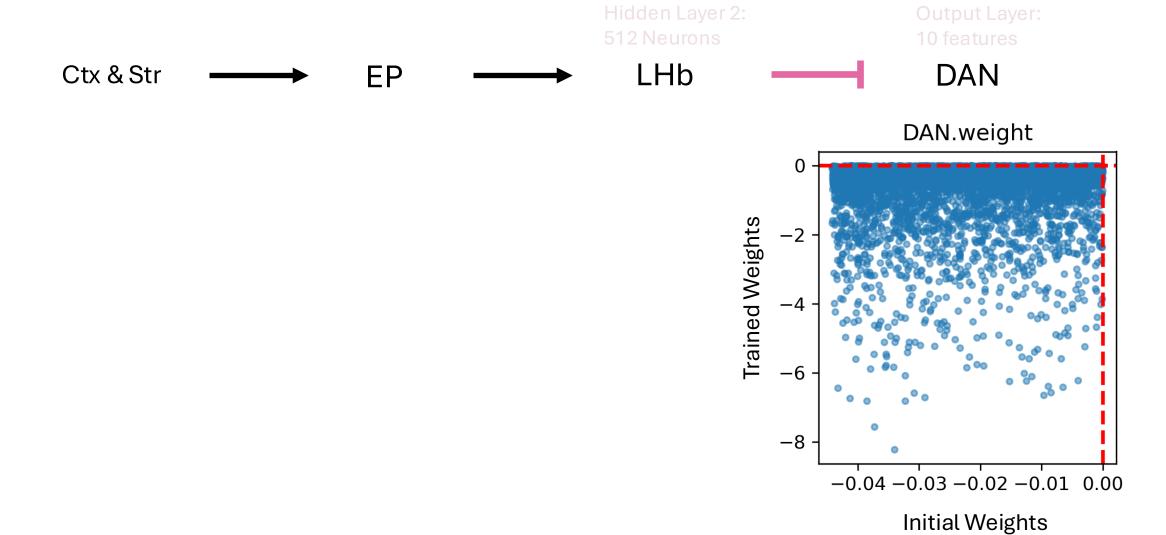
Constructor init function

```
def __init__(self, in_features=784, h1=512, h2=512, out_features=10, dropout_rate=0.5, real = False, combine_EI = False, dales_law = False):
    super().__init__()
    self.real = real
    self.dales_law = dales_law
    # create layers
    self.EP = nn.Linear(in_features, h1)
    self.bn1 = nn.BatchNorm1d(h1)
    self.LHb = nn.Linear(h1, h2)
    self.bn2 = nn.BatchNorm1d(h2)
    self.DAN = nn.Linear(h2, out_features)
```

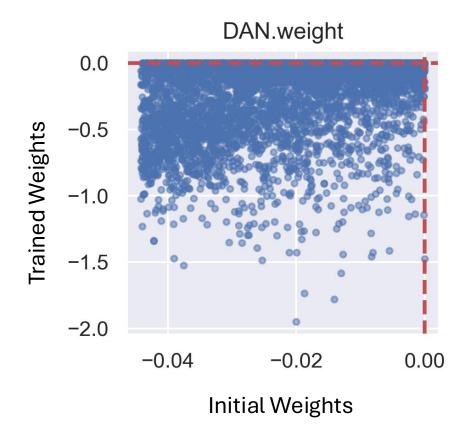
```
def forward(self, x):
    x = x.view(x.size(0), -1)
    x = F.relu(self.bn1(self.EP(x)))
    x = F.relu(self.bn2(self.LHb(x)))

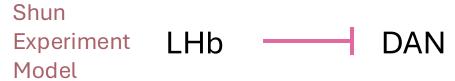
# pure negative -> DAN
    if self.real == True:
        x = -torch.abs(x)
    x = self.DAN(x)
```

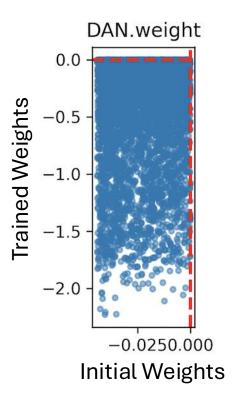
True LHb — DAN



True LHb — DAN









Shun Experiment Model Code: True LHb-DAN

Constructor init function

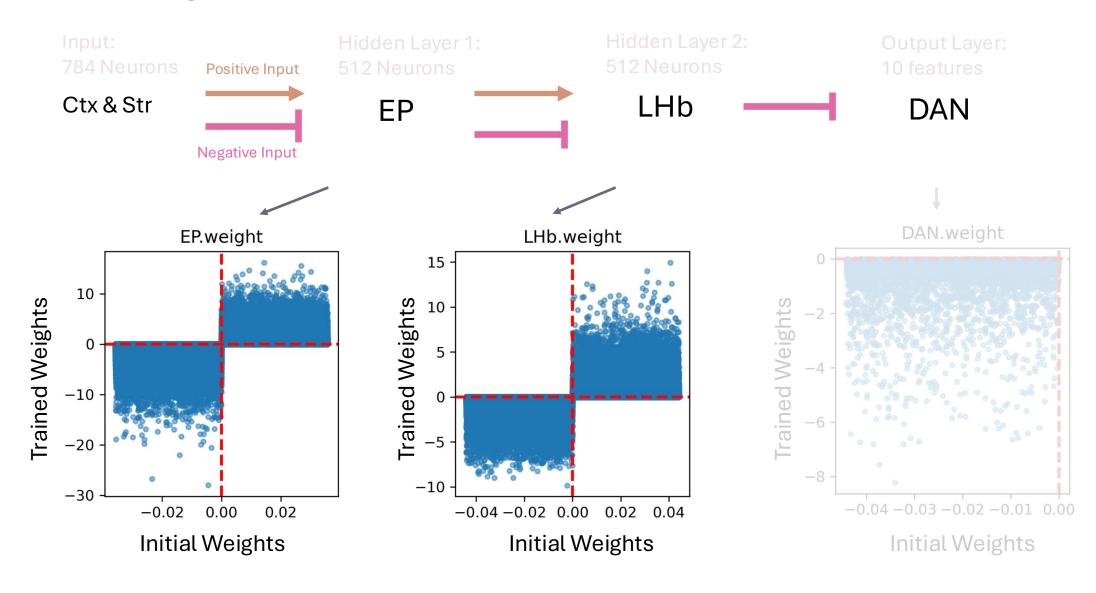
```
def __init__(self, in_features=784, h1=512, h2=512, out_features=10, dropout_rate=0.5, real = False, combine_EI = False, dales_law = False):
    super().__init__()
    self.real = real
    self.dales_law = dales_law
    # create layers
    self.EP = nn.Linear(in_features, h1)
    self.bn1 = nn.BatchNorm1d(h1)
    self.LHb = nn.Linear(n1, h2)
    self.bn2 = nn.BatchNorm1d(h2)
    self.bnA = nn.Linear(h2, out_features)

# initialize DAN as purely inhibitory
    if self.real == True:
        self.apply(self.absolute_val)
```

```
def forward(self, x):
    x = x.view(x.size(0), -1)
    x = F.relu(self.bn1(self.EP(x)))
    x = F.relu(self.bn2(self.LHb(x)))

# pure negative -> DAN
    if self.real == True:
        x = -torch.abs(x)
    x = self.DAN(x)
```

Fixed-Sign Excitatory and Inhibitory: Combined Stream



```
def __init__(self, in_features=784, h1=512, h2=512, out_features=10, dropout_rate=0.5, real = False, combine_EI = False, dales_law = False):
    super().__init__()
    self.real = real
    self.dales_law = dales_law
    # create layers
    self.EP = nn.Linear(in_features, h1)
    self.bn1 = nn.BatchNorm1d(h1)
    self.LHb = nn.Linear(h1, h2)
    self.bn2 = nn.BatchNorm1d(h2)
    self.DAN = nn.Linear(h2, out_features)
   # initialize DAN as purely inhibitory
    if self.real == True:
        self.apply(self.absolute_val)
   # combined EI/ dale's law
    EP_LHb_DAN_pos_neurons, EP_LHb_DAN_neg_neurons = {}, {}
    DAN_pos_neurons, DAN_neg_neurons = {}, {}
   # neurons will only project pure excitatory/inhibitory
    with torch.no_grad():
        for name, param in self.named_parameters():
            if combine_EI == True:
                print(combine_EI)
                if "weight" in name:
                    # categorize neurons as excitatory/inhibitory
                    EP_LHb_DAN_pos_neurons[name] = torch.sum(param.data, axis = 0) >= 0
                    EP_LHb_DAN_neg_neurons[name] = torch.sum(param.data, axis = 0) < 0</pre>
                    # make neuron all excitatory/inhibitory
                    param.data[:, EP_LHb_DAN_pos_neurons[name]] = torch.sign(param[:, EP_LHb_DAN_pos_neurons[name]]) * param[:, EP_LHb_DAN_pos_neurons[name]]
                    param.data[:, EP_LHb_DAN_neq_neurons[name]] = -torch.siqn(param[:, EP_LHb_DAN_neq_neurons[name]]) * param[:, EP_LHb_DAN_neq_neurons[name]]
            elif self.real == True:
                if "DAN.weight" in name:
                    DAN_pos_neurons[name] = torch.sum(param.data, axis = 0) >= 0
                    DAN_neg_neurons[name] = -torch.sum(param.data, axis = 0) < 0
                    # make neuron all excitatory/inhibitory
                    param.data[:, DAN pos_neurons[name]] = torch.sign(param[:, DAN pos_neurons[name]]) * param[:, DAN pos_neurons[name]]
                    param.data[:, DAN_neg_neurons[name]] = -torch.sign(param[:, DAN_neg_neurons[name]]) * param[:, DAN_neg_neurons[name]]
    # keep track of weights
    self.EP_LHb_DAN_pos_neurons = EP_LHb_DAN_pos_neurons
    self.EP_LHb_DAN_neg_neurons = EP_LHb_DAN_neg_neurons
    self.DAN pos neurons = DAN pos neurons
    self.DAN_neg_neurons = DAN_neg_neurons
```

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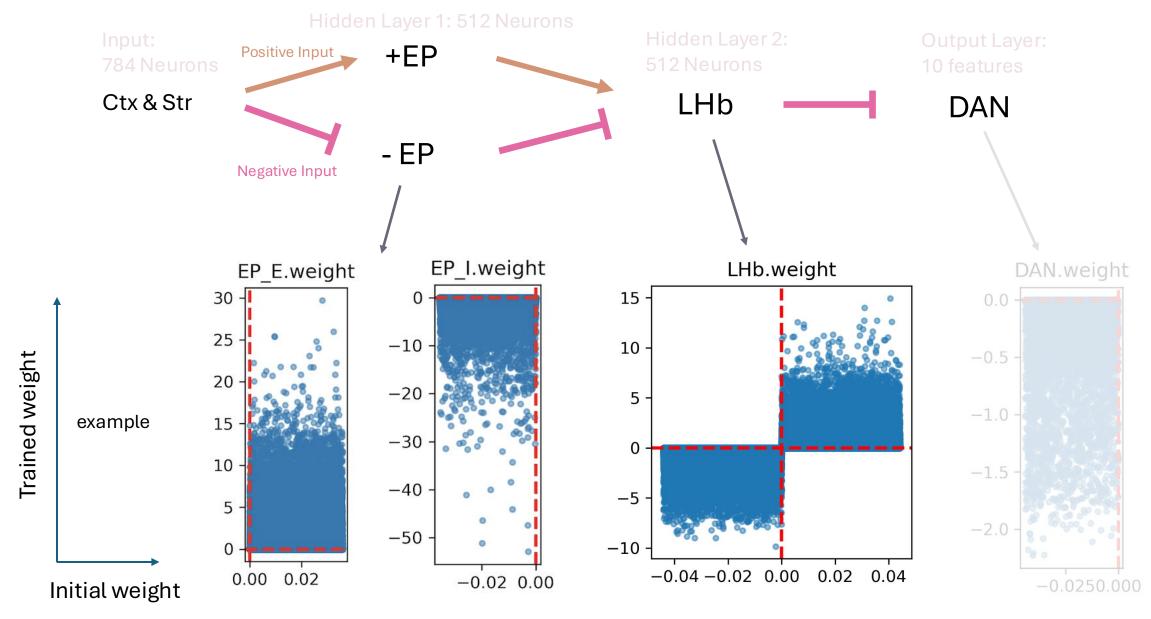
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Fixed-Sign: Combined Stream

Fixed-Sign Excitatory and Inhibitory: Split Stream



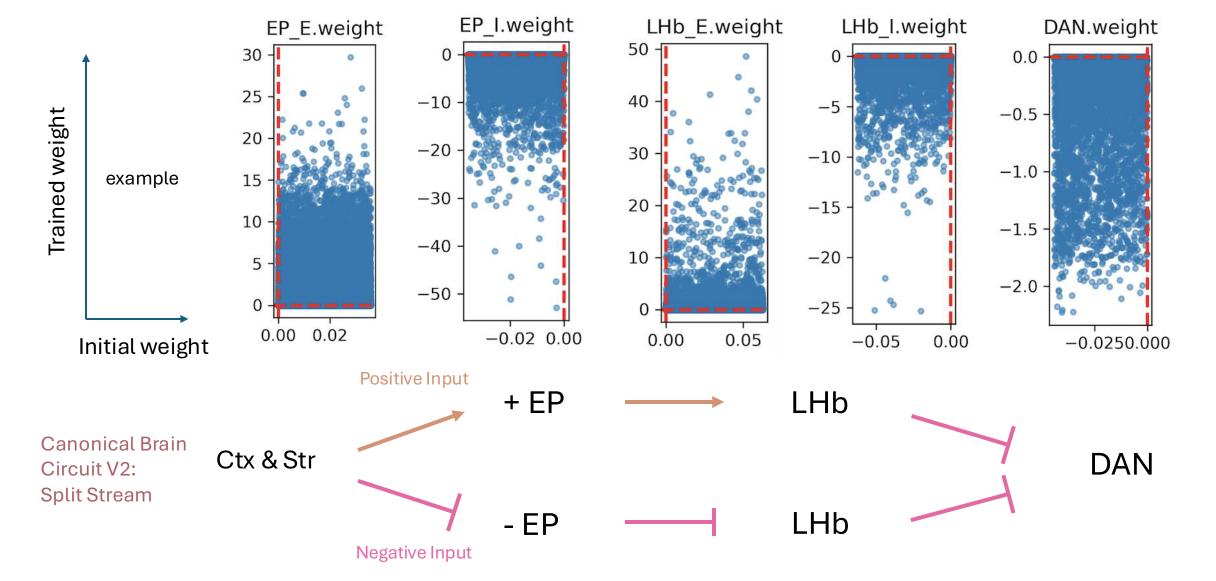
Shun Experiment Model Code: Split Stream EP only

Constructor init function

```
def __init__(self, in_features=784, h1=512, h2=512, out_features=10, dropout_rate=0.5):
    super().__init__()
    # 50% E and I
    num\_excitatory\_h1 = int(0.5 * h1)
    num_inhibitory_h1 = h1 - num_excitatory_h1
    num_excitatory_h2 = int(0.5 * h2)
    num_inhibitory_h2 = h2 - num_excitatory_h2
    # Create lavers
    self.EP E = nn.Linear(in features, h1)
    self.EP I = nn.Linear(in features, h1)
    self.bn1 E = nn.BatchNorm1d(h1)
    self.bn1 I = nn.BatchNorm1d(h1)
    self.LHb = nn.Linear(h1, h2)
    self.bn2 = nn.BatchNorm1d(h2)
    self.DAN = nn.Linear(h2, out features)
    # initialize EP_E, EP_I, DAN as strictly E or I
    self.apply(self.absolute_val)
    # keep track of weights
    self.init weights = self.record params(calc sign=False)
```

```
def forward(self, x):
   x = x.view(x.size(0), -1)
   # EP
   x e = F.relu(self.bn1 E(self.EP E(x)))
   x i = F.relu(self.bn1 I(self.EP I(x)))
   # Converge into LHb
   x = x e + x i
   x = F.relu(self.bn2(self.LHb(x)))
   # Pure Negative LHB to DAN
   x = -torch_abs(x)
   x = self.DAN(x)
    return x
```

Fixed-Sign Excitatory and Inhibitory: Split Stream (EP and LHb)



Shun Experiment Model Code: Split EP and LHb

Constructor init function

```
def init (self, in features=784, h1=512, h2=512, out features=10, dropout rate=0.5):
   super(). init ()
   # 50% E and I
   num excitatory h1 = int(0.5 * h1)
   num inhibitory h1 = h1 - num excitatory h1
   # Create layers
   self.EP_E = nn.Linear(in_features, num_excitatory_h1)
   self.EP I = nn.Linear(in features, num inhibitory h1)
   self.bn1 E = nn.BatchNorm1d(num excitatory h1)
   self.bn1_I = nn.BatchNorm1d(num_inhibitory_h1)
   self.LHb E = nn.Linear(num excitatory h1, h2)
   self.LHb_I = nn.Linear(num_inhibitory_h1, h2)
   self.bn2 E = nn.BatchNorm1d(h2)
   self.bn2_I = nn.BatchNorm1d(h2)
   self.DAN = nn.Linear(h2, out_features)
   # initialize EP_E, EP_I, LHb_E, LHb_I, DAN as E or I
   self.apply(self.absolute_val)
   # keep track of weights
   self.init weights = self.record params(calc sign=False)
```

```
def forward(self, x):
   x = x.view(x.size(0), -1)
   # EP
   x e = F.relu(self.bn1 E(self.EP E(x)))
   x_i = F.relu(self.bn1_I(self.EP_I(x)))
   # LHb
   x_e = F.relu(self.bn2_E(self.LHb_E(x_e)))
   x_i = F.relu(self.bn2_I(self.LHb_I(x_i)))
   # converge to DAN
   x = x e + x i
   # Pure Negative LHB to DAN
   x = -torch_abs(x)
   x = self_DAN(x)
    return x
```

Summary of Networks	Input: 784 Neurons	Hidden Layer 1: 512 Neurons			Hidden Layer 2: 512 Neurons		Output Layer: 10 features
Standard MLP	Ctx & Str	Mixed Input	EP	→	LHb		DAN
EP-LHb — DAN: Shun Experiment Model: Corelease	Ctx & Str		EP		LHb		DAN
Canonical Brain Circuit V1: combined streams	Ctx & Str	Positive Input Negative Input	EP		LHb		DAN
Canonical Brain Circuit V2: split streams (EP and LHb)	Ctx & Str		+ EP		LHb	7	DAN
			- EP		LHb		
Canonical Brain Circuit V3: split streams (EP only)	Ctx & Str		+ EP		LHb		DAN
		—	- EP				

Task for the network: F-MNIST

Part 1: original fMNIST

Part 2:

shuffled fMNIST



Average Test Accuracy

